

# Quantum Geometry (Super-Symmetry for Dummies)

That's why they call it golf – all the good words were taken.

Anonymous

It seems as though our natural languages are cluttered by misapplications of good words to important basics. For instance, it would be fabulous if the word “atom” had never been applied to the basic structure we now know as an atom. Democritus originally coined the term to apply to that which could not be divided. Of course atoms can be divided in countless ways, we now know, starting with sub-atomic particles and drilling many orders of magnitude down from there. Similarly, geometry is riddled with misnomers.

Traditional geometry is the basis of all mathematics. It is an axiomatic system of logic using the concept of point space. Recursion of points produces more points, lines, planes and solids. If we conceptualize this system as the nesting of a single function, we can describe it as follows:

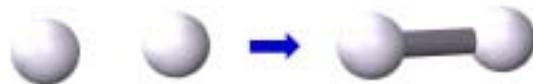
$x = \text{point}$   
 $f(x) = \text{line}$   
 $f(f(x)) = \text{plane}$   
 $f(f(f(x))) = \text{solid}$

However a point is seen as a dimensionless entity, and this is an exceptionally hard concept to illustrate. How does one graphically demonstrate a non-dimension? Of course years of casual usage makes us entirely comfortable with the concept, and we've become accustomed to seeing “points” on a printed page.

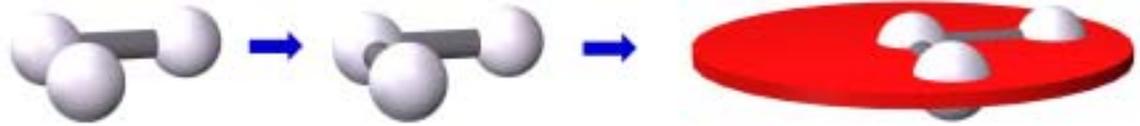
$x = \text{point}$



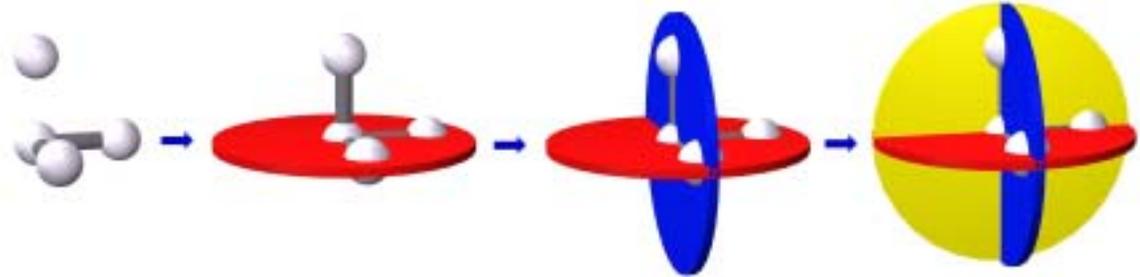
$f(x) = \text{line}$



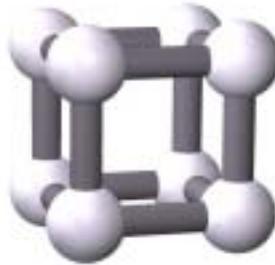
$f(f(x)) = \text{plane}$



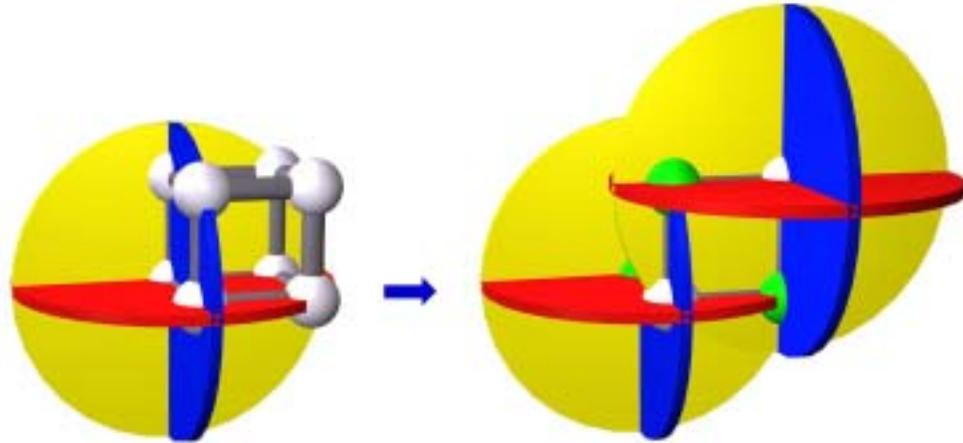
$f(f(f(x))) = \text{solid}$



This system quantizes distance, but does not quantize angle. Consequently, a continuum of angle is required, which produces a complimentary continuum of distance. The only angle intrinsic to the system is a right angle, so it is natural that the cube is the fundamental solid in traditional geometry.



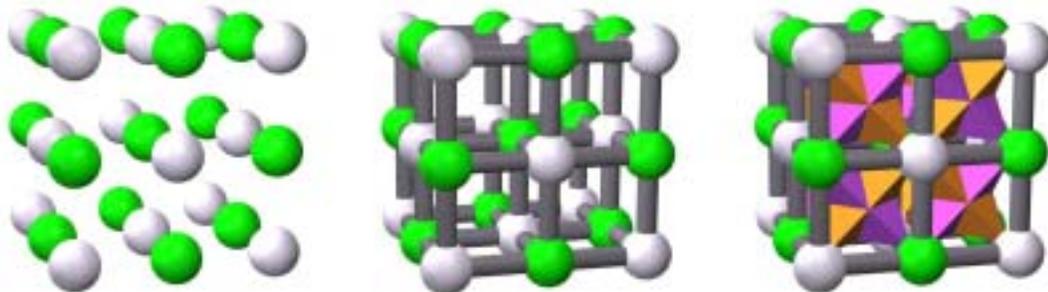
Points generate planes, so planes cannot have thickness. The quantum dimension of distance is derived from the difference between locations of two points, or two planes.



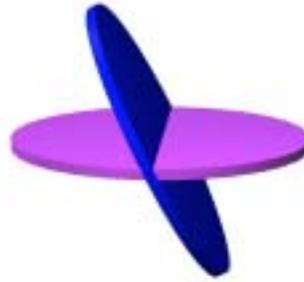
If we adopt a protocol that only allows discrete points in three-dimensional space, then only discrete angles between lines can be generated. We know that certain angles can never be generated because certain solids cannot be generated in this space. For instance, a dodecahedron cannot be generated, because discrete points can never perfectly align; therefore, the angles in a dodecahedron will not be discretely quantized in this space. However, a cube is dual to an octahedron and contains two tetrahedrons, so they all can comfortably exist within the system.



If points in such a way fill space, then these shapes should also fill it, and the duality of the tetrahedrons in the cube should be apparent.

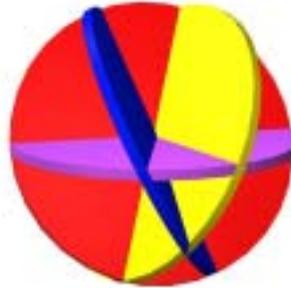
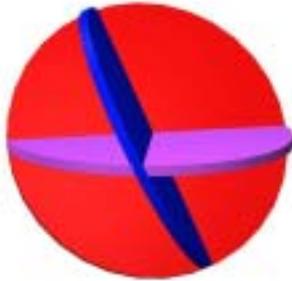






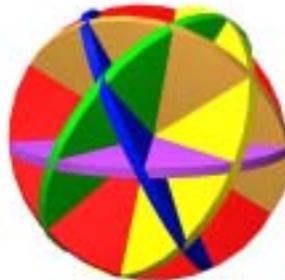
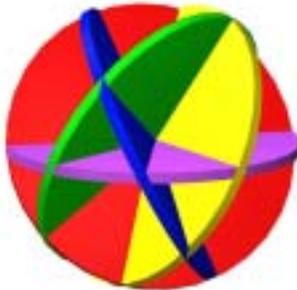
$f(f(x)) = \text{point}$

$f(f(f(x))) = \text{shape}$



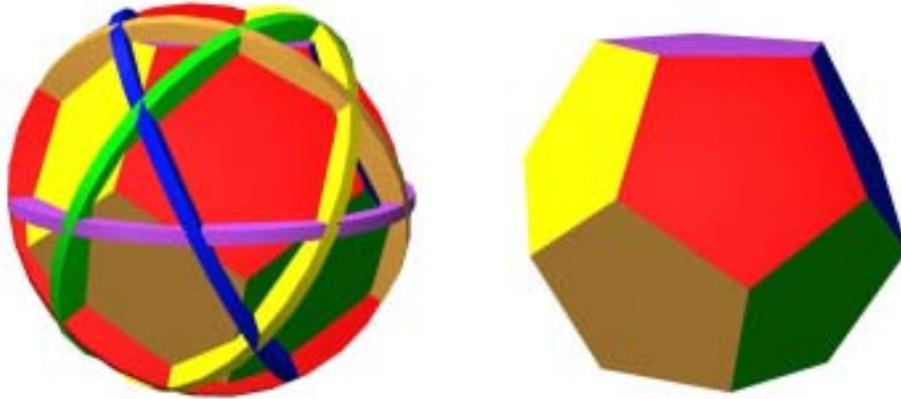
$f(f(f(f(x)))) = \text{solid}$

$f(f(f(f(f(x)))))) = \text{all solids}$

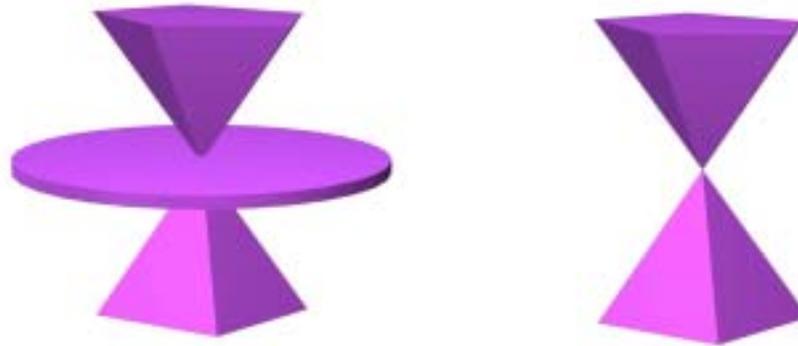


The most notable difference between the two systems of geometry is the inversion of points and planes in the hierarchy. In point space three points are required to form a plane, but in plane space three planes are required to form a point. Points continue to be dimensionless objects, but they no longer underpin the dimensions of length and angle. The next most notable difference is in the concept of angle. In point space, angle is not iterated; it is derived from lines. Specifically, the relationship between two lines in a plane generates an angle. In plane space the intersection of two planes generates an angle, and the intersection of two angles generates a relative angle in a plane.

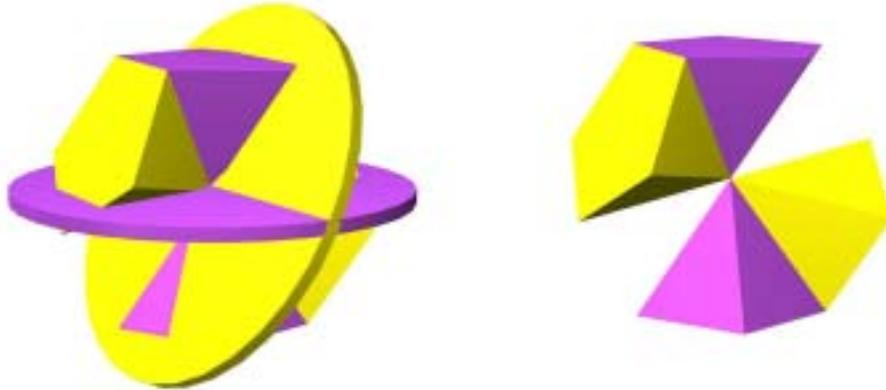
Despite the length dimension of a plane, we can still conceive of a point as a dimensionless entity, and in the case of six intersecting planes there are 20 points. To help visualize the concept of a point in this system we will imagine the solid made by the intersection of the six iterated planes.



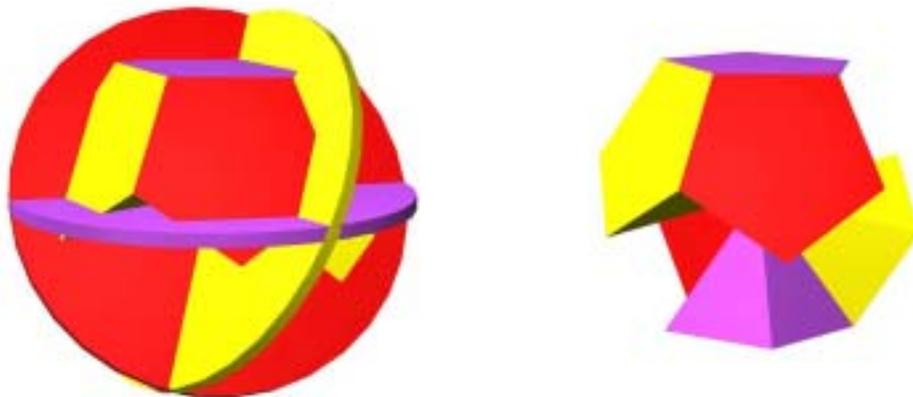
Let's call this the quantum dodecahedron; it is the atomic level of the system, and is itself not dimensionless. The distance between parallel faces is one plane thickness. These illustrations have reduced the thickness of planes relative to the quantum dodecahedron to merely demonstrate relative orientations not relative thickness. If we remove all but one plane from the intersection we can see the contribution of a single plane to the intersection.



Adding a second plane back into the intersection produces the following relationship of two planes.



The third plane in the intersection produces a point.

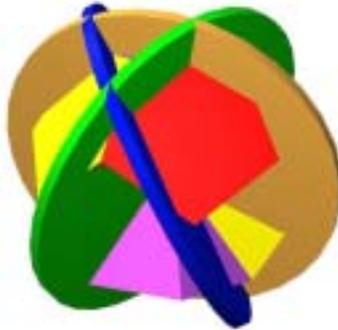


There are two discrete segments to this intersection: an upper and a lower. In isolation there is no real need to differentiate between the two segments. However, if we imagine the system as comprised of not just single planes but infinite layers of planes, then there is a need to differentiate between the upper and lower portions of the intersection. For instance, lets imagine the purple planes that lie above and below this intersection.

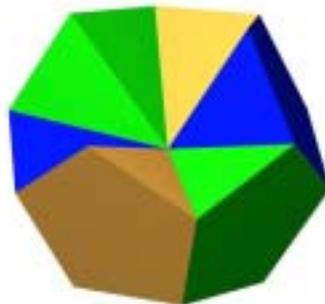


The purple plane above the intersection will see the point defined as Red – Yellow – Purple, and the plane below the intersection will see it as Red –

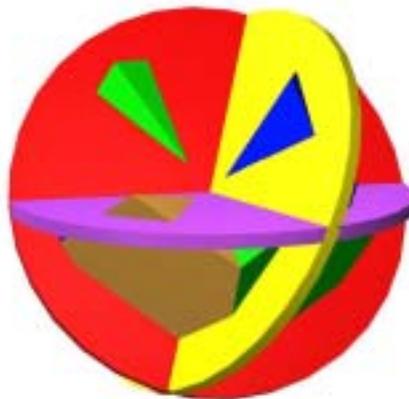
Purple – Yellow. Therefore, the system presents a logical way to determine position of a plane relative to a point. The other issue that is less intuitive is the status of the remaining three planes in the intersection relative to the point.



It is as if these three planes are not present at this particular point; however, they are present in the quantum dodecahedron.



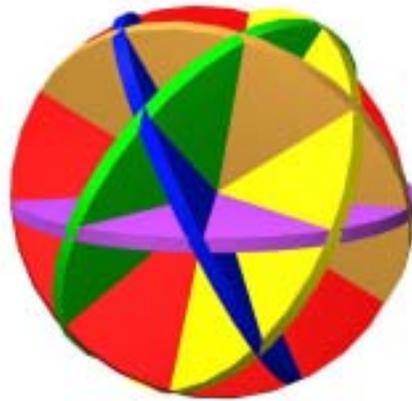
Similarly, these “missing planes” at a point maintain a logical relationship to the planes participating in the defining intersection of three planes.



Therefore we have identified three logical qualities of every plane at a point. There is an upper quality, a lower quality and an absent quality. We can assign the following symbols to these qualities.

- “+” = upper
- “-” = lower
- “0” = absent

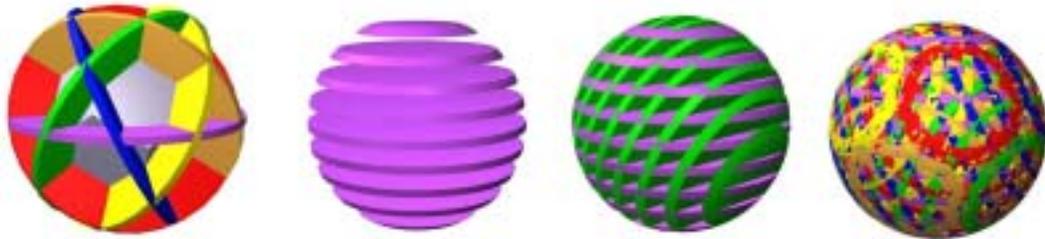
Using these trinary symbols we can now construct a concise description of the twenty discrete points in a quantum dodecahedron. We can provide all of the relevant information in a table with 120 cells – a truth table if you will.



	Red	Yellow	Blue	Purple	Orange	Green
1	+	+	+	0	0	0
2	+	0	+	+	0	0
3	+	+	0	0	+	0
4	0	+	+	0	0	+
5	+	0	0	+	0	-
6	+	0	0	0	+	-
7	0	+	0	-	+	0
8	0	+	0	-	0	+
9	0	0	+	0	-	+
10	0	0	+	+	-	0
11	0	0	-	-	+	0
12	0	0	-	0	+	-
13	0	-	0	+	0	-

14	0	-	0	+	-	0
15	-	0	0	0	-	+
16	-	0	0	-	0	+
17	0	-	-	0	0	-
18	-	-	0	0	-	0
19	-	0	-	-	0	0
20	-	-	-	0	0	0

We can now use this information as a basis for building virtually any quantum shape by infinitely layering all of the planes.



It is curious that dodecahedrons cannot fill space, but dodecahedral planes can. All the Platonic and Archimedean solids can be easily defined within this system. For instance, we know that eliminating points from the above truth table can create five cubes and ten tetrahedrons. We also can organize symbols to create an icosahedron and octahedrons. Scaling is also a simple matter of adding a global quantifier to the table, opening the door for combinations of solids of varying sizes.

There are many disorienting consequences of these changes in geometry, but all operations of point space can be performed in plane space. The opposite is not true. The operations of plane space are all performed with real numbers. In point space the construction of simple elements, such as circles and dodecahedrons cannot be achieved with real numbers alone. point space requires a continuum of numbers brought about by the absence of quantized angles. Numbers not included in the set of real numbers do not exist in quantum geometry. They are achieved through relative properties of the system. Even Pi becomes a real number, one that is relative to scale.

Because point space is an axiomatic system of logic, it has been used to produce matrices of logic. Quantum geometry can likewise be used to generate logic matrices different from traditional geometry. The matrices of plane space embody the matrices of point space; but again, the opposite does not hold. This becomes apparent when we translate the trinary information in the above table into binary information. To do this, we will map the above six-color quantum dodecahedron onto the four-color “genetic” dodecahedron that we developed earlier.

Binary to Trinary Translation Table

	Red	Yellow	Blue	Purple	Orange	Green	
Green Yellow	+	0	0	0	0	0	0
Green Blue	0	+	0	0	0	0	0
Green Red	0	0	+	0	0	0	0
Blue Red	0	0	0	+	0	0	0
Red Yellow	0	0	0	0	+	0	0
Yellow Blue	0	0	0	0	0	0	+
Yellow Green	-	0	0	0	0	0	0
Blue Green	0	-	0	0	0	0	0
Red Green	0	0	-	0	0	0	0
Red Blue	0	0	0	-	0	0	0
Yellow Red	0	0	0	0	-	0	0
Blue Yellow	0	0	0	0	0	0	-

It is readily apparent that the translation involves the addition of six new color combinations to the six that we have been using. Therefore, a translation of the above dodecahedron truth table will require an addition of 120 cells, bringing the total to 240.

												
1	1	1	1	0	0	0	0	0	0	0	0	0
2	1	0	1	1	0	0	0	0	0	0	0	0
3	1	1	0	0	1	0	0	0	0	0	0	0
4	0	1	1	0	0	1	0	0	0	0	0	0
5	1	0	0	1	0	0	0	0	0	0	0	1
6	1	0	0	0	1	0	0	0	0	0	0	1
7	0	1	0	0	1	0	0	0	0	1	0	0
8	0	1	0	0	0	1	0	0	0	1	0	0
9	0	0	1	0	0	1	0	0	0	0	1	0
10	0	0	1	1	0	0	0	0	0	0	1	0
11	0	0	0	0	1	0	0	0	1	1	0	0
12	0	0	0	0	1	0	0	0	1	0	0	1
13	0	0	0	1	0	0	0	1	0	0	0	1
14	0	0	0	1	0	0	0	1	0	0	1	0
15	0	0	0	0	0	1	1	0	0	0	1	0
16	0	0	0	0	0	1	1	0	0	1	0	0
17	0	0	0	0	0	0	0	1	1	0	0	1
18	0	0	0	0	0	0	1	1	0	0	1	0
19	0	0	0	0	0	0	1	0	1	1	0	0
20	0	0	0	0	0	0	1	1	1	0	0	0

One might conclude that a binary view of trinary information would neglect exactly half of the information. A view of the genetic code as built around quantum logic would build shapes in plane space, as opposed to point space. Quantum logic can be viewed as a twelve-symbol binary system. This logic simultaneously delivers information about position and angle, because the two forms of information are inseparable in quantum geometry. Our application of the logic of point space has effectively hidden from us half of the information in the genetic code – the stereochemistry half. Here's what the assignments look like when they are translated into a quantum geometry twelve-symbol format.

Isoleucine			AUU	AUC	AUA	
Phenylalanine			UUU	UUC		
Valine			GUU	GUC	GUA	GUG
Leucine	UUA	UUG	CUU	CUC	CUA	CUG
Methionine						AUG
Tryptophan						UGG
Alanine			GCU	GCC	GCA	GCG
Glycine			GGU	GGC	GGA	GGG
Cysteine			UGU	UGC		
Tyrosine			UAU	UAC		
Proline			CCU	CCC	CCA	CCG
Threonine			ACU	ACC	ACA	ACG
Serine	AGU	AGC	UCU	UCC	UCA	UCG
Histidine			CAU	CAC		
Glutamate					GAA	GAG
Asparagine			AAU	AAC		
Glutamine					CAA	CAG
Aspartate			GAU	GAC		
Lysine					AAA	AAG
Arginine	AGA	AGG	CGU	CGC	CGA	CGG
STOP	UGA				UAA	UAG

The linear model views this table as a 4-64 relationship. From the context of a dodecahedron the code becomes a 12-120 relationship. If each of the four nucleotides is taken within context and its positional value is considered, then the code can distinguish between twelve distinct nucleotide symbols. From this perspective codons become syllables in words that mean peptide bonds, and there are potentially more than 64 syllables. This kind of thinking is not without precedent. Harold Morowitz, a master bio-physicist and expert in emergence, suggested to me a parallel to the Pauli exclusion principle in quantum physics. I had to go back to freshman chemistry to see what he meant. Pauli postulated that no two electrons could share the same quantum numbers. This means that each electron carries a unique quantum value, and in this way each electron is

informative. In fact, according to Dr. Morowitz, matter itself is informative due to the pruning nature of Pauli's exclusion principle. I can't argue with that.

Rafiki is proposing a Pauli-like exclusion principle of its own. In the Rafiki code no two nucleotides can share the same value; therefore, twelve are required. Since only four brands of nucleotide are used in the actual code, the context of each nucleotide becomes essential, and the only context available is the nearby body of nucleotides. This is a model of overlapping contexts – it is a network model. The full set of codon permutations takes on a new hue, as illustrated in the following table:

 UUU	 Phe	 Phe	 Phe	 Phe	 Phe	 Phe
 UUG	 Leu	 Leu	 Cys	 Cys	 Val	 Val
 UUC	 Phe	 Phe	 Ser	 Ser	 Leu	 Leu
 UUA	 Leu	 Leu	 Tyr	 Tyr	 Iso	 Iso
 GCA	 Ala	 Arg	 Asp	 Gln	 Ser	 Thr
 GGG	 Gly	 Gly	 Gly	 Gly	 Gly	 Gly
 GGA	 Gly	 Gly	 Glu	 Glu	 Arg	 Arg
 GGC	 Gly	 Gly	 Ala	 Ala	 Arg	 Arg
 GGU	 Gly	 Gly	 Val	 Val	 Trp	 Trp
 ACU	 Thr	 His	 Iso	 Leu	 Tyr	 Ser
 CCC	 Pro	 Pro	 Pro	 Pro	 Pro	 Pro
 CCU	 Pro	 Pro	 Leu	 Leu	 Ser	 Ser
 CCA	 Pro	 Pro	 His	 His	 Thr	 Thr
 CCG	 Pro	 Pro	 Arg	 Arg	 Ala	 Ala
 UGA	 STOP	 Val	 STOP	 Asp	 Met	 Ser
 AAA	 Lys	 Lys	 Lys	 Lys	 Lys	 Lys
 AAU	 Asn	 Asn	 Iso	 Iso	 STOP	 STOP
 AAC	 Asn	 Asn	 Thr	 Thr	 Gln	 Gln
 AAG	 Lys	 Lys	 Arg	 Arg	 Glu	 Glu
 CUG	 Leu	 Ser	 Arg	 Cys	 Ala	 Val

I have barely started playing with the logic of quantum geometry, but I am optimistic that further investigation will yield a more accurate logical mechanism of the genetic code, and therefore allow us to translate all of the information therein. It seems as though certain relationships are a natural fit, and a simple language is behind it. This language gives a better distribution of relationships than the second order binary approach currently in vogue. For instance, the data shows that only 5% of peptide bonds are in the cis configuration. A quantum code would better support that language, as there is a one in twenty chance of two codons being total opposites in their planar configurations. Could this be the signal for a cis bond, and all the rest are trans by default?

Other patterns are intriguing, such as the relationship between the start signal Methionine, , and the three signals for STOP , , . This cluster is directly opposite the “middle” of the code in the area of proline , which is the king of cis bonds. Could there be a correlation between mutations attempting cis bonds and translation termination? It is also interesting to note the non-Gamow-like distribution of the planes within each assignment cluster. This is another striking illustration of the spreading of assignments. Is there a primitive arithmetic utilized by this spreading?

I do not have definitive answers to these, or the more specific question, “what precisely is the language of the genetic code?” More data is needed. However, I feel that this symbol translation will be helpful in finding those answers. More importantly, we should begin to recognize the abilities inherent in a dodecahedral system. Not only does a dodecahedron tessellate in a sequential pattern, thus supporting the storage mechanism of a double helix, it also perfectly carries the leverage mechanisms for information translation. Therefore, the dodecahedron is a great choice for both genetic information storage and translation.

## LCA

It is easy to ring a bell, but it is impossible to un-ring a bell. A bell once rung cannot be un-rung; it can keep ringing or it can stop ringing. The same is true for two bells, three bells, a million bells. If a million bells ring at the same time they make a ringing sound unlike any single bell, but the collective phenomenon will be like a single bell in that it cannot be reversed or undone.

A scientist might hear a ringing sound, analyze it, speculate about various properties, and trace the sound to its origin. He can then request that a bell ringer stop ringing his damn bell. This would be a linear process from sound to silence, cause and effect, but what if the ringing was complex? If the ringing had multiple tones, volumes, pulsations, and came from all directions, what linear process could the scientist use to trace the origin of the ringing? In this case the origin of the ringing is probably multiple bells and multiple ringers in multiple places acting throughout time at different intervals. None of the individual bell ringers could draw a comprehensive map of the complex ringing sources, their methods, or their meaning. Perhaps the scientist succeeds in silencing a single ringer, but more will fill his spot once he's gone. The scientist has failed to achieve even the partial goal of his linear process. Each bell ringer can interact with his fellow ringers by hearing and ringing. No additional contact or special instructions are required in order for this system to produce exceptionally complex behavior, music if you will. Because all of the ringers are connected, the system has all sorts of complex properties and abilities that transcend the abilities of a single bell and a single ringer. Trying to understand the entire system in a linear fashion will obscure the total properties of this non-linear system. Cause and effect of the system transcend cause and effect of any single agent. It is a fallacy to equate the single bell phenomenon to the complexity of the multi-bell system.

The concept of a last common ancestor is somewhat like the bell-ringer's fallacy in that it belies the notion that ancestry is somehow a linear process. It is true that we can draw ancestral lines between virtually any organic beings, but doing so is less enlightening, and potentially more blinding than it might first appear. Very few people fail to recognize that humans share ancestry or blood lines, because it is logical to believe that everybody alive today had parents, and their parents had parents and so on. Each person's ancestry spreads out generally by orders of two with each generation, and ancestries overlap. Groups of roughly one to ten people living today share one or both parents, but groups of hundreds share great-great grand parents. Therefore the people living today share ancestors, and the number of shared ancestors must get smaller as we go backward in the ancestry. You cannot share an ancestor at one level and un-share them at the next, so the process will converge moving backward. Call it what you want, Adam, Eve, Last Common Ancestor(s), the ancestry process will converge on two individuals. All of us humans living today has a common ancestor back there somewhere, but so what - how important is that person?

Humans comprise a tiny portion of the biomass on the earth, and the title of Last Common Ancestor is subject to change at a moments notice. It has the

potential to change by many orders of magnitude, depending on the reference frame. Consider the possibility that there are only three members of a particular species on earth. Let's say we discover that there is a super-human sub-specie of humans, but there are only three members: you, me and another guy (hopefully you are a woman). Suppose that you and I find out we are actually siblings, we have the same dad, and dad had a half-sister that is the mother of the other guy. Our whole family tree is dead except for us three. The Last Common Ancestor (LCA) of the super-human specie is our grandpa, Grandpa LCA, call him Adam, is the champion and titleholder for super-humans. There are only two generations between all living members of the super-human specie and LCA. Suppose the third guy dies, so now the title of LCA passes to our dad, Adam Jr., and the distance between all living members and their LCA has been cut in half. We have a new champion for no particular reason other than some guy we don't even know just died for some possibly random reason (the world is a dangerous place).

Somebody in the human species could die tomorrow and shift the title of human LCA to somebody else way back in time. So what? There were hundreds of millions of "humans" alive at the time of LCA, but there was no way to identify that individual as anything other than a descendant of the previous LCA. Finding the LCA of all human's alive today is interesting and it has its uses, but we must keep it in perspective relative to Life on this planet. Because we logically conclude that a small, highly specialized portion of the biomass today shares a common ancestry, can we also conclude that all biomass can be traced backward to a single cell? Why would we want to?

Let's get even funkier. If LCA's exist for humans then they probably also exist for elephants. All living elephants have a last common ancestor. Suppose your worldview allows you to believe that all mammals alive today have an LCA, the elephant LCA and the human LCA would then also have an LCA, an elephant-human LCA. That individual is probably more interesting than any LCA we've yet imagined here, but consider a single elephant today and call her Fee-Fee. You and Fee-Fee have an LCA, but it is not necessarily the same as the LCA that Fee-Fee and I share, and it almost certainly is not the same as the elephant-human LCA, which is subject to change at a moment's notice. Even our "lines" of descent aren't really lines - they are bushes. Therefore, LCA's are subject to whimsical definitions based on relatively arbitrary criteria. We can ballpark a line, but we can never really draw one, and why would we want to? This is a subtle bias that naturally skews the emphasis to individuals, and we can draw a line between any two individuals so we somehow think that we must. What about plants, insects, bacteria, fungi or viruses?

Another way to attack the problem is to turn it upside-down. If we start with a single organism, you for instance, and begin graphing ancestry, two-by-two, it is easy to see that this graph will undoubtedly expand back into history (some graphs will expand faster than others, i.e. readers in Indiana vs. Kentucky). At some point this graph will reach a maximum expansion, but could it ever expand to include all of the existing biomass on the planet? This is highly unlikely, and it would have to be repeated for every living thing on the planet

today, and the configuration of biomass on this planet has changed through time. It then logically follows that not every living thing descends from the exact same ancestry. We cannot pick a time in history, or a collection of carbon and crown it with the ultimate title of “origin of life”. Life is an assembly of precursors. Our parents were our precursors, and their parents were their precursors. This process will expand, not contract back through time. At any moment in Earth’s history we might view the total collection of carbon as “biomass” and recognize some interesting patterns or properties, but whatever that is, it had atomic and molecular precursors. To somehow imagine that at some level and some time this process were different would be to imagine two different processes, and this would then require a splice between the two processes that does not exist. We can pick milestones or interesting stages, but the origin of life on earth was the origin of the earth. The bell ringer’s fallacy is to try to trace this complex process back to any other single source and draw a line.

Ancestry is not a linear process despite our misguided desire to view it as such. It is a multi-input, multi-output process. Ancestry is a combinatorial network of non-random nodes through time. Some nodes are huge and others are small, but they all must overlap due to the combinatorial nature of the process. Sexual reproduction is now the dominant perpetuating strategy of the combinatorial network, and this exacerbates the illusion of linearity. We have blood “lines” on two sides. None of the nodes are neutral; they all have an impact on their own fate as well as the fate of other nodes. The view that this process is somehow a linear chain of events is the bell ringer’s fallacy that sends us on a fool’s errand of searching for “missing links” in the chain. Rather, we would be better served to hunt for hidden tiles in a continuous mosaic.

Historically all of the nodes are fixed, but as a practical matter they are all transient. All of the nodes are bells that have rung once and can never be un-rung or rung again. At any given time there is a vastly larger collection of organisms that will not produce descendants than those that will. This was the basis of Darwin’s fabulous insight. It follows that any later stage organism in the process will have a vastly larger collection of past relatives than future relatives. Organisms are related to organisms that don’t reproduce as well as those that do. At what time and what level moving backward would this ratio reverse? My answer is that it would not. It is a fundamental property of the process.

Life is a dynamic, ever shifting pattern. The existence of an overall pattern remains relatively constant, but the actual pattern is never the same from one moment to the next. Consider a stationary stick in a moving stream. The surface of the stream may be flat, but the shape of the water around the stick will be something other than flat. This shape will remain constant despite the fact that none of the water making it is constant. The water is perpetually replaced by new water, but the shape of the water around the stick remains. Life is constant, but the pattern of Life is ever changing. We would no more think to trace the origin of the water pattern around the stick to a single water molecule than we would trace the pattern of Life to a single amino acid. There is a constant process and a force behind the water pattern, and so too there is with Life, and this can be the focus of a meaningful search.

Diamond burns to  $\text{CO}_2$  – no ash. Graphite can be burned, and as we know, organic hydrocarbons burn fabulously. What is the meaning of all this burning? Carbon, regardless of its present form, is carbon. The only special property of organic carbon is the pattern it forms across the current and past biomass. It is a fascinating pattern on any scale of size or time, but it is a pattern none-the-less. The carbons that are you have a fabulous story to tell, I'm sure, but it is not the same collection of carbon you were born with. Your carbon is flowing around the pattern that is you as water flows around a stick. Compared to water molecules it seems that carbon flows slowly around us, but compared to the flow of electrons in molecules water flows glacially, and compared to diamond our carbon flows like photons around a Christmas ornament. Think about the pattern that is you and how much it has changed in such a short time. Carbon is entering and leaving the pattern as we speak. Think of how the pattern of carbon changes in your head as you read this sentence, the force of change being the symbols on this page. Think about how much carbon has been added to the pattern. You started as a single cell and now look at you. It is a sure bet that the pattern that is you has never been the same from one nanosecond to the next, and no two patterns will ever repeat.

At the correct level of reference, the same can be said of diamond, but it is far less dramatic. Think about the magnitude of change occurring right now in your body compared to an equivalent mass of diamond. You must maintain two phase transitions at all times: gas to liquid and liquid to solid. If you stop breathing, or stop circulating blood, your carbon pattern will take a drastic turn toward entropy. It is not despite these phase transitions that you exist, it is because of them. They are the fuel behind the engine of change. They are the chaos that feeds the interface with order. Change is the hallmark of Life and carbon patterns are the canvas for change.

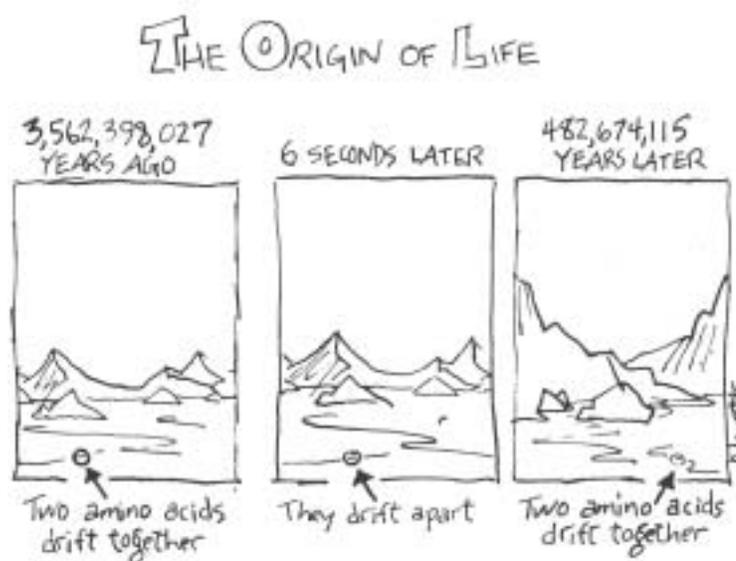


FIGURE 7.1

It is within this framework that any “last common ancestor” explanation of features in the genetic code fails to pass the giggle test. This answer belies a failure to understand the question. We can identify many features of Life that will be common to all forms of life on this planet, but their genetic code is unlikely to be one of them. It is too complex, and simplifying it to a linear, unchanging relationship is not instructive. We could go one level lower and identify DNA and proteins as a common theme to all life, but this is not the same as saying that all life has the exact same relationship between DNA and protein. There are three things here that need to be addressed: DNA, protein, and the relationship between the two. The genetic code is the latter. Starting at the base we could say that all Life is made of matter or atoms. We could say that all Life includes carbon and water and some other contaminants. We can say that nucleotides and amino acids play a role in all Life, but now we are skipping a level. There are patterns of atoms that lead to nucleotides and amino acids, and shapes characterize these patterns. If the relationship between these molecules is to play a central role then the relationship between their shapes must also be addressed. It is precisely this relationship between shapes that allows the progression of molecular complexity to continue. Without that relationship, endless regularity is all that is possible. Without that relationship, addition of atoms will proceed on a relatively ordered basis, and change becomes a monumental problem, not a necessity.

One wonders why LCA is important at all. Debates rage, and thinly veiled name calling is ritualistically indulged. The reason is that LCA is linear God. It is the creator of the universal code and father to all living things. LCA is an axiom of biological evolution, a dogmatic philosophical doctrine. Should it be? Debate about LCA is good, but unfortunately the sides are loaded. The debate is emotionally charged, raging over which God is more palatable – creationist God or linear God. Everyone must have his God, even the atheist, but some are more specific about articulating their God than others. I will not articulate mine here, and I will not discourage another from chasing his own, but I will offer words of caution. Never say or do anything you don't want repeated back to you on the stand (best advice given in med school).

A single cell, or a single molecule, or a single atom as the origin of Life is a complete non-sequitor, a fairy tale without empiric teeth. I ask you, how many condors would it take to perpetuate the species? A condor is a big, durable thing. What chance does a primitive crystal or cell have? What are the chances that anything alive today might be the father of all living things in the future?

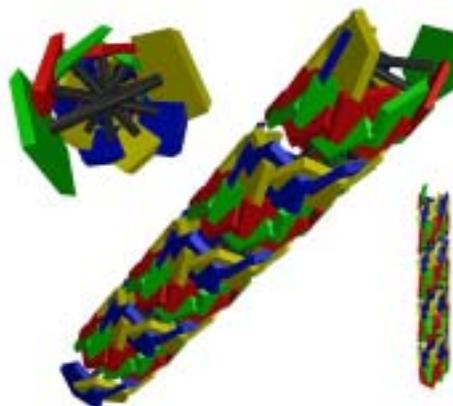
Precursors, precursors, precursors, bazillions and bazillions of precursors. The smaller you go, the more there must be.

Why the insistence on only one? The answer is simple: the genetic code is the lynchpin of an unfathomably complex system. It is highly improbable as a random occurrence, yet random processes are clearly involved. We struggle to imagine how it arises once, and to imagine it arising repeatedly is mathematically

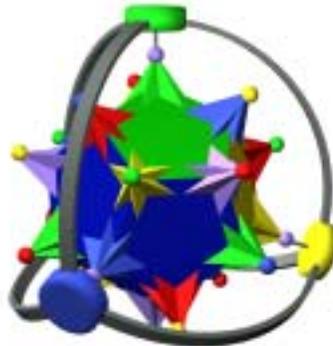
unappealing. The LCA theory holds that the genetic code ONLY HAD TO ARISE ONCE. After the arrival of this single cell God, the rest of the universe must have formed a protective, all respectful cocoon to preserve the gifted one. Life was finally able to flourish in all its glory. The vengeful procreative prowess of the single one was then able to rid the planet of descendants of all fellow molecules, creating a functional imperative that reigns today throughout all cells and all time. This is one talented cell, but after all, it is God - for some.

If the biomass today represents a Circle of Life, then the shape moving backwards in time is a cylinder. Worshippers of an LCA God insist on a cone contracting backwards to a point that represents single-cell LCA. I have problems with this fable on mathematical grounds, and ironically it runs against grain with Darwin's mechanism of natural selection. Darwin's brilliant insight was that Life could not support an expanding cone forward, so a constant force must refine the circle, and the result will be descent with modification. It is the circle that ultimately gets modified, and it is the circle that is subjected to the force. If it is historically a cone, Darwin should predict a backwards expansion, not contraction. I am proposing that we consider reversing fields entirely. Instead of searching for a point in time and space, something that is rare and fragile, let's look for something that is ubiquitous and durable. Through massive numbers and endless time, something interesting can emerge, but it won't be traceable to a single point in space or time.

It is fun and enlightening to extend this exercise of searching for commonalities of Life beyond the confines of our planet. Mike McNeil is enamored with this game. He is intrigued by the idea that we might identify some icon of Life in the universe so that we can create a greeting card. Contact with extraterrestrials will likely start with some form of pattern recognition. We will notice a pattern in electromagnetic radiation that might indicate unmistakable hallmarks of Life, just as we are now broadcasting them. What is the most insightful pattern we could send or receive? There are many good candidates. We could send this:



and the recipient might turn from his receiver and comment to his spouse, “our neighbor carbons on earth just figured out their hard drive.” Mike suggests that we send the following image with the caption, “We get it”.



## Crystal code

DNA is a crystal. It is unusual in that it is a crystal based on dodecahedral symmetry. Dodecahedrons, unlike other symmetries, will only tessellate in one dimension. This oddity allows a dodecahedron to crystallize in a logically sequential fashion; therefore, DNA can act as a seed for the sequential formation of other crystals.

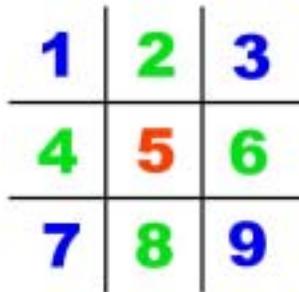
Typically a seed crystal exhibits two properties in the process of seeding growth of a crystal. First, seed crystals usually become embedded within the crystalline structure whose growth they seed. Second, the crystal growth that is stimulated by the seed is of a uniform type. DNA is an aberration on both of these counts. It neither becomes embedded, nor does it seed a single symmetry of crystal growth. By not becoming embedded in the crystal growth DNA is able to repeatedly seed numerous crystals. By having seed properties of multiple symmetries DNA is able to direct its own replication, as well as the growth of alternate symmetry forms, such as proteins. The relationship between the symmetry of DNA and its alternate seeded crystal forms is the foundation of the logic in the genetic code.

It is hubris to expect our neighbors to share our love of carbon, but it is not a bad guess. It is statistically feasible that Life exists everywhere in the universe, and at some level there are likely similarities between Life here and anywhere. Shape is the most likely jumping off point. Carbon is the most likely next level up in complexity, but silicon has got to be attractive to somebody somewhere. We must first ask about the constraints, and our imaginations currently constrain us to molecules, which are themselves constrained by shapes. If anything becomes constrained to lines, it will not be a line of points, it will be a line of shapes. The “line” in the process is better viewed in this light as a sequence. Both the constraint of shape and the constraint of sequence have something to offer to the process. Something more robust can emerge from them.

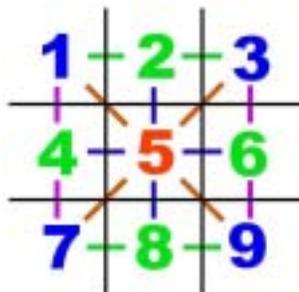
It is ironic that we began to explore the potential for silicon Life on this planet in the 50's and 60's, about the same time that we “broke” the genetic code. Each influenced the other, and not necessarily in a productive way. We became resigned to the idea that computers would lead to an “electronic brain” in no time flat. It was seemingly just a matter of brute force, but it didn't work out that way. It appears that the linearity of binary logic was a serious impediment to simulating Life-like behavior in silicon, and the ability to hard wire pathways of logic is not all that and a bag of chips. We now have more sophisticated tools that turn on concepts of “fuzzy logic”. Agent-based systems of dynamic logic networks have proven that machine learning is a viable destination. Complexity can in fact emerge from simplicity in silicon, and progress is relatively rapid, but the transcendence of matter into mind has proven more complicated than imagined. Odds are good that the ultimate path will in no way appear linear.

Progress made in artificial life should be applied to our study of traditional biology. In the realm of a-life there is no room for meaningless codes, frozen accidents and single-agent systems - the three horsemen of the “one-dimensional” paradigm of the genetic code. Dr. Morowitz described to me the term “frozen accident” as a dirty word. He says that it is an intellectual copout, and I couldn't agree more – it is the f-word. It displaces necessary intellectual work in favor of a comfortable fairy tale. The result has been a preference for theories of pan-spermia, because they focus questions of earth's origin of Life to pinpoint locations in time and space; whereas all such questions are better considered in the context of networks.

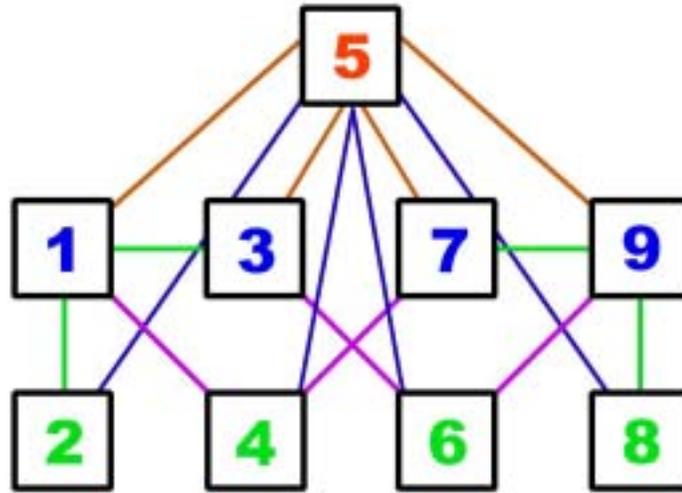
To illustrate this I will share an experience I had in programming a machine learning game of tic-tac-toe with my young son. The first step was to break the game board into addressable cells.



The next step was to define all possible ways to win a game.



We then defined all of the cells in terms of their winning possibilities.



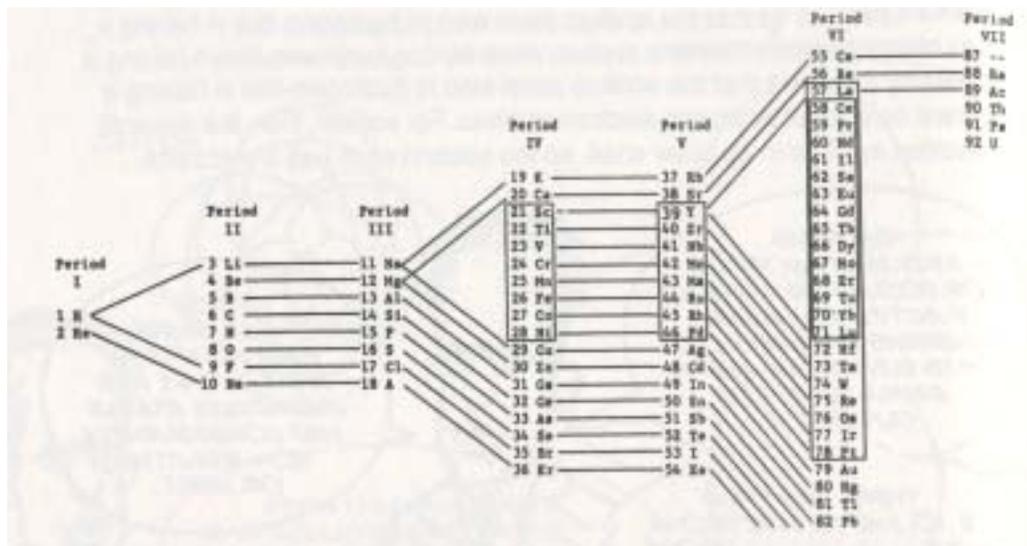
This provides a graph of the network of all winning games of tic-tac-toe games. No single cell has a corner on the market for winning, and no possible winning play can involve only one cell. This first struck me as a map of winning strategies in business. My friend, John Bender, is a master entrepreneur, and he preaches this doctrine about business. He describes it in terms of self-interest. If the goal is winning, then your self-interest lies in helping other people win. If cell "5" is the leader of a business, the only way he can win is by participating in a winning effort that involves other cells, such as employees, suppliers, and customers. Then it struck me that it might be a universal pattern of competition. It is hard to imagine any competitive endeavor that involves a single-cell winner. This is nowhere truer than in the competitive pattern of Life. Winners are actually vast networks of winners, not individual winners. The fierce competition for survival is marked by a pattern of networks.

- Symmetry → networked
- Carbon → networked
- Nucleotides → networked
- Codons → networked
- tRNA → networked
- Amino acids → networked
- Peptide bonds → networked
- Proteins → networked
- Cells → networked
- Organisms → networked
- Species → networked
- Life → networked

In this light the genetic code within organic evolution becomes a network of networks. Winners are not chosen on an individual basis, rather they are chosen on their properties within the total network. There is no way to carve a component from the network and study it in a vacuum.

The problem now is in defining “self” so that self-interest can be evaluated. Richard Dawkins brought the problem to a head in his book “The Selfish Gene.” He suggests that the appropriate scale for the question of self-interest lies at the gene level. I would go one further and suggest that it lies at the code level. Regardless, the question pre-supposes that the universe has the ability to operate on a “self”. Of course we know that it does, but an undifferentiated universe would not have this ability, so differentiation must be the first step in this process. In the tic-tac-toe universe, each cell can be identified as self in terms of a meta-level called “player”. Each cell can be defined as either player or not-player. If it is not-player then it is either “competitor” or it is nothing. It is a simple trinary system of valuation to hold a simple competition. We humans have the curious ability to identify ourselves as self, and this identity persists through time. The universe therefore has a property that allows a persistence of self. We go on to identify with family, community, nation, species, etc. This is interesting on a human level, but it is more so on the level of a hydrogen atom, or on a macromolecular level, or on the level of a body of collective mass such as the earth, sun or solar system. Without this persistent differentiation in the universe nothing of interest would emerge.

Emergence is a phenomenon of networks, not individuals. Individuals are required to form the networks, but individuals are not competitive entities without the networks. When one network emerges, it serves as the basis of the emergence of more networks. We then find an accumulation of emergences. Human thought then is predicated on the emergence of biological neural networks, a point beautifully demonstrated by Morowitz in *The Emergence of Everything*. Just as organic evolution is marked by networks, so too is the physical universe. It was this type of discovery by Neils Bohr in the periodic table of elements that marked the spectacular advances in quantum chemistry.



Bohr typed out a fractal nesting of individual elements into a periodic network of elements. The lynchpin of the network is the set of quantum numbers and Pauli's observation that no two components (electrons) within an individual (atom) could share the same identity, in this way giving matter its informative value. An electron is an electron, but within an atom they are all distinguishable by some metric. Each electron attains a unique value of self.

These then are the two principle ingredients (in my book) for the existence of Life in the universe – self and emergence. The universe provides these ingredients from the get go, and the rest is history. Without this perspective we seem content to search for historic winners of single-cell games of chance. I see the pattern differently. Just as winners of tic-tac-toe emerge from networks of winning components, Life emerges from huge networks of winning networks. A one-dimensional paradigm that views the process as fundamentally without logic will never properly illuminate this process. We then are left resorting to creationist stories of space rocks kick-starting a “frozen accident” here on earth. This only displaces the intellectual work of understanding to another time and another planet.

## Concluding

This has been fun, but all good things must end. I have taken a decidedly non-linear path to the end, and I'm sure this has led to some confusion. It always does. Allow me to wrap up some of this mess.

“Science is really the search for simplicity.”

Claude A. Villet

Science operates by adopting paradigms. These paradigms lead scientists in specific directions in their searches for empirical evidence of phenomena within their fields of expertise. Most often evidence accumulates in a pattern at odds in some way with the accepted paradigm. Eventually this creates a crisis of explanatory power for the paradigm. When this happens, a revolution must occur, and a new paradigm is adopted. It is always a messy, unpleasant business.

The eagerness to adopt a “one-dimensional” paradigm of the genetic code should have created an immediate crisis, but it did not. It was, in the parlance of OJ, a rush to judgement, and scientists have happily accumulated a mountain of contradictions over the past several decades. In this day and age, when we are so open to the importance of emergence in nature, it is time that we explicitly address the lack of explanatory power offered by the one-dimensional paradigm.

The first red flag should have been wobble - and when wobble proved incapable of effectively limiting a tRNA population below sixty-four, the crisis should have become acute. From there, we can easily find a drawer full of anomalies that cannot be adequately handled by the linear model. Why only twenty amino acids? Why all L-amino acids? Why is there so little variation in a process that is clearly capable of change? What is the inherent logic that allows such precision, diversity and consistency in translating a double helix into a protein?

Moving from the general anomalies of the non-specialist to the specific anomalies in cutting edge molecular biology, today we find the crisis growing ever bigger. The linear model is worse than useless in explaining the following.

### Empiric Observations

1. Synonymous codons are not always functionally synonymous.
2. Codons require context.
3. Some codon combinations cannot be translated within a genome.
4. GC content drives codon usage.
5. Codons can disappear entirely from genomes.
6. tRNA populations vary between genomes.
7. Codon usage and tRNA expression is correlated.
8. Codons can specify more than one tRNA within a genome.
9. One tRNA can recognize more than one codon.

10. tRNA molecules are not homogenous within or between genomes.
11. Xenogenetic sequences produce translation difficulties.
12. Synonymous mutations can alleviate xenogenetic translation difficulties.
13. Primary structure determines tertiary structure in proteins.
14. Primary sequence analysis has failed to accurately predict secondary structure.

It usually takes a child to note the emperor's lack of apparel, and a reckless heretic to insight a revolution. The failure of the linear model can be attributed to a fundamental flaw: it denies the need for context. It is not just blind to the context of codons, it is blind to the context of everything. The fundamental tenet of Rafiki is a need for context, and the fundamental context of the genetic code is the dodecahedron - all other features must be evaluated within it. Similarly, all features of the universe manifest as patterns, and all patterns are products of their context, which is itself a pattern. Of course this viewpoint makes some simple things much less intuitive, but that is the nature of nature. What could be simpler for our terrestrial purposes than a stationary earth? But this turns out to not be the case. What could be simpler than a one-dimensional code? Not just a clever comparison of two historical paradigms; this is a demonstration of the same historical mistake. The one-dimensional paradigm causes faulty data collection and interpretation of the genetic code exactly like a stationary earth paradigm forces our view of the heavens. Prior to Copernicus, it wasn't so much a question of whether or not the earth was actually moving; it was more a question of whether the earth could be used as a fixed reference. The answer is no. Heavens and earth are mutual contexts, just as every component of the genetic code is a context for every other component within the logic of the code.

There is undoubtedly a loss of simplicity. As an illustration we can see that ordinary arithmetic becomes ponderous within the context of a dodecahedron. The simple case of calculating "potential" codons in a linear model ( $4 \times 4 \times 4 = 64$ ) becomes an exercise in metaphysics within the dodecahedron. Harking back to the thought experiment involving the drawing of three colored chips from a bag containing three sets of four colors, we can attempt to calculate codons. We get a perplexing result. The first chip drawn could be any of the twelve in the bag. However, even after it is drawn we cannot know its exact identity, other than its color. The second chip could be any chip that contacts any of the faces that "might" represent the first chip. This excludes three of the remaining eleven chips. The third chip could be any of the four colors. This means that within the context of the dodecahedron there are  $12 \times 8 \times 4 = 384$  number of ways to draw three chips from the bag. Coincidentally, this is exactly twice the number of nucleic acids required to fully illustrate the linear model. As if this is not bizarre enough, even after the drawing we still do not necessarily know the exact identity of the three chips, unless they are all different colors. The drawing itself requires the context of prior and subsequent drawings to precisely determine its outcome.

Subtle changes in the premises of the thought experiment have a chaotic impact on the results. This is why it is not possible, for me at least, to make

definitive pronouncements about the exact structure and mechanisms of the language. I am confident, however, when I proclaim that there is more than one dimension of information contained in the code. This should have been obvious just by looking at data that has been around a long time. However, a paradigm can be a powerful lens, or it can be a powerful fog when looking at data.

Every component of the genetic code requires context from, and provides context to every other component. Just as in drawing chips, no single component, such as a single nucleotide, or a single codon, or a single amino acid, can be removed from its context and accurately interpreted. There are no absolutely stationary bodies in the solar system of genetic information. The system must be viewed as a whole to appreciate the patterns it makes and the logic behind it. There must be some sort of logic behind it; otherwise, it could never arise in the first place, let alone perform its magic so consistently. The Rafiki Model easily handles the simple anomalies in the linear model. More exciting, it generates so many new questions that science can keep busy for a while in vetting it. Some of the more difficult questions, if they are to be answered to anyone's satisfaction, will require more powerful, certainly more bizarre tools, such as quantum geometry. On this score particle physicists have spent the last decade using super-symmetry to peel a layer of "meaningless" from the one-dimensional onion. They have successfully caught a glimpse of the underlying logic and gone so far as to call for a periodic table of assignments. Rafiki goes farther. Rafiki demands a search for relevant context, whereas the one-dimensional paradigm demands that context cannot exist - it effectively halts all relevant searches. We can never be clear on exactly what the context is for all things, but within Rafiki the fundamental context for the genetic code is a dodecahedron. On this we can be clear.

"Although I am fully convinced of the truth of the views given in this volume..., I by no means expect to convince experienced naturalists whose minds are stocked with a multitude of facts all viewed during a long course of years, from a point of view directly opposite mine. ...(B)ut I look with confidence to the future – to young and rising naturalists, who will be able to view both sides of the question with impartiality."

Charles Darwin  
Origin of Species

To paraphrase Norbert Weiner, I am not a mathematician. I am also not a scientist. I am a heretic and a troublemaker. It is my job to make trouble, my stock and trade. There are millions of working scientists who have been given splitting headaches by my musings; otherwise I have failed to do my job. My intent is to give normal people permission to be creative in their approach to critical thinking about the things around us. I ask them to ask questions, and create their own poetry about the universe. I am an artist working in the medium of the mind. I have set out to sculpt this malleable metal in a new, hopefully

interesting shape. The tools of my trade are questions, not answers, and on that score I will ask the following:

- Can the genetic code carry stereochemistry?
- How might the genetic code carry stereochemistry?
- Does the genetic code carry stereochemistry?
- What ramifications do the answers to the above questions pose?

As far as I can tell, the first question rarely if ever gets asked; therefore the rest are moot. The answer to question number one is always a dogmatic, “no” - end of debate. Sorry, but my view says that it not only *could*, but it *should* have a say in the stereochemistry of Life.

A reasonable answer to the second question can be partially given by the observation that the “best” way to view the genetic code - in a numerically unbiased way - is on the surface of a regular solid, or better yet, a sphere.

The third question requires beakers, and messes, and work, but the fourth question is where we can have some fun.

Talk amongst yourselves.

I summarize my answers as follows:

The genetic code is part of a complex crystallization process that we call Life. The currently accepted linear model holds that the genetic code is a one-dimensional, sequential, non-overlapping relationship between nucleic acids and amino acids. This model has proven insufficient in explaining the multi-dimensional process of translation between nucleic acids and amino acids. An alternative to the linear model proposed here, the Rafiki Model of the genetic code, differs from the currently accepted one in three important ways.

1. The genetic code embodies two fundamental forms of information regarding translation. First, it carries information about the stereochemistry of peptide bonds. Second, it carries amino acid sequence information.

The primary structure of a polypeptide results from the information contained in the genetic code. The amino acid sequence of a polypeptide is merely a sub-set of the total information translated from the nucleic acid sequence.

2. The genetic code has a geometric foundation of coincident symmetry from all five regular solids. Information in this system is based primarily on the symmetry relationships between the tetrahedron and the dodecahedron.

Erwin Schrödinger proposed that Life is an aperiodic crystal. He was essentially correct, but every repeatable crystal structure requires a simple, repeatable symmetry to enable consistent construction of molecular

morphology. Aperiodic crystals are by definition not constructed on repeating symmetry, and therefore a simple map directing consistent morphology is difficult to imagine. However, a map of the symmetry relationship between solids can generate tremendous complexity, and for all practical purposes this relationship functions in a simple, aperiodic way.

The genetic code is based on the interaction of symmetries, essentially mapping the relationships between them. The genetic language is a language of shapes, primarily translating dodecahedrons into tetrahedrons.

3. The genetic code is a hierarchical system of combinatorial, molecular elements. Nucleic acids are the base element in the system. These combine in triplets (codons) to specify a tRNA molecule. The tRNA molecules combine, presumably in quartets (peptons), to define a peptide bond. Peptide bonds combine to define the primary structure of proteins.

The primary sequence of proteins can be determined by examining either the primary structure of polypeptides or the sequence of nucleic acids, but the peptide bonds cannot be determined by examining nucleic acid sequence alone. Only by examining the combination of tRNA molecules in a pepton can the precise peptide bond be determined from the code.

Therefore, the complete genetic code in an organism is a system that must conceptually include mRNA and tRNA. Ribosomal RNA participates by providing a structural base for mRNA during translation, as well as providing the enzymatic activity of peptide bond formation. In this way rRNA might be viewed as an active voice in the genetic code as well. A protein's primary structure is the fundamental output of the genetic code, and amino acids are the monomeric units of that output.

Rafiki assimilates these new conceptual elements into a model of the genetic code. This model provides a more robust and accurate understanding of the complex crystallization process we know as Life. From this perspective, we can recognize that variation in the nature of tRNA populations from one organism to another naturally occurs, and therefore the system is no longer constrained to universality. The relationships between regular solids, however, are universal.

The Rafiki Model **helps** explain many of the perplexing phenomena being discovered today at an ever-accelerating pace, phenomena that cannot be explained adequately by the linear model.

## After word

“Modern physics will prove that an elephant can hang from a cliff with his tail tied to a daisy.”

Oliver Stone  
JFK

Michael Crichton is an excellent author who writes fictional stories about real science. *Jurassic Park* is about chaos, and *Prey* is about emergence. These are both important scientific tools for building models about the natural world. The villain in both of Crichton’s stories is the same as the villain in Mary Shelly’s *Frankenstein*. It is not a person, and it is not even the monster; the villain is scientific hubris. The real hubris is not about our ability to apply technology, it is about universal truths and our ability to discover them. The universe is constructed in a way that shuns simple systems, but we are limited to understanding the universe by first constructing simple models. Our models will always take us only so far toward understanding, and our ability to predict and control systems will always be limited. Crichton’s process for building a monster in *Prey* is a dead-nuts ringer for the process that is building the genetic code.

Question #71 How do you determine the height of a building using a barometer?

- A) Take barometric pressure readings at base and top, and do complicated math.
- B) Drop the barometer from the top of the building, time its fall, and do complicated math.
- C) Remove the recording tape from the barometer and use it as a tape measure.
- D) Offer the architect of the building a nice barometer if he will tell you the height of the building.

The “correct” answer is completely dependant on the context of the question. Is this a test in meteorology or business? What are the accuracy requirements and time constraints? How nearby is the architect, and what is the e-bay value of the barometer? We must model the system of the questioner and the system being questioned. (How would you like to have me in one of your classes?)

I am told that we are “reasonably certain” about the sequence of events after the first  $10^{-35}$  of a second following the big bang. I’m reasonably sure that we are - but hell - I’m not reasonably certain about what I had for lunch yesterday. The folks expressing their certainty about this alchemy look remarkably like the people who were reasonably certain that the earth is stationary. Most models are dubious representations of reality, and when they propose linear events across vast time and space they become more so. The primary culprit is our language, or our system of numbers and how they are used.

While our mathematics is far advanced from the ancient Greeks, our appreciation of the nature of numbers is still primitive. We can learn something from everyone, and we might glean a thing or two from the ancient Greeks as well. Our best models are dependent on numbers, and they will always be overly simplistic.

“In 1931 the mathematician Kurt Godel proved his famous incompleteness theorem about the nature of mathematics. The theorem states that within any formal system of axioms, such as present-day mathematics, questions always persist that can neither be proved nor disproved on the basis of the axioms that define the system. In other words, Godel showed that there are problems that cannot be solved by any set of rules or procedures.

Godel's theorem set fundamental limits on mathematics. It came as a great shock to the scientific community, since it overthrew the widespread belief that mathematics was a coherent and complete system based on a single logical foundation. Godel's theorem, Heisenberg's uncertainty principle, and the practical impossibility of following the evolution of even a deterministic system that becomes chaotic, form a core set of limitations to scientific knowledge that only came to be appreciated during the twentieth century.”

Steven Hawking  
The Universe in a Nutshell

Blaise Pascal was a brilliant mathematician that intuited what Godel proved. Pascal recognized that his most cherished skills and models were incapable of giving him the answers to his most important questions. When his questions turned to God, he avoided the trap of hubris. He knew that God, if he exists, is a force of nature incapable of yielding to any model Pascal could contrive. So Pascal found an elegant solution in which he posed for himself a wager. Smart money bets on God, according to Pascal. For him the wager paid off, because he was then able to appreciate his life all the more. Not everyone can do this. I suffer from a lack of Pascal's intelligence, but I always like to bet with smart money.

This is not an anti-science diatribe; it is science revelry. Science is a systematic investigation, and it has the inherent capacity to change its models. It is based on the premise that models are never “right” they are just good or bad depending on the context. They can be useful or not. The worst models are not the ones that are wrong, they are the ones that cannot be wrong. As Pauli noted about a model proposed by Heisenburg, “that's so bad it's not even wrong.” Hawking takes a positivist approach on this that I find most enlightening. We do not have to abandon science because of its limitations; we can embrace it. Crichton correctly warns us, however, to carefully examine the questions, methods, interpretations and applications of the fruits of science. By now we should realize that each new step leads to a new direction.

What does the pattern of Life have to say about all this?

**Universe**  
**String**  
**Quark**  
**Sub-Atomic Particle**  
**Atom**  
**Molecule**  
**Macromolecule**  
**Life**  
**Thought**  
**Universe**

I can't really say, but it should be a powerful voice in the debate. In the universal progression of complexity, Life is not an isolated exception. If it is indeed a specific case of a general rule, then it should not be specially exempted from the processes of the rest of the universe. Life is not a single, fragile entity focused to a point in time and space, it is a ubiquitous, durable, agent-based system spread across vast areas of time and space. Our view of the universe must decide if Life is the exception or the rule. If there is indeed a line in the universe across which Life can be compartmentalized, then we must identify that line. If not, then perhaps the process of Life can be used as the model of the universe, and vice-versa. Perhaps the universe is an agent-based system, and the agents of the universe are the same or similar to the agents of Life. Perhaps the SORT function we visited earlier is acting as some universal force that organizes and complexifies the universe.

**SORT( FILL(universe) ) = UNIVERSE**

Agent-based systems are necessarily complex. The king of complexity is Stuart Kaufman. He has proposed a fourth law of thermodynamics that would provide a metric for time and complexity in the universe (atta boy). He does a nice job of differentiating this new law from the second law of thermodynamics, which essentially says that the universe is steadily going to disorganized crap. The process of Life appears to be at odds with the second law, so Dr. Kaufman is respectful of this. I am not very respectful of anything, so I say trash the second law – that's my job. I never liked that law anyway. If the agents of life are a clue to the agents of the universe, then perhaps we can imagine a model where the two act in the same fashion. In this model a self-organized, complex universe would emerge, and the second law would look different. Instead of velocity of entropy, it would reflect a force producing acceleration of self-organizing complexity. What name could we give this force? We could find evidence, I'm sure, if we had the right light and knew where to look. Perhaps the universe hardens instead of expands. This, at least, I will leave to the experts.

## Finally

“The human mind is not capable of grasping the Universe. We are like a little child entering a huge library. ...The child knows that someone must have written those books. It does not know who or how.”

Albert Einstein

History is riddled with entertaining pronouncements of scientific finality. We are constantly told that all answers are within our grasp, or close at hand. The data suggest otherwise. In fact, the more we learn, the more there is to learn, which is nice in my opinion. The process keeps us very busy, as well it should. Rafiki does not hold the ultimate answer. It cannot because of the nature of the questions, nothing can. Rafiki is an interesting, shiny seashell. It might attract our attention, briefly, but we must not lose sight of the beaches and oceans they meet. The universe is big, beautiful, and remarkably complex; in it we are bounded only by our imagination.

Imagination is more important than knowledge

Albert Einstein