GENETIC ENTROPY

Dr. J.C. Sanford

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About the Author

Dr. John Sanford has been a Cornell University Professor for more than 30 years. He received his PhD from the University of Wisconsin in the area of plant breeding and plant genetics. While a professor at Cornell, John trained graduate students and conducted genetic research at the New York State Agricultural Experiment Station in Geneva, NY. At Cornell, John bred new crop varieties using conventional breeding and then became heavily involved in the newly-emerging field of plant genetic engineering. John has published over 100 scientific publications and has been granted several dozen patents. His most significant scientific contributions during the first half of his career involved three inventions: the biolistic ("gene gun") process, pathogen-derived resistance, and genetic immunization. A large fraction of the transgenic crops (in terms of numbers and acreage) grown in the world today were genetically engineered using the gene gun technology developed by John and his collaborators. John also started two biotech enterprises derived from his research, Biolistics, Inc., and Sanford Scientific, Inc. John still holds a position at Cornell (Courtesy Associate Professor), but has largely retired from Cornell and has started a small non-profit organization, Feed My Sheep Foundation (FMS).

Through FMS, John has conducted research in the areas of theoretical genetics and bioinformatics for the last 14 years. This book was the "first fruits" of those efforts.

Dedication and Acknowledgements

I feel I could only write this book by God's grace, and acknowledge and thank Him as the Giver of every good thing. This book is dedicated to the memory of Dr. Bob Hanneman, my graduate thesis advisor, who encouraged me in my science and provided an example for me regarding faith and godliness. I would like to thank my wife, Helen, for her unswerving support. I thank the many scientists who went before me, who courageously questioned the "Primary Axiom". Special thanks to my scientific colleagues who have collaborated with me during the last decade, doing research that strongly validates all of the themes of this book. These colleagues include Walter ReMine, John Baumgardner, Wes Brewer, Paul Gibson, Rob Carter, Franzine Smith, Chase Nelson, Chris Rupe, and others. I thank Lloyd Hight and Chris Rupe for this book's artwork.

J.C. Sanford

Genetic Entropy

Foreword

By Dr. John Baumgardner

During the past half century, the scientific enterprise has opened a door into an almost surrealistic, Lilliputian realm of self-replicating robotic manufacturing plants, with components whirring at tens of thousands of RPM, automated parcel addressing, transport and distribution systems, and complex monitoring and feedback control systems. Of course, this is the realm of cell and molecular biology. It is a realm in which tens of thousands of different kinds of sophisticated nanomachines perform incredible chemical feats inside the living cell. Above and beyond this cellular complexity is the equally complex realm of the organism, with trillions of cells working in astonishing coordination, and above that is the realm of the brain, with its multiplied trillions of neural connections. Confronted with such staggering complexity, the reflective person naturally asks, "How did all this come to exist?" The standard answer given to this question is what the author of this book calls "the Primary Axiom" (random mutations filtered by natural selection).

Genetic Entropy represents a probing analysis of the fundamental underpinnings of the Primary Axiom. In particular, it focuses on the genetic software that specifies life's astounding complexity. The author points out that, for higher organisms, and certainly for humans, the extent of these genetic specifications, called the genome, is vast. Not only is the genome huge, it is also exceedingly complex. It is filled with loops and branches, with genes that

regulate other genes that regulate still other genes. In many cases, the same string of genetic letters can code for entirely different messages, depending on context. How such an astonishing information structure has come into existence is clearly an important question. But the author introduces a further question, namely, how can the human genome even be *maintained* against the degrading effects of the billions of new deleterious mutations that enter the human population each generation?

Concerning the Primary Axiom, the author acknowledges that, as a professional geneticist, he discerned no serious problems with its theoretical underpinnings for many years. He confides that during his training in graduate school he accepted this primarily by trust in the authorities, rather than by genuine personal understanding. At that point he felt he had no choice – he thought this abstract and highly mathematical field was beyond his own ability to assess critically. It was not until much later in his professional career that he became aware of how unrealistic and how vulnerable to critical analysis were the crucial assumptions on which the Axiom rests. The author concludes that most professional biologists today are just like he was earlier in his career. Most simply are not aware of the fundamental problems with the Axiom. This is because the Axiom's foundational assumptions are not critiqued in any serious way, either in graduate classes, or in graduate level textbooks, or even in the professional literature.

The conceptual models that population genetics has offered to the rest of the professional biology community, presented in the guise of mathematical elegance, have at their foundations a number of unjustifiable assumptions. The Primary Axiom, it turns out,

depends on these assumptions for its support. Most professional biologists are simply not aware of this state of affairs.

The field of population genetics deals largely with complex mathematical models that attempt to describe how mutations are passed from one generation to the next after they arise, and how they affect the survival of individual members of a population in each generation. The reality of these conceptual models depends critically, of course, upon the realism of the assumptions on which they are built. In this book the author exposes the obvious lack of realism of many of the most crucial assumptions that have been applied for the past 75 years. Most professional biologists, like the author during the earlier part of his professional career, base much of their confidence in the Primary Axiom on claims derived from these conceptual models that have employed observationally unjustifiable assumptions. Most biologists today are unaware that the claims of population genetics to which they were exposed in graduate school can no longer be defended from a scientific standpoint. Most, therefore, can hardly imagine that when realistic assumptions are applied, population genetics actually repudiates the Axiom.

Genetic Entropy is a brilliant exposé on the un-reality of the Primary Axiom. It is written in a challenging but accessible style, understandable by non-specialists with a modest background in either genetics or biology. At the same time, this book has sufficient substance and documentation to cause the most highly trained biologist to seriously rethink what he or she probably has always believed about the Primary Axiom. In my opinion, this book deserves to be read by every professional biologist and

biology teacher in the world. To me it has the potential of changing the outlook of the academic world in a profound way.

John Baumgardner has a PhD in geophysics from UCLA and worked as a research scientist in the Theoretical Division of Los Alamos National Laboratory for 20 years. He also received an MS degree in electrical engineering from Princeton University, where he first became aware of information theory and later its implications for biological systems. He is an expert in complex numerical simulations, and was instrumental in development of the computer program Mendel's Accountant – *currently the most realistic numerical simulation of the mutation/selection process.*

Prologue

In retrospect, I realize I have wasted much of my life arguing about things that don't really matter. It is my sincere hope that this book can actually address something that really does matter. The issues of *who we are*, *where we come from*, and *where we are going* seem to me to be of enormous importance. This is the real subject of this book.

Modern thinking centers around the premise that man is just the product of a pointless natural process (undirected evolution). This widely-taught doctrine, when taken to its logical conclusion, leads us to believe that we are just meaningless bags of molecules, and in the final analysis, nothing matters. If false, this doctrine has been the most insidious and destructive thought system ever devised by man. Yet, if true, it is at best meaningless, like everything else. The whole thought system which prevails within today's intelligentsia is built upon the ideological foundation of undirected and pointless Darwinian evolution.

Modern Darwinism is built upon what I will be calling "The Primary Axiom". The Primary Axiom is that man is merely the product of *random mutations* plus *natural selection*. Within our society's academia, the Primary Axiom is universally taught, and almost universally accepted. It is the constantly-mouthed mantra, repeated endlessly on every college campus. It is difficult to find professors on a typical college campus who would even consider (or dare) to question the Primary Axiom. It is for this reason that the overwhelming majority of youth who start out believing that

there is more to life than mere chemistry – will lose that faith while at college. I believe this is also the cause of the widespread self-destructive and self-denigrating behaviors we see throughout our culture.

What if the Primary Axiom were wrong? If the Primary Axiom could be shown to be wrong, it would profoundly affect our culture and I believe it would profoundly affect millions of individual lives. It could profoundly change the way we think about ourselves.

Late in my career, I did something that would seem unthinkable for a Cornell professor. I began to question the Primary Axiom. I did this with great fear and trepidation. I knew I would be at odds with the most "sacred cow" within modern academia. Among other things, it might even result in my *expulsion* from the academic world. Although I had achieved considerable success and notoriety within my own particular specialty (applied genetics), it would mean stepping out of the security of my own safe niche. I would have to begin exploring some very big things, including aspects of theoretical genetics which I had always simply accepted by faith. I felt compelled to do all this, but I must confess that I fully expected to hit a brick wall. To my own amazement, I gradually realized that the seemingly "great and unassailable fortress" which has been built up around the Primary Axiom was really a house of cards. The Primary Axiom is actually an extremely vulnerable theory. In fact, it is essentially indefensible. Its apparent invincibility derives largely from bluster, smoke, and mirrors. A large part of what keeps the Axiom standing is an almost mystical faith – which the "true-believers" hold – regarding the omnipotence of natural selection. As I went deeper, I began to see that this

unshakable faith in natural selection is typically coupled with a degree of ideological commitment which can only be described as religious. I started to realize (again with trepidation) that I might be offending the religion of a great number of people!

To question the Primary Axiom required me to re-examine virtually everything I thought I knew about genetics. This was the most difficult intellectual endeavor of my life. Deeply entrenched thought patterns only change very slowly (and, I must add, painfully). What I eventually experienced was a complete overthrow of my previous understanding. Several years of personal struggle resulted in a new and very strong conviction that the Primary Axiom was definitely wrong. More importantly, I became convinced that the Axiom could be *shown* to be wrong to any reasonable and open-minded individual. This realization was both exhilarating and frightening. I realized that I had an obligation to openly challenge this most sacred of cows. I also realized I would earn for myself the intense disdain of many of my colleagues within academia, not to mention very intense opposition and anger from other high places.

What should I do? It has become my conviction that the Primary Axiom is insidious on the highest level, having a catastrophic impact on countless human lives. Furthermore, every form of objective analysis I have performed has convinced me that the Axiom is clearly false. So now, regardless of the consequences, I have to say it out loud: ***the Emperor has no clothes***.

I invite the reader to carefully consider this very important issue. Are you really just a meaningless bag of molecules, the product of nothing more than random molecular mutations and reproductive

filtering? As you read this book, I am going to ask you to wrap your mind around something very challenging but also very exciting. I contend that, if you will invest a reasonable mental effort and follow just a handful of fairly simple arguments, I can persuade you that the Primary Axiom is false. Can you imagine anything more radical or more liberating? To the extent that the Primary Axiom can be shown to be false, it should have a major impact on your own life and on the world at large. For this reason, I have dared to write this book, which for some will be blasphemous treason and for others – revelation.

If the Primary Axiom is wrong, there is a surprising and very practical consequence. When subjected only to natural forces, the human genome must degenerate over time. Such a sober realization has more than just intellectual or historical significance. It should rightfully cause us to personally reconsider the basis of our hope for the future.

Update *– Since the initial writing of this book, a series of dramatic new developments have been published, all of which powerfully reinforce the central themes of this book. These developments include the demonstration of the nonlinear nature of the genome, the poly-functional nature of many of the nucleotides which make up higher genomes, the fact that the genome encodes much more information than was even recently thought possible, and the collapse of the fallacy that most of the human genome is just "junk" or "silent" DNA. I have added in italics, very brief "Author's updates" on these various points at the end of most chapters. I have also added Chapter 11 which summarizes the major new scientific developments.*

The Genome is the Book of Life. Where Did it Come From?

Newsflash – The genome is an instruction manual.

An organism's *genome* is the sum total of all its genetic parts, including all its chromosomes, genes, and nucleotides. A genome is an instruction manual that specifies a particular form of life. The human genome is a manual that instructs human cells how to be human cells and instructs the human body how to be the human body. There is no information system designed by man that can even begin to compare to the sophistication and complexity of the genome.

