The Truth About Evolution

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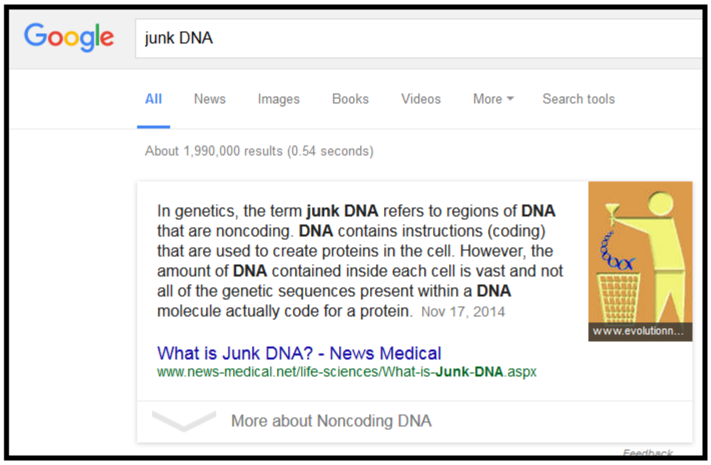
Abstract

The purpose of this report is to debunk Darwin's theory of evolution and any variant theory that relies on the natural rate of mutation to explain the origin of new genes. We construct a model of DNA and show that the minimum rate of mutation needed to produce humans within the geological age of the Earth is too high. It is much higher than any realistic model of random mutations. The calculation presented here should end the evolution debate, at least in its Darwinian limit. Other problems with evolution are discussed.



In genetics, the term **junk DNA** refers to regions of **DNA** that are noncoding. **DNA** contains instructions (coding) that are used to create proteins in the cell. However, the amount of **DNA** contained inside each cell is vast and not all of the genetic sequences present within a **DNA** molecule actually code for a protein. Nov 17, 2014

What is Junk DNA? - News Medical
www.news-medical.net/life-sciences/What-is-**Junk**-**DNA**.aspx

FIG. 1. A common definition of what constitutes junk DNA. Note the garbage can illustration.

Junk DNA is a term floated in pseudo-intellectual circles as if scientists have identified a scab on the end of the DNA molecule that can be safely scraped off to engineer humans free from the junk DNA plague. At what may or may not be the dawn of the age of genetic engineering, the danger posed by such ludicrous thinking cannot be understated. Consider figure 1. Scientists do not yet understand the genome and there is no reason to think what they have defined as *coding for a protein* should be the definitive consideration in genetics. Please appreciate how inane it would be for the field of genetics to invent itself and just a few decades later declare junk the part of the genome which remains mysterious. It is true that DNA in plasmids and telomeres (and such) may be junk, but it is much more important that we don't know for sure. In fact, we don't have a scientific reason to assume so. This is part of a troubling trend in science where concepts that are poorly understood become classified as irrelevant.

If inter-dimensional aliens are trying to enslave and eat humanity, it may be vital for them to crop these regions from our genome because they give us a natural immunity to aliens. Why do people think there is junk DNA? How long before a geneticist asks for a grant to remove the "non-coding" DNA from human genetic material so he may grow experimental children?

There are two definitions of junk DNA. First is the one that the scientists use about non-coding DNA. The definition is known but it is not known if the definition adequately characterizes the real situation or agrees with the situation that will be predicted by geneticists in the future. The other definition for junk DNA is the one that will be used by voters if they ever vote on genetics. In that case, junk DNA refers to the part of the genome that is junk. Consider this ballot initiative: *Should doctors be allowed to help patients by removing junk DNA?* How did Google's algorithm find the information characterized by figure 1?

A lot of the smartest people don't go into science because they recognize how chronic mismanagement of programs leads to unproductive professional practices. Among scientists, the quants can be thought of as the best and brightest. After the rigorously quantitative fields there are other fields which are also called science. Genetics occupies the middle ground when geneticists attempt to describe the non-equilibrium quantum statistical mechanics of large biological molecules with 2D square matrices of active and recessive gene combinations. From the group of aspiring genetic scientists, the bio-tech industry extracts sound bites and blurbs about results which quickly become illogified. The truth-comes-from-authority meme gets a lot of likes in the big groupthink and bullshit ends up in Google's top result.

And so it is with Darwin's theory of the evolution of new species by the random appearance of new mutant genes which are then selected by Nature as improving fitness: the origin of species by natural selection. Just as interspecies DNA changes are not well-described in N by N matrices, we argue here that Nature is not well-described by evolution. This writer's first reaction to hearing Darwin's theory was one of intuitive agreement; however, the big problems soon crystallized. In fact it does seem reasonable that animals could evolve per Darwin's prescription but it would take much longer than the age of the Earth.

Another problem with evolution is that creationism is isomorphic to any theory for why the very first thing started living on the particular day that life first arose.

Regarding the agreement of evolution with the fossil record, this paper's main result is a paradox in that geology or evolutionary biology must be wrong. Until we can show which one, the theory of evolution will remain unphysical because geology takes precedence. Furthermore, classical thermodynamics predicts that life would never start because the organization of the first self-replicating DNA molecule was a catastrophic decrease in entropy from the time when there were no self-replicating molecules. If one assumes that life started despite thermodynamics, then it is reasonable to see that life could evolve. Upon closer inspection, we will show that even if life did start for some reason, the rate of random fitness-improving (FI) mutations that is observed in modern laboratory experiments implies an evolutionary timescale much greater than the geological age of the fossil record.

The astute reader might ask, "If life starting is non-physical, who cares about physicality?

I'm alive so the point is moot." The reader is astute indeed. Everything that happened was definitely physical so there is a problem with thermodynamics since the observation of life more or less disagrees. Giving away the answer, the discrepancy is probably accounted for in a thermodynamics like that described by Prigogine. Due to the special non-equilibrium problem in which all life exists at the cusp of an unzipping DNA molecule, there is probably some special consideration about pattern formation that will allow complex biological problems to be solved in the appropriate physical framework.

Darwin's theory requires, as with junk DNA, a disambiguation to separate evolution and adaptation. This simple clarification of terminology is sufficient to truncate a large volume of evolutionary debate space. In evolution, new genes appear and then the environment selects them for fitness. In time, many of these new genes collect in a species' genome and it is said to be a distinct species from its progenitor species. In adaptation, genes that occur rarely in a species' genome become ubiquitous as some rare trait becomes needed for survival. There are no new genes in adaptation and therefore this process can never lead to new species.

The typical example of adaptation is bacteria and that they can be observed to become resistant to antibiotics. This is cited as evolution but usually it is not evolution. It is possible that new FI (Φ) genes appear in the lab and if so the evolutionists should show that the real observed rate agrees with the rate required to accommodate the geological age of the fossil record. Here we argue that this is impossible. The normal development of antibiotic resistance occurs when there is some small percentage of the parent population that already had the immunity genes. This includes the population that was originally immune and also the non-immune population which did carry some subset of the immunity genes. In the end, all the offspring that don't inherit the perfect combination of genes die and then the whole species is resistant. The resistant bacteria did not change species just because the other ones died. This is adaptation via the reorganization of genes which were already part of the bacterial genome.

Consider a physical theory: general relativity. GR has made many successful predictions; the small corrections it predicts gives us a GPS system that works. If we don't make the corrections, the signal from the satellites is wrong by exactly how much GR says it should be. In evolution no one has ever said, "This species will turn into another species," and then seen that happen. If Darwin's theory is about the origin of species, then the only observation

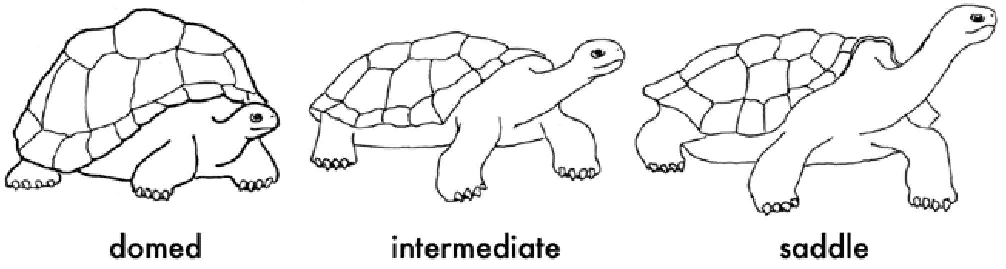


FIG. 2. Darwin concluded that the saddle shell evolved so that the tortoise could eat higher leaves. An epigenetic explanation might refer to a persistent signal in the tortoise's nervous system when it struggles through life with a sore neck yearning for the leaves which are just out of reach.

that can confirm it is the genesis of a new species in a way consistent with evolutionary principles. Darwinian evolution by the natural selection of multitudes of miraculous mutant genes is not on par with the verifiable theories that evolutionists persistently compare it to.

Figure 1 illuminated the wrongness of broadly accepting definitive statements that claim to characterize scientific beliefs. Epigenetics is a new field which studies how organisms can control the DNA of their offspring in a direct "epigenetic" response to the environment. It is well possible that DNA categorized as non-coding junk is responsible for the epigenetic effects. Such effects may allow creatures to adapt to changing conditions more quickly than is possible via random mutation. Junk DNA is an anachronistic abstraction handed to us by the long legacy of genetic studies whose axioms did not include epigenetic considerations. Which of the axioms that will be held by geneticists in future generations are not yet considered by those currently fixated on protein coding?

Consider Darwin's data. One canonical example from Galapagos is the birds that became darker than their South American ancestors in response to the darker volcanic rocks. Another is the tortoises whose shells morphed (figure 2) to allow their necks different ranges of motion in response to the varying height of edible vegetation on the each island. Darwin's approach was undoubtedly scholarly but his result fails to conform to modern standards of scientific rigor. In this way Darwin's 1859 book contrasts with that of his contemporary Maxwell who published a more famous book on electromagnetism in 1865.

Darwin concluded Galapagos' birds and tortoises evolved from ancestors that were distinct by having more children when they had beneficially mutated DNA. However, the Galapagos birds were still birds and the tortoises were still tortoises so the application of

FIG. 3. Wiener dog.

the data to interspecies evolution is questionable. However, we will grant this and continue to analyze the typical case: over a very, very long time the animal gains so many positive changes that it becomes a new species and all Nature's animals, even the silly ones (figure 3), came from that.

Darwin did not show that the Galapagos animals evolved new genes. Consider the birds long ago swept from the mainland in a storm. They found the volcanic Galapagos rocks much darker than their old environment. Darwin hypothesized *and concluded* that as the birds lived there, there were so many mutations that some of them made the birds have new, better camouflage. Darwin did not rule out the possibility that the color of the birds' feathers can be strongly influenced by epigenetic rather than genetic effects.

Darwin did not show that the genes which make the birds dark were not in the mainland population. It is possible that feather color is influenced by very many genes and the dark feather gene combination does sporadically occur in the mainland population. Darwin never showed that there were new genes, only new traits. It makes sense that natural selection would favor the combination of genes that gives the birds darker feathers but that says nothing about new genes. Furthermore, it is possible that the epigenetic code in the bird

DNA – which may meet the non-coding technical criterion for junk DNA – sensed that the birds needed darker feathers to blend in among the new Galapagos rocks. The purpose of the epigenetic code may be to deliberately give the progeny darker feathers instead of waiting for it to happen randomly.

If the result was epigenetic, that could account for the appearance of the new trait on a much faster timescale than when the genes appear randomly. In the epigenetic case, the entire island population quickly starts successive generations of darker birds. In the random genetic case, one has to wait a very long time for the random mutation that increases fitness, and then that particular animal also has to be the grandparent of the entire current population. There are a number of problems here.

It is unlikely that the animal will be born with a Φ mutation *and* will be positioned in an environment that is optimized for offspring *and* that those optimal conditions continue over very many generations until the first mutant animal's increment of fitness conquers the entire genome of the parent species. Keep in mind how unlikely it is for any one gene to conquer a whole branch of evolutionary life and also how many times that would have to happen for one species like a fish to evolve into something like a triceratops.

Be clear, the unlikeliness of any animal being at one of these interspecies family tree apex positions must be multiplied by the further unlikeliness of being mutated in a way that improves fitness.

Consider the case when the combination of genes that make dark feathers was always in the bird species and dark feathers did occur sometimes on the mainland. In general the mainland birds were lighter, but they weren't identical and perhaps sometimes this combination of genes did show up. This would be more common than albinism. All the albino genes are in the genome even when they do not commonly occur in the combination that causes albinism. The frequency and arrangement of the genes in the genome isn't what defines a species. Different species have different genes and the fact that the combination for dark feathers becomes ubiquitous doesn't mean that there are new genes. Maybe there were new genes but Darwin did not have sufficient controls on his data to demonstrate his conclusions. What can geneticists with ornithological leanings tell us today?

Here we will present a calculation. Consider what Wikipedia tells us about physical calculations on its statistical mechanics wiki.

> “In physics there are two types of mechanics usually examined: classical mechanics and quantum mechanics. For both types of mechanics, the standard mathematical approach is to consider two ingredients:
>
> 1. The complete state of the mechanical system at a given time, mathematically encoded as a phase point (classical mechanics) or a pure quantum state vector (quantum mechanics) [*which reduces to a classical phase point through contraction with a dual vector*].
>
> 2. An equation of motion which carries the state forward in time: Hamilton’s equations (classical mechanics) or the time-dependent Schrödinger equation (quantum mechanics).”

The third type of mechanics not mentioned is statistical mechanics. We emphasize that it is not possible to simulate evolution of the non-life state into the life state with well-known statistical mechanics because that simulation will always say life does not start. The QFT Hamiltonian function is the sum of the system’s kinetic and potential energies so the Hamiltonian equations of motion will not show a reduction in entropy. Such energy flows are constrained by the 19th century thermodynamic principles. Instead of Hamilton’s or Schrödinger’s equations we will use the equation $y = mx + b$. It describes the linear accumulation of Φ genes required for the DNA in each evolutionary bin to evolve into the next. The result here is a physical calculation because the number of genes in each kind of species (its complete state) can be measured in the lab.

We will define six states from the fossil record and require that one evolve into another according to the fossils’ geological ages. We choose coarse grained bins to lump the evolutionary ancestry of humanity into the following groups: prokaryotes, eukaryotes, multicellular, animals, mammals, humans. By analyzing a genetic representative of each bin, we can infer the minimum mutation rate required for humans to evolve in the four billion years since the surface of the Earth cooled enough for life to immediately start.

We will compute an approximation for how many generations of life there have been on Earth. We directly constrain the mutation rate of evolutionary history with this number. The genome size and intergenerational timescale of each bin is assumed to be that of the following representative organisms: e. coli, complex amoeba, lichen, worm, mouse, human. The data model is given by table 1.

Table 1. Evolutionary data model

Time (10^9yr)	Δt (10^9yr)	Class	Example	Genes (Mb)	ΔG (Mb)	Reproduction	N (10^9)
$t_5 = -4.0$	2.0	prokaryotes	e. coli	5	*na*	20min	52560
$t_4 = -2.0$	0.5	eukaryotes	amoeba	300	295	30min	8760
$t_3 = -1.5$	0.7	multicellular	lichen	30	30	1hr	6132
$t_2 = -0.8$	0.6	animals	worm	100	70	1day	219
$t_1 = -0.2$	0.2	mammals	mouse	2,700	2600	1mo	2.4
$t_0 = 0.0$	*na*	humans	human	3,000	300	13yr	*na*

ΔG_0 and ΔG_4 are nearly equal so there is as much evolution in the most recent two hundred million years as in the first two billion. Since the intergenerational timescale of mice is two thousand times slower than e. coli we see the fossil record suggests new mutant genes are accumulating about twenty thousand times faster now than in geologically early times. This is not motivated by any evolutionary theory, but rather by experimental geology. Why is it evolving so much faster now?

One of many possible rebuttals to this attempt to clarify what is known about evolution will be to invoke a varying rate of mutation. It will claim the mutation rate seen in the lab isn't too slow for the fossil record because the rate was higher when the fossil bodies were being deposited. That's wrong because evolutionary geology requires it to have been slower in earlier times as so clearly demonstrated by $\{\Delta G_0, \Delta G_4\}$. However, consider that when the rates of quantum mechanical processes (such as mutation) are allowed to vary, the rate of formation of radioactive carbon isotopes in the atmosphere must also vary in kind. Varying the rate of mutation invalidates any data reliance on radiocarbon or other nuclear dating techniques and the house of cards crumbles. Carbon dating relies on a steady flux of new radiocarbon through history.

Indeed there is an error when geological dating relies on constant rates but evolution relies on accelerating rates (table 2). In brief, mutations in DNA are essentially caused by the same random cosmic rays that make the radiocarbon. Indeed, radiocarbon is known as a cosmogenic nuclide and all the causes of Darwinian mutation are at least indirectly cosmogenic. The theory of evolution does not have sufficient gravitas to overturn trusted geological methods of approximation. It is possible that radiodating methods are not as reliable as thought but evolution has no bearing on those problems.

The data model creates life four billion years ago with five megabases (Mb) of genetic code. We will examine only the subsequent rate of evolution. Each chronological evolutionary step shows an increase in genetic material except at the ΔG_3 step where the coherent cellular multiplex enters the fossil record. ΔG_3 describes the evolution from eukaryotic amoebae to simple multicellular lichen. It is smaller than the other ΔG because the first two billion years of life evolved cells too big and it turned out to be better to make smaller specialized cells with smaller genomes. In that a number must be chosen, we strongly underestimate that it only required $\Delta G_3 = 30$Mb of random new genes for the complex amoebae to become lichen. This may be the greatest source of error in this calculation but the number is so conservative that the result here will still serve as a bound. Accounting for any errors could only make evolution appear even more far-fetched.

For $\Delta G \neq \Delta G_3$, the minimum number of new genes during each step of evolution is found by subtracting the size of the old genome from the new. The simplifying assumption is that every mutation was Φ and there were no evolutionary dead ends where new Φ genes were lost. If every random mutation is assimilated into the species' genome, ΔG is the minimum number of new genes that had to appear for each bin to evolve into the next. Even under these many optimizing assumptions, the Earth is not old enough for evolution to have happened yet. Of course if the Earth and life itself are eternal, then geology is wrong and that is independently interesting.

We can calculate the rate of new genes per generation with $R_i = \Delta G_{i-1}/N_i$.

Table 2. Results

Time	Example	R (10^{-6})	$\mathcal{Z}$
t_5	e. coli	5.61	178,000
t_4	amoeba	3.42	292,000
t_3	lichen	11.4	87,700
t_2	worm	11,900	84
t_1	mouse	125,000	8

Obviously these numbers R have no inherent meaning. What would it mean for less than one gene to appear per generation? If more than one new Φ gene was improving fitness *and* being assimilated by every member of the species in every generation, then the genetic code wouldn't be stable at all. There would be no well-defined notion of distinct species and we could stop the calculation right now. Distinct species are observed in Nature and in fact species stasis is observed among many of the distinct species found in the fossil record. Species stasis describes the situation when the same kind of fossil appears in the fossil record over potentially hundreds of millions of years without appearing to evolve at all. Species stasis is a strong observational constraint on the theory of evolution that cannot be ignored in a proper treatment.

While R is not so useful, we can take its inverse $\mathscr{Z}$ to find the average number of model generations that pass between Φ mutations. Evolution has to fit the whole fossil record, not just part of it. Feynman said, “It doesn’t matter how beautiful your theory is, it doesn’t matter how smart you are. If it doesn’t agree with experiment, it’s wrong.” The theory of evolution is wrong because it does not agree with geological experiments.

$\mathscr{Z}_1$ tells us that a new Φ gene will appear once in every eight generations of mice. That is very easy to confirm or deny with data that already exists. Furthermore, the evolutionary history agreed upon by the evolutionists predicts very many more species between mice and humans than we have used. Each distinct species had a distinct genome and the 300 Mb used for ΔG_0 is hugely too small. ΔG_0 is the case when the mouse evolved directly into a human via the most efficient possible accumulation of new mutant genes. In fact, all the ΔG are hugely too small ensuring that the real answer can only appear even more unlikely than the bound derived here.

The easy falsifiability of $\mathscr{Z}_1$ holds true for $\mathscr{Z}_2$ and comparable experiments on worms. Surely these experiments have been done and will show mutations resulting in coherent new genes that improve fitness are too rare. If the molecule is mutated, keep in mind that only a small subset of all random mutations result in something that is still viable genetic code. Most mutations will not result in the random appearance of genetic code. Even when the mutation produces code, it is unlikely that the code will improve fitness with respect to the code that already stood the test of natural selection. Existing data should further demonstrate the same for the bins at high $\mathscr{Z}$. If bacteria are gaining new genes at this rate, let the evolutionists demonstrate the new genes and that they increase fitness so much that they are likely to spread through entire species’ genome within geological history.

