The Crystal Concept of Genetic Information

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Definition:

Life on Earth represents a single crystal system that has been growing and evolving on Earth's surface since its formation. The universal laws of this system are based in chemistry, which are themselves successively based in physics, mathematics and logic.

The genetic code is a set of logical relationships based in spatial symmetries through time. By executing this code over a long period of time, the molecules of Earth have generated and accumulated information via an iterative process of competitive learning known as Natural Selection.

The molecular sets we now recognize as the codon table reflect these laws and this process, but they are a thing entirely separate from them, and many things more than just codons and amino acids. They are not merely products of this process; they are active participants that elaborate on the process in space through time. They participate in the generation of yet more molecular sets that also generate and accumulate information, and this too represents whole new related sets of logical relationships in space through time – new codes.

Current concepts in Geochemistry and Biochemistry are necessary but inadequate for understanding either of these two disciplines fully, and there is no current general concept that logically ties the two together. The Crystal Concept of Genetic Information bridges this gap.

Explanation:

The above is a basic definition of the concept to be further explained, developed and explored. It was born of a simple idea, but I mistakenly believed at first that it implied a simple concept. In reality, it is not a single, simple idea; it is a collection of simple ideas that all go toward a concept that is unfathomably difficult. It is a general concept that is difficult to define, explain, understand, develop and explore. It might ultimately prove to be the most difficult concept in all of human thinking; however, it is a logically valid concept with many obvious and important epistemic and pragmatic consequences.

As I explored this concept, I discovered many things. Mainly, I discovered the gaping conceptual chasm that exists between basic concepts in Geochemistry and Biochemistry today. Not only does this gap obviously exist, it is fortified and exacerbated by the natural thoughts and languages used in pursuit of these separate disciplines today. The Crystal Concept of Genetic Information (CCGI) is intended to bridge that conceptual gap. The bridge will need to be built from the bottom up, borrowing not just ideas and languages from both, but from a broad range of other intellectual disciplines as well. Once built, this bridge will not only take from all of these disciplines, but it will give back handsomely to them as well.

I will attempt to explain this concept in more detail, and it is helpful to begin this explanation with a listing of the simple ideas that go toward creation of the larger concept. They will serve as general principles to guide the process. Each of these ideas contains many concepts that also will require elaboration and development. The Principles are not presented in order of simplicity or importance, or in the order of discovery. They are presented in a simple, logical order that might allow each to build upon the others, culminating in the creation of a basic rendering of the general concept in full. The full concept is understood to be not fully developed, but merely positioned in such a way that it can be further understood, explained, explored and developed. It is a start point, not an end point.

List of Principles:

1. The necessary concepts are based in logic, but all necessary ideas and vocabularies are yet to exist.

2. They depend both on simplicity and complexity.

3. They depend on basic concepts of Information.

4. Information depends on basic notions of logic, space and time.

5. They depend on Natural Selection.

6. Concepts of Biochemistry are necessary but not adequate.

7. Concepts of Geochemistry are necessary but not adequate.

8. Atoms "compete" within crystals.

9. Past crystal behavior determines future crystal behavior.

10. Paleo-chemistry illuminates contemporary biochemistry.

11. The genetic code represents at least two entirely different things.

12. The genetic code illuminates past, present and future biochemistry.

I will now explain each of these principles in more detail, trying to keep it as brief as possible, yet giving enough detail to each so that the general argument can be made clear.

Principle 1:
The necessary concepts are based in logic, but all necessary ideas and vocabularies are yet to exist.

The Crystal Concept of Genetic Information was developed by me in a virtual ideological vacuum. I do not have the resources or ability to define, explain and develop this concept beyond a primitive level. It requires a language that simply does not exist. It requires words and ideas that either do not yet exist, or do exist and their meanings need to be more precisely defined to suit the needs of this concept. It must borrow from existing languages that are either incomplete or ill-suited for this purpose.