The complex nature of the genome can only be appreciated when we begin to grasp how much information it contains. When you assemble the little red wagon you bought for your child, there is a booklet that tells you how to put it together. The size of the booklet is deceptive. It does not contain all the information needed for fabricating the component parts, or for manufacturing the steel, rubber, and paint. The complete instruction manual would actually be a very large volume. If you compiled all the instruction manuals associated with creating a modern automobile, it would fill a library. That library would be very large if it included the

information needed for making all the components for creating the robotic assembly lines. Likewise, the manuals required for creating a fighter jet and all its components, computers, and assembly lines would comprise an extremely large library. The manuals needed for building the entire space shuttle and all its components and all its support systems would be truly enormous. Yet the *specified complexity* of even the simplest form of life is arguably greater than that of the space shuttle. Try to absorb the fact that the jump in complexity from a bacterium to a human being is arguably greater than the jump from the little red wagon to the space shuttle. There is simply no human technology that serves as an adequate analogy for the complexity of a human being. The genome is the instruction manual encoding all the information needed for that human life!

We are only beginning to understand the first dimension of this book of life: a linear sequence of four types of extremely small molecules, called nucleotides. These small molecules make up the individual steps of the spiral-staircase structure of DNA. These molecules are the letters of the genetic code, and are shown symbolically as A, T, C, and G. These letters are strung together like a linear text. They are not just symbolically shown as letters, they are very literally the *letters* of our instruction manual. Small clusters or motifs of these four molecular letters make up the *words* of our manual, which combine to form genes (the *chapters* of our manual), which combine to form chromosomes (the *volumes* of our manual), which combine to form the whole genome (the entire *library*).

A complete human genome consists of two sets of 3 billion individual letters each. Only a small fraction of this genetic library is required to directly encode the hundreds of thousands

of different types of human proteins and the uncounted number of functional RNA molecules found within our cells. Each of these protein and RNA molecular types are essentially miniature *machines*, each with hundreds of component parts, and with its own exquisite complexity, design, and function. But the genome's *linear* information, which is equivalent to many complete sets of a large encyclopedia, is not enough to explain the complexity of life.

As marvelous as all this linear information is, it must only be the first dimension of complexity within the genome. The genome is not just a simple string of letters spelling out a linear series of instructions. It actually embodies multiple linear codes that overlap and constitute an exceedingly sophisticated information system embodying what is called *data compression* (Chapter 9).

In addition to multiple, overlapping, linear, language-like forms of genetic information, the genome is full of countless loops and branches, like a computer program. It has genes that regulate genes that regulate genes. It has genes that sense changes in the environment and then instruct other genes to react by setting in motion complex cascades of events that can then respond to the environmental cue. Some genes actively rearrange themselves, or modify and methylate other gene sequences, basically *changing* portions of the instruction manual.

Lastly, there is good evidence that linear DNA can fold into two- and three-dimensional structures (as do proteins and RNAs), and that such folding probably encodes still higher levels of information. Within the typical non-dividing nucleus, there is reason to believe there are fabulously complex three-dimensional arrays of DNA, whose 3-D architecture controls higher biological functions.

The bottom line is this: the genome's set of instructions is not a simple, static, linear array of letters – but is dynamic, self-regulating, and multi-dimensional. There is no human information system that can even begin to compare to it. The genome's highest levels of complexity and interaction are probably beyond the reach of our understanding, yet we can at least acknowledge that these higher levels of information exist. While the linear information within the human genome is extremely impressive, the non-linear information must obviously be much greater. Given the unsurpassed complexity of life, this has to be true.

All this information is contained within a genomic package that is contained within a cell's nucleus – a space much smaller than a speck of dust. Each human body contains a galaxy of cells – more than 100 trillion – and every one of these cells has a complete set of instructions, directing the cell's own highly-prescribed duties. The human genome not only specifies the complexity of our cells and our bodies, but also the functioning of our brains. The structure and organization of our brains involves a level of organization entirely beyond our comprehension.

As we recognize the higher-order dimensions of the genome, I believe we can readily agree with Carl Sagan's oft-repeated statement that each cell contains more information than the Library of Congress. Indeed, human life is more complex than all human technologies combined. **Where did all this information come from, and how can it possibly be maintained? This is the mystery of the genome.**

The standard answer to the origin of biological information is that *mutation* and *selection* have created all biological information. This is the fundamental basis of the *Neo-Darwinian Theory*. It says that all genomes (instruction manuals) must have derived from a simple initial genome via a long series of mutations (typographical errors) and lots of natural selection (differential copying). This is the *Primary Axiom* of biological evolution: **Life is life because random mutations at the molecular level are filtered through a reproductive sieve acting on the level of the whole organism.**

What is an axiom? An axiom is a concept that is not testable but is accepted by faith because it seems obviously true to all reasonable parties. On this basis, it is accepted as an Absolute Truth. In this book, I am going to urge the reader to ask the question, "Should we accept today's Primary Axiom?" If the Primary Axiom could be shown to be wrong, it would mean that we would need to re-examine many other popular ideas, because the Primary Axiom has been so foundational to the establishment of modern thinking. This would justify a *paradigm shift* of the highest magnitude (a paradigm shift is a change in a fundamental idea that previously governed a group's collective thinking), and would allow us to completely reevaluate many of the deeply entrenched concepts which frame modern thinking.

It is important that we put the Primary Axiom into a framework that is honest and also realistic to our mind's eye. I would like to propose an honest analogy which very accurately characterizes today's Primary Axiom. My analogy involves the evolution of transportation technologies, as outlined below.

In our little red wagon analogy, the first primeval genome encoded the assembly instructions for the first wagon. That simple genomic instruction manual was copied by an invisible mechanical scribe, to make more instruction manuals. Each newly copied manual was used to make a new red wagon. However, the scribe, being imperfect, made errors. So each wagon came out differently. Each wagon had its own unique instruction manual taped to its bottom. When the first wagons were junked, their instruction manuals were lost with them. New copies of instruction manuals could only be imperfectly copied from the manuals of the immediately preceding generation of wagons, just before they were to be discarded. Since the copying of instructions was sequential (rather than using an original master copy), errors accumulated over time in every manual, and the resulting wagons started to change and vary. The accumulating errors are, of course, our analogy for mutations.

Are you uneasy with this picture? No doubt you realize we are looking at a deteriorating situation. Information is being lost, instructions are becoming degraded, and the wagons will doubtlessly deteriorate in quality. Eventually, the system will break down, the manual will become complete gibberish, and workable wagons will become extinct. We will examine this problematic aspect of mutation in more detail in Chapters 2 and 3.

At this point, we introduce our hero, natural selection. Natural selection is like a judge, or quality control agent, deciding which wagons are suitable models for further copying. Natural selection, as the judge, instructs the scribe not to copy manuals from inferior wagons. This represents differential reproduction (reproductive sieving), better known as *selection*. But it is important to understand

there is never direct selection for good instructions, only for good wagons. As we will see, this is very important. Mutations are complex and happen at the molecular level, but selection can only be carried out on the level of the whole organism. The scribe and judge work entirely independently. Working on the level of molecules, the scribe is essentially blind; being extremely near-sighted, he can only see individual letters while he is copying. The judge is also nearly blind, but he is extremely far-sighted. He never sees the letters of the manual, or even the wagon's individual components; he can only see the relative performance of the whole wagon.

The scribe can be envisioned at the beginning of a robotic assembly line. He copies programs for the robots by blindly and imperfectly duplicating older programs, one binary bit at a time. The quality control agent looks at the performance of the finished wagons, and decides which wagons are better than others. The programs from the wagons he has chosen are then given to the scribe for the next round of copying and assembly.

In this way, many defective wagons can be eliminated, and so most errors in the instructions might presumably be eliminated. More exciting, some rare spelling errors might result in *better* wagons, and so the judge can instruct the scribe to preferentially copy these instructions. The process of evolution has begun!

Let us now examine the feasibility of the selection process as a mechanism for improving genomic information. The information within the instruction manual might not only be *improved* by this process, but it can also be *expanded*. If the imperfect scribe

occasionally copies an extra (duplicate) page out of the manual, we might start adding information. Naturally, a duplicate page in an instruction manual is not really new information. In fact, it will invariably confuse and disrupt the reading of the manual. But again, the judge only allows copying of manuals from *good wagons*. So, bad duplications might presumably be eliminated and harmless duplications might be preserved. Now these harmless duplications will also begin to have copying errors within them, and some of these errors *might* create new and useful information, like instructions for new functional components in the wagon. With a little imagination, perhaps we can picture a variety of duplications eventually evolving, via misspellings, and specifying something entirely new, like an internal combustion engine, or wings, or an on-board computer navigational system. Hence we have a scenario whereby a little red wagon can, through a series of typographical errors, evolve into an automobile, a plane, or even the Space Shuttle.

But this analogy does not go far enough, because a human being is much more complex than a space shuttle. In fact, our *phenome* (the entire body including the brain), is immeasurably more complex than any known technology. Perhaps we can come closer to the mark if we imagine our little red wagon being transformed into the fanciful *Starship Phenome*, complete with warp-speed engines and a holodeck (Figures 1a-d, pp. 12-14). The Primary Axiom says that misspellings and some differential copying can simultaneously explain the library (the genome) and the starship (the phenome) illustrated in Figure 1d.

We must now ask, "Could misspellings and selective copying really do this?" A correct understanding of *selection* is essential

for evaluating the merit of the Primary Axiom. No intelligence is involved in this scenario. The scribe is really just a complex array of senseless molecular machines that blindly replicate DNA. The judge is just the tendency for some individuals to reproduce more than others. Many people unconsciously attribute to natural selection a type of supernatural intelligence. But natural selection is just a term for a blind and purposeless process whereby some things reproduce more than others. It is crucial we understand that our scribe and our judge have neither foresight nor intelligence. Their combined IQ equals *zero*.

Isn't it remarkable that the Primary Axiom of biological evolution essentially claims that typographical errors and limited selective copying within an instruction manual can transform a wagon into a spaceship in the absence of any intelligence, purpose, or design? Do you find this concept credible? It becomes even more startling when we realize that the spaceship was in no way pre-specified under the Primary Axiom, not even in the mind of God. It truly "just happened" by accident. The spaceship is essentially just a *mutant wagon*. Yet this illustration is actually the best analogy for describing the Primary Axiom. The only weakness of this analogy is that there is no human technology that can compare to the actual complexity of life, and thus there is no human information system that can compare to the human genome.

This whole analogy stands in sharp contrast to the false picture portrayed by Dawkins (1986). The famous Dawkins argument, built around the phrase "methinks it is like a weasel", involved a *pre-specified language* and a *pre-specified message* being systematically uncovered through a simple-minded process

equivalent to children's games such as "20 Questions" or "Hangman". In Dawkins' model, both the phrase and the carefully crafted and finely tuned method of uncovering it were intelligently designed and purposeful. Furthermore, his selection scheme allowed for direct selection of genotype (misspellings) rather than phenotype (wagon performance). Briefly, Dawkins set up a simple computer program which started with a simple random array of letters, having exactly the same number of characters as the phrase "methinks it is like a weasel". He designed his program to then begin to randomly mutate (change) the letters. When a new letter fell into place which matched the phrase "methinks it is like a weasel" the program would select the "improved" message. Obviously it would not take long for such a little program to create the desired phrase. However, even to make this simple program work, Dawkins had to carefully design the replication rate, the mutation rate, and other parameters to get the results he wanted. He also needed to impose perfect selection for each and every individual letter, each and every generation. This program supposedly proved that evolution via mutation/selection is inevitable (not requiring any intelligent design). Obviously, Dawkins used an intelligently designed computer, and then he used his own intelligence to design the program, to optimize it, and even to design the pre-selected phrase. For many reasons (see Chapter 9), Dawkins' argument cannot honestly be used to defend the Primary Axiom (which does not allow for the operation of any intelligence, purpose, or forethought, and does not allow for direct selection for any misspellings themselves).

In this book we are going to examine some basic aspects of genetics and determine if the known facts about the human genome are

compatible with the Primary Axiom. As you read, if you come to the point where you feel that the Primary Axiom is no longer obviously true to all reasonable parties, then you should feel rationally obligated to reject it as an *axiom*. If the Primary Axiom cannot stand up as an axiom, it should be treated as an unproven hypothesis, subject to falsification.

2014 Update *– A milestone book was published in 2013 entitled "Biological Information – New Perspectives" (see* ***BINP.org****). This book was the compilation of research papers from a symposium held at Cornell University (Marks et al., 2013). These papers were authored by 29 well-credentialed scientists representing a very wide range of scientific disciplines. The 29 authors were in broad agreement regarding the true nature of biological information.* ***The nature of biological information systems is much more like an elaborate computer system than a book.*** *The DNA is like the cell's hard drive. The millions of RNA and protein molecules, and all their interactions, are like the active memory or RAM of the cell. Every individual gene functions as an executable computer program (indeed - there are multiple programs per gene). Each one of the protein and RNA molecules within a cell is itself a simple program (algorithm). The DNA, RNA, protein and countless other molecules are in constant communication with each other – constituting something like a vast internet system within every cell. Using data visualization techniques it has now been shown that higher genomes are remarkably similar in structure to executable computer programs (Seaman, 2013).*

For updated information on the topic of Genetic Entropy visit the website ***GeneticEntropy.org.***

Figure 1a. Some assembly required…

A little red wagon is not information, but it requires information to specify its assembly. A typical assembly booklet is not really all the information required to specify the production of a wagon. The truly complete production manual would be a very substantial book, specifying the production of all the components (wheels, etc.), and all raw materials (steel, paint, rubber).

Figure 1b. A library of information.

The complete instructions needed to specify a modern automobile would comprise a substantial library. If the assembly was to be done entirely by machines (no "intelligence" required), the information, including that required for making and programming the robots, would be massive, comprising a phenomenal collection of books.

Figure 1c. Many layers of information.

The complete instruction manual needed to specify a fighter jet, including its on-board computer systems and all the manufacturing and support systems inherent in creating and maintaining such a system, would be a massive library. Imagine the instructions if every component had to be made robotically!

Figure 1d. A galaxy of information...

The library shown above represents the human genome (all our genetic information). The spaceship represents the human phenome (our entire body, including our brain). We cannot really imagine how extensive the library would have to be were it to specify the fictional S.S. Phenome, complete with warp-speed engines and a holodeck. Wouldn't it have to be much larger than the Library of Congress? Yet it can be reasonably argued that a human is still more complex than a hypothetical S.S. Phenome. What type of starship could reproduce itself?

Figure 2. The nature of genetic information...

The genome appears to us as a linear array of letters: A, T, C, G. The actual genome is 3 million fold greater than the sequence shown above. To view just half of your own genome, you would have to view 10 nucleotides every second, for 40 hours per week, for 40 years! The apparent simplicity of this language system is deceptive. A higher genome, almost certainly, must comprise a great deal of data compression (see Chapter 9), as well as a great deal of non-linear information. Except for certain short portions, we cannot view the genome as simply a linear text, like a book. Much of the information content is probably found in 3-dimensional structures, as is the case with folded proteins.

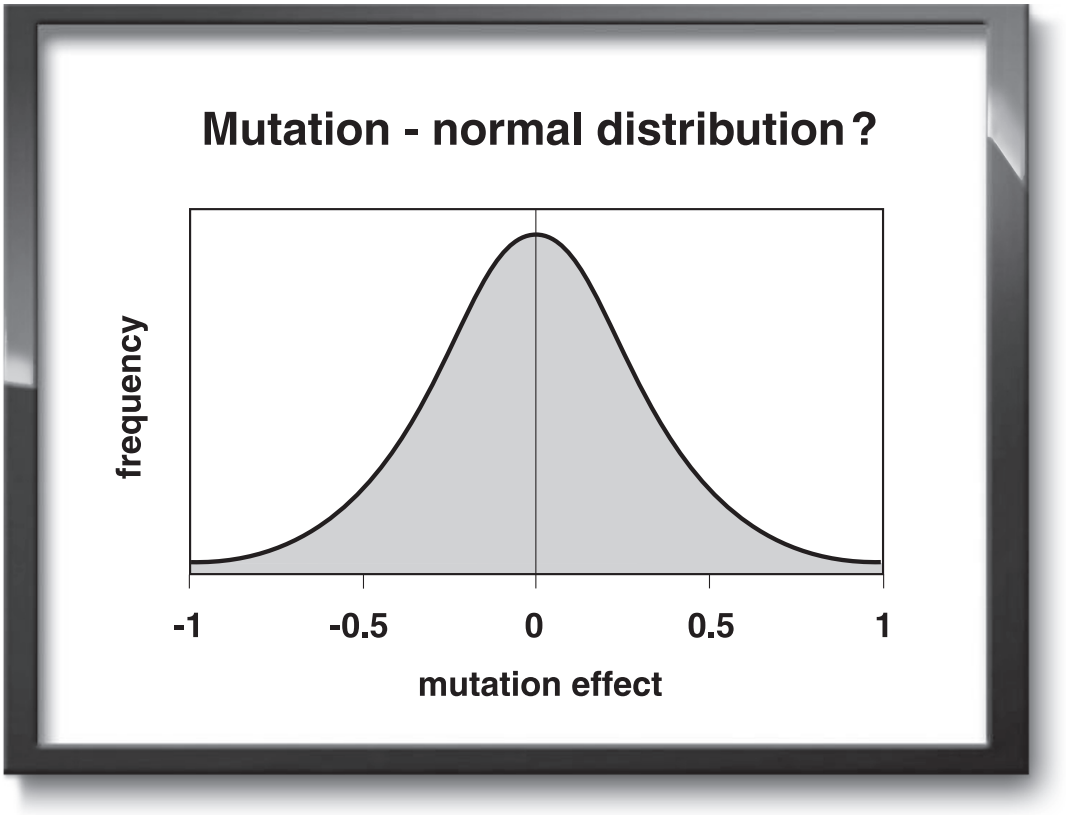

Figure 3a. Distribution of mutational effects on fitness – the naive view.

The naive view of mutations would be a bell-shaped distribution, with half of all mutations showing deleterious affects on fitness (left of center), and half showing positive effects on fitness (right of center). With such a distribution it would be easy to imagine selection removing some bad mutations and amplifying some good mutations, inevitably resulting in evolutionary progress. However, we know this is a false picture.

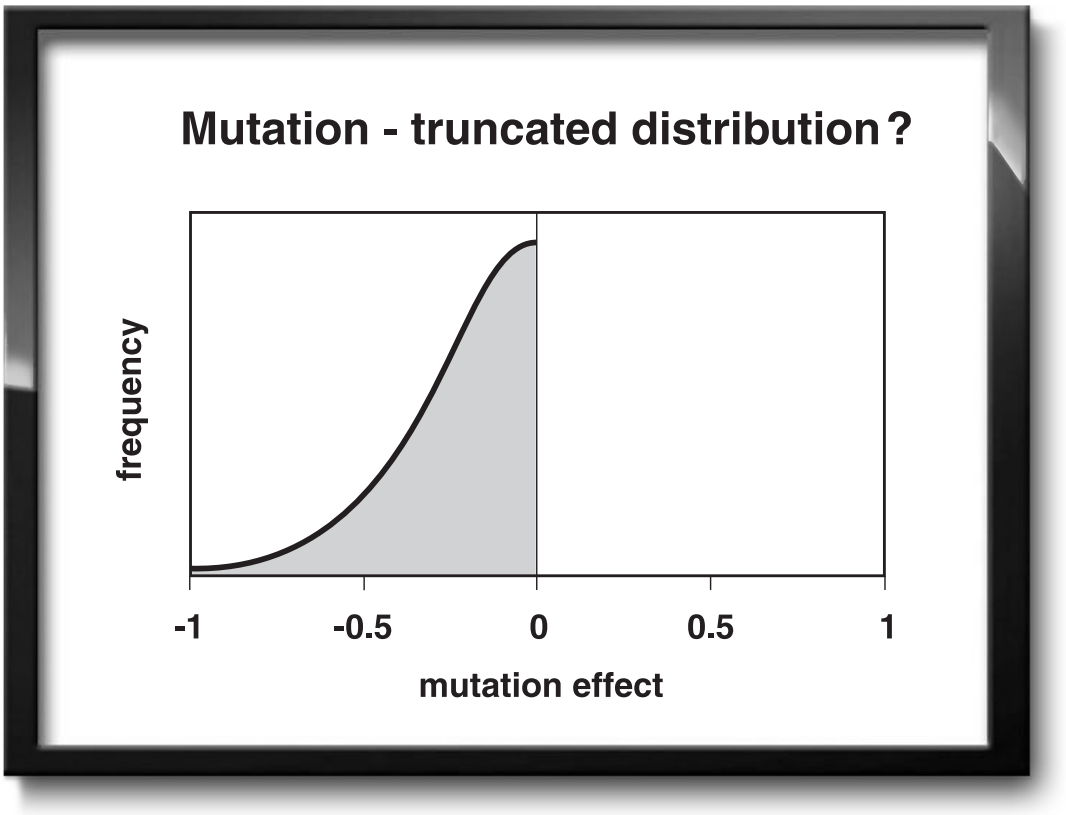

Figure 3b. Mutational effects on fitness – almost never beneficial.

Population geneticists know that nearly all non-neutral mutations are deleterious, and that mutations having positive effects on fitness are so rare as to be typically excluded from such distribution diagrams. This creates major problems for evolutionary theory. But this picture is still too optimistic.

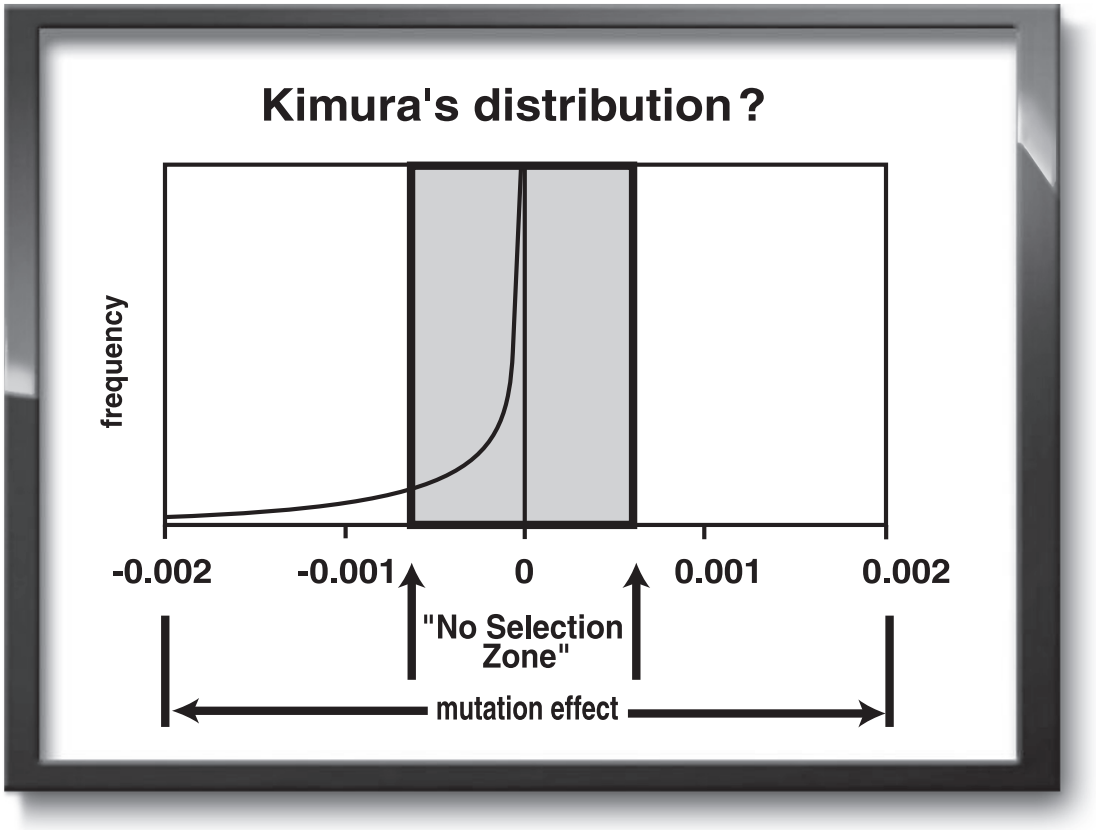

Figure 3c. Mutational effects – harmful effects usually very slight – invisible to natural selection.

Population geneticists know that mutations are strongly skewed toward neutral. Just like in an instruction manual, a few misspellings will be lethal but most will be *nearly harmless*. The nearly-neutral mutations create the biggest problems for evolutionary theory. This diagram is adapted from a figure by Kimura (1979). Note that the lower scale has changed – instead of ranging from -1 to +1, the scale ranges from -0.002 to +0.002. Kimura and his colleague, Ohta, are famous for showing that most mutations are nearly-neutral, and therefore are not subject to selection. Kimura's "no-selection zone" is shown by the grey box.

The general shape of this curve is important, but the precise mathematical nature of this curve is not. While Ohta feels the mutation distribution is exponential, Kimura feels it is a 'gamma' distribution (Kimura, 1979). However, regardless of which specific mathematical formulation best describes the natural distribution of mutation effects, they all approximate the picture shown above.

Geneticists agree that the frequency of highly deleterious mutations is almost zero (off the chart), while "minor" mutations are intermediate in frequency. Minor mutations are believed to outnumber major mutations by about 10-50 fold (Crow, 1997), but near-neutrals vastly outnumber them both.

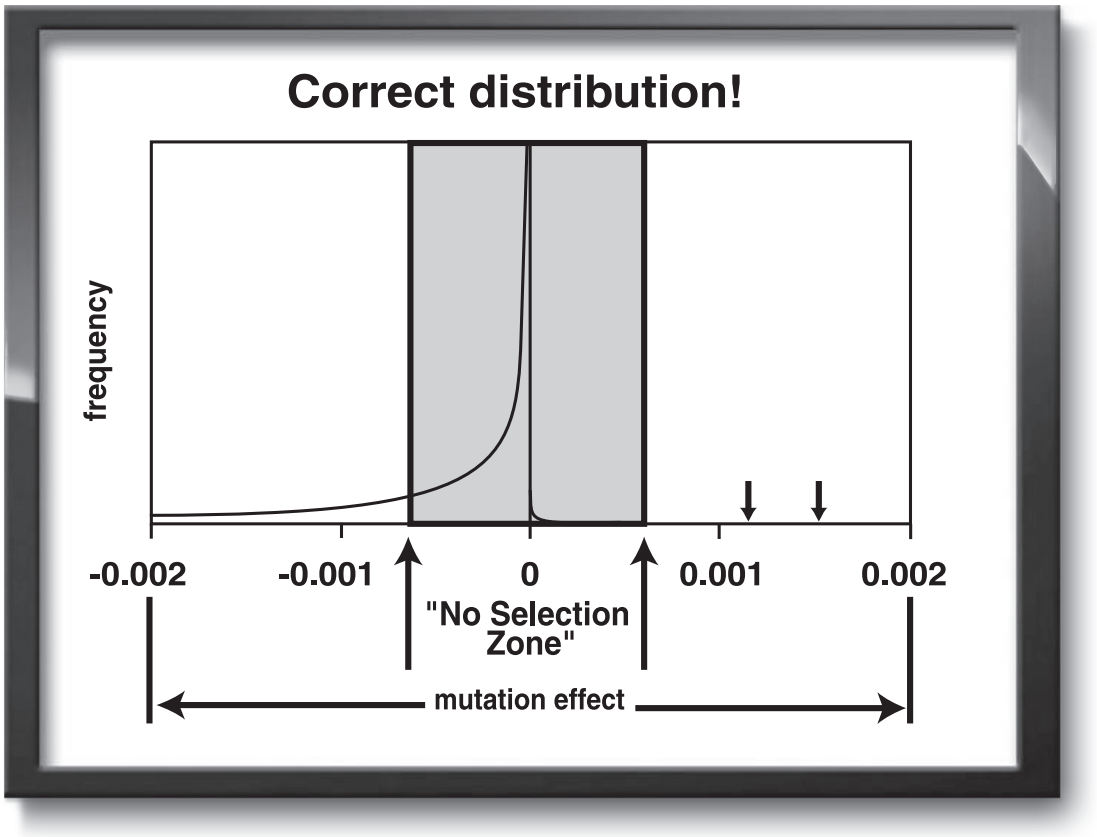

Figure 3d. Mutation effects – rare beneficial mutations do happen, but are generally un-selectable.

Kimura's Figure (3c) is still not complete. To complete the figure we really must show where the beneficial mutations would occur, as they are critical to evolutionary theory. Their distribution would be a reverse image of Kimura's curve, but reduced in range and scale, by a factor of somewhere between one thousand to one million. Because of the scale of this diagram, I cannot draw this part of the mutation distribution small enough, so a relatively large curve is shown instead. Even with beneficial mutations greatly exaggerated, it becomes obvious that essentially all beneficial mutations will fall within Kimura's "no-selection zone". This completed picture, which is correct, makes progressive evolution on the genomic level virtually impossible. Adaptation to a special circumstance can still happen, due to extremely rare high-impact beneficials – which are isolated anomalies (shown by arrows to the right of the "no-selection zone"). These rare beneficial mutations almost always involve loss of function and are therefore unproductive in terms of "forward evolution".

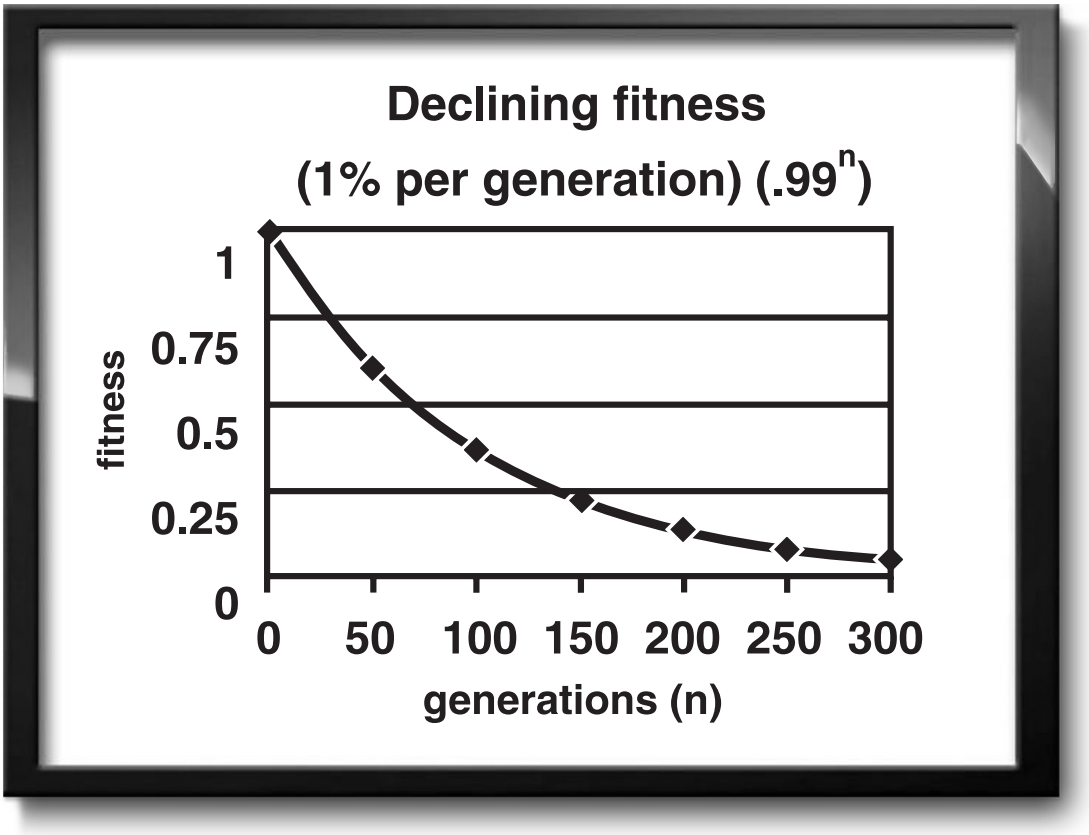

Figure 4. The consequence of genetic entropy.

Dr. Crow (1997) indicated that the fitness of the human race is presently degenerating at 1-2% per generation due to the accumulation of mutations. A 1% decline in fitness per generation (beginning with a fitness of 1) is plotted for a hypothetical human population over a period of 300 generations (6,000-9,000 years). The resulting pattern seen is a classic biological decay curve. This type of progressive loss of fitness would clearly lead to dramatic degeneration of the human race within the historical timeframe.

Figure 11. Degeneration of the genome, degeneration of man, and degeneration of mankind.

We experience it on a personal level, and we see it all around us. It is "genetic entropy", and there is nothing man can do to halt it. It is biologically inevitable. It is part of why species go extinct, and it is why we are all individually in the process of dying.

What Hope?

Newsflash – There is a hope.

As you have so diligently stayed with me all the way through this book, and have now reached its end, perhaps you will not be offended if I diverge from what has been a scientific discussion and touch upon the philosophical. I would like to humbly put before you my own personal conclusion regarding where our hope lies.

When I was young, I accepted the fact that I was going to die, and that all of the people I loved were going to die. I accepted it, but it robbed me of joy, to say the least. I was taught that there was still one hope: that the world was getting better. Science was advancing. Culture was advancing. Even mankind was getting better. Through our efforts, we could make the world a better place. Through evolution, we could evolve into something better. Through *progress,* we might eventually defeat death itself. Perhaps we might someday even reverse the degeneration of the universe! My personal hope was that I might in some small way contribute to such progress. I believe that this basic hope was shared, to a

large extent, by my entire generation[1].

I now believe this was a false hope. I still believe we should diligently apply ourselves to making this a "better world", and to be responsible stewards of the world we have been given. But I see our efforts as a holding action at best. While science can reasonably hope to prolong life, it cannot defeat death. Degeneration is certain. Our bodies, our species, and our world are all dying. It is simply not in our power to stop this very fundamental process. Isn't this obvious when we look around us? So where is the hope? If the human genome is irreversibly degenerating, we must look beyond evolution in order to have a hope for the future.

One of my reviewers told me that the message of this book is both terrifying and depressing. He suggested that perhaps I am a little like a sadistic steward on board the Titanic, gleefully spreading the news that the ship is sinking. But that is not correct. I hate the consequences of entropy (degeneration). I hate to see it in my own body, in the failing health of loved ones, or in the deformity of a new-born baby. I find it all absolutely ghastly, but also absolutely undeniable. Surely a real steward on the Titanic would have a responsibility to let people know that the ship was sinking, even if some people might hate him for it. I feel I am in that position. Responsible people should be grateful to know the *bad news*, so they can constructively respond to it. If we have been putting all our hope in a sinking ship, would it not be expedient to recognize this and abandon the false hope? It is only in this light that we

[1]*Kimura, 1976: "Shall we be content to preserve ourselves as a superb example of living fossils on this tiny speck of the universe? Or, shall we try with all our might, to improve ourselves to become supermen, and to still higher forms, to expand into the wider part of the universe, and to show that life after all is not a meaningless episode?"*

can appreciate bad news. Only in the light of the *bad news* can we really appreciate the *good news* – that there is a lifeboat.

Even as we cannot create life, we cannot defeat death. Yet I assert there is One who *did* create life and who designed the genome. I do not know how He did it, but somehow He surely made the hardware, and He surely must have written the original software. He is called the Author of Life (Acts 3:15 – NIV). I believe the Author of Life has the power to defeat death and degeneration. I believe this is the ***Good News***.

It is my personal belief that Jesus is our hope. I believe that apart from Him there is no hope. He gave us life in the first place, so He can give us new life today. He made heaven and earth in the first place, so He can make a *new* heaven and earth in the future. Because He rose from the dead, we can be raised from death, even the death which is already enveloping us. In these profound yet simple truths, I believe there is a true hope. I believe this hope is unshakable, because I believe it is founded on the One who is eternal. It is a hope that has withstood the attacks of time and the corruption of religion. It is a hope freely available to anyone who would receive it today. I humbly put before you this alternative paradigm for your consideration – Jesus is our one true hope.