If somehow there is so much uncertainty in the calculation that the bound is refuted and the observed mutation and genetic dissemination rates, $\mathscr{Z}$ and Q, are achievable in Nature, then it will become necessary to also refer to the many other problems with evolution to show why it doesn’t make sense and fails as a verified scientific theory. For instance, the rate of the appearance of new genes is not the main hurdle for evolution. The bottleneck before new species appear is that the new Φ genes have to randomly appear *and* those genes have to spread through thousands of generations of descendants. The rate Q of that process is smaller than the rate $\mathscr{Z}$ calculated here.

Another large problem is that interspecies evolution relies on discrete jumps in the number of chromosomes in some unique specimen that lived and died at a certain time. The model of small mutations in which one or a few base pairs is added per N evolutionary steps is totally wrong. The Φ mutation has to have an entire chromosome consisting of many thousands of base pairs all appearing together at once. The statistical mechanics of large particle ensembles will show that such a large random fluctuation is unlikely to have occurred even once in the lifetime of the universe.

There may be some predilection for mutations to appear similar in structure to the non-mutant variants, but for an entire new chromosome to improve fitness by chance is something that has to be observed to be believed. When a human is born with the wrong number of chromosomes fitness is typically decreased. An example is Down's syndrome which both increases infant mortality and adversely affects fitness in adulthood.

There is no reason to conclude that life with many chromosomes can evolve from life with fewer chromosomes. Tens of thousands of random mutations must simultaneously coalesce in one particular laboratory organism to create a well-ordered (*but random!*) chromosome that luckily is also a huge boon to fitness. Even if that is observed, there are still other problems that must be addressed before Darwin's theory can be deduced as a unique conclusion.

Consider one effect mentioned above that will further retard the evolution of new species. In the model here, all the mutations happened along a single genetic lineage. The number of possible mutant ancestors in which the original genes could have appeared is not limited by the large number of all possible ancestors. Instead it is limited by the small number of grandparents in the lineage of the first member of the child species that is mutated enough to quality as such. An example is to point out that the mouse is not the product of the evolution of all the worms. The mouse is only the product of the worms that were his ancestors.

Note well, the mouse did not inherit Φ genes from any member of the worm species that was not in the small subset of worms that can call the first mouse their grandchild. That means the huge majority of Φ mutations that occurred during the epoch of worms were not passed into the genome of mice.

The critical reader might cite a perceived reliance on the line drawing fallacy but *en garde!* We can draw a line between worms and mice. Worms and mice have different numbers of chromosomes so it is very clear what is what. Remember, there is no such thing as 23.9 chromosomes. Chromosomes always appear in integer multiples.

Inasmuch as we have said no to evolution, an alternative is offered. The typical physical frame of the evolutionists is that of the big explosion. The universe started so life must have also started at some finite time later. In that framework, Prigogine's ideas about non-equilibrium pattern formation may be sufficient to resolve one or more biological paradoxes.

Another framework is the eternal universe model with the attendant eternal life. This model is easily reconciled with biblical creation. Consider a general closed time-like curve (CTC). The typical example is a circle but here consider a circle with a null point as described by the theory of infinite complexity. The null quality of the null point is that from the perspective of a life form, the value at the null point is null. As demonstrated in the paper *Ontological Physics* by this writer, the entire infinite body of all possible information is in the null point and it can be associated with God. The eternalness of God can be the hypercomplex internal structure of the null point as finite life forms exist on the finite circular interval $(0, 2\pi)$. This model allows for interesting hypotheses such as: *Do dinosaur bones appear so large due to a persistent rounding effect on the part of the big computer in the sky?*

Consider the biblical but noncanonical story of the Anunaki and the Nephilim that was recently adapted in the movie *Prometheus.* In the original version of the story, aliens came down in space ships and bred with the native earthlings. They taught the men to use metal and they taught the women to wear make up. While this does not explain the origin of life, it does explain the origin of modern humans.

Consider trees. They reproduce a lot slower than other life. Evolution predicts their supposed appearance on Earth about 350 million years ago. If we generously assume trees can reproduce at 10 years old, that's 35 million total generations of trees. Big Brazilian rain forest trees, magnolias, date palms, and even the five thousand year old Bristlecone pines all evolved in that 35 million generations. That's only seventy thousand Bristlecone lifetimes for all of trees to exist.