I have made every attempt to base this concept and the argument for its further development in the language of simple logic. As with any concept or argument, if a premise or conclusion is false, then the concept or argument will fail.

I will therefore define and label some of the simpler arguments so that they can be referenced as the description of the general concept is built. I will label each argument with a capital letter, and label each statement of the argument with a number. Hopefully, this will facilitate explanations and future debate.

Argument A

1. There is a conceptual gap between existing concepts in Geochemistry and Biochemistry.

2. The gap can be bridged.

3. The Crystal Concept of Genetic Information (CCGI) logically bridges that gap.

Argument B

1. Logic and information represent a fundamental, universal binary existence. In other words, each can only exist in the presence of the other. There is no logic without information, and there is no information without logic. Logic and information represent two different things whose existence is mutually dependent.

2. Logic and information exist in space and time.

3. Molecular information is a form of information that must involve components of both space and time.

4. Genetic information is - at least in part - a form of molecular information.

Argument C

1. Logic is the foundation of all valid concepts, languages and arguments.

2. Mathematics provides basic ideas, concepts and languages based in logic.

3. Any understanding of physics is based on mathematics.

4. Our concept of modern chemistry is based on quantum physics.

5. Geochemistry is a logical subset of all chemistry.

6. Biochemistry is a logical subset of geochemistry.

Argument D

1. We can call any set of rules and logic that leads to the formation of a thing a code of that thing, or perhaps a genetic code.

2. Our understanding of the genetic code of atoms is embodied in the periodic table of elements.

3. There are rules of logic operating in space and time that allow interactions between atoms to form molecules, or what we can call a genetic code of molecules.

4. As molecules form, they will bring with them new rules of logic operating in space and time that allow interactions between molecules, which then form more molecules. Therefore, there are progressively more complex genetic codes of molecules.

5. There are specific genetic codes of molecular behavior. They depend upon the specific molecules and the specific circumstances of their relationships. These codes become more specific and complex as the molecules become more specific and complex.

6. As sets of molecules change, the specific rules governing their behavior changes with them.

7. The rules that lead to the formation of molecules and molecular sets can remain the same, even as the rules governing the behavior of the sets can change. **This is a key concept.**

8. The rules that generate molecular sets and the rules that govern their behavior will be different sets of rules. Despite this, they can share common elements of basic logic in space and time.

9. The periodic table of elements is the logical foundation of all genetic codes of molecules. Each molecular code built from this will always be more specific and more complex than the codes below them.

10. Our current understanding of the genetic code of molecules in protein synthesis is embodied, in part, in the codon table.

11. A codon table can reflect both the rules of its formation, and the rules governing its behavior simultaneously.

Argument E

1. We can know the chemistry of Earth's core, surface, and atmosphere as it might have been before Life existed on Earth. We can call this Paleo-Chemistry.

2. We can know the chemistry of Earth's core, surface, and atmosphere as it is today. We can call this Geochemistry.

3. There are many known, simple differences between Paleo-Chemistry and Geochemisty.

4. The known differences between Geochemistry and Paleo-Chemistry can be broadly attributed to the processes of Life, which we can call Biochemistry.

5. The processes of Life must first act on Paleo-Chemistry to produce Biochemistry.

Argument F

1. The codon table has been empirically established as representing a valid relationship between a set of codons and a set of amino acids.

2. There are a set of numerical relationships within the codon table.

3. The molecules that execute the genetic code have been empirically established to have certain geometric features.

4. Sequential languages for DNA replication and protein synthesis have been empirically established.

5. DNA replication is a base 4 language.

6. Protein synthesis is a base 4 to base 20 language.

7. DNA replication and protein synthesis both represent sequential changes of molecules in space through time.

8. A perfect dodecahedron represents a logical set of spatial symmetries.

9. A perfect cube represents a logical set of spatial symmetries.

10. A perfect tetrahedron represents a logical set of spatial symmetries.

11. The tetrahedron is a logical subset of the cube, and the cube is a logical subset of the dodecahedron.

12. These spatial symmetries are reflected in a large set of numeric relationships.

13. These relationships can be sequentially linked.

14. The numeric relationships can be used to form a base 4 language that reflects the logical change in spatial relationships through time.

15. The logical relationships of spatial symmetry are perfectly coincident with the empiric facts of Biochemisty – on every conceivable metric.

16. The coincidence could represent cause and effect, or not.

17. If there is cause and effect, the spatial relationships must be the cause, because they cannot be the effect. They are objective, and the object is clearly stated – it is a perfect dodecahedron.

18. The coincidence is too great to not represent cause and effect.

19. The logical spatial relationships in space through time are the cause of the known empiric facts of Biochemistry.

This list of simpler arguments has now been stated so that they might be further elaborated, understood and debated. I will reference them as I advance through the explanation of the general concept.

Principle 2:
The concepts within CCGI depend both on simplicity and complexity.

One must often hold mutually opposing views simultaneously. CCGI requires that one simultaneously understand the simplicity and complexity of genetic information. It is imperative that the two not be confused, and that the appropriate view is applied in every particular instance.

There is plenty of precedence for this dual concept between simplicity and complexity. Perhaps the best precedent in science is our current understanding of an electron. It must be seen both as a particle and a wave. When we see it as a particle; it is a particle. When we see it as a wave; it is a wave.

The initial model of the atom was built by Niels Bohr. He first viewed an electron as a particle orbiting a nucleus. This led to a relatively simple model of the atom that was useful for certain things, but it failed in other necessary uses.

The model was made more complex by Schrödinger, Heisenberg and Pauli, who all contributed to building a wave model of the atom. The new model was more difficult to conceptualize, but it was more useful. Elements of the simpler model were incorporated and remain conceptually useful, but the complex wave model has now supplanted it.

A similar analogy can be drawn from modern law. The United States of America is a system of laws. The United States Constitution is the genitor of that system and those laws. The Constitution itself is not a law, but a system that generates not just the laws but the actors and institutions that organize, create and execute those laws. Although the Constitution itself can be amended, it remains unchanging in its essence. The actual actors, institutions, and laws are in constant flux. New actors bring new laws with them. The Constitution is simple and unchanging, but the system of laws it spawned is complex and in constant flux.

These analogies speak directly to the current general concepts regarding genetic information, and specifically regarding the genetic code. The initial model is far too simple, and it is now failing in simple and obvious ways. It is a particle view where a wave view is obviously required. It has corrupted the very language used to describe it and the things it is used to describe. It is impossible to have a proper understanding of the genetic code and genetic information by starting with a demonstrably false premise of total simplicity.

The genetic code and genetic information can be made simple in one way, to be sure, but it will always need to be understood from a view of total complexity. There is perhaps nothing more complex in the entire universe, save for the universe itself.

Principle 3:
The core concepts of CCGI depend on an essential understanding of Information.

This is an expansion of Arguments B and D.

It is impossible to have any logical discussion about genetic information without a basic understanding of information.

I believe that at bottom all information involves the existence of logic. Our current understanding of information in its many forms always requires a notion of quantity, and then the notion of making a choice from that quantity. The choice requires some form of logic, and so the choice contains and quantifies that logic in some way. This is what we call information.

In a very simple example, I have two apples and ask you which one you want. You point to one based on your logic for making that choice. I hand you the apple. This represents "one bit" of information, it contains one bit of logic, and it results in an action – me giving you an apple.

Information and logic are rarely this simple or clear, but no matter how vague or complex the concept might become, we simply must have an understanding of information, a precise definition for it, and words to describe it before we begin a discussion of a genetic code in particular, and genetic information in general. The codon table is merely a specific instance of molecular information. Molecular information is a more general concept within the yet more general concept of genetic information - which is precisely the point made in Argument D.

We currently have no working definition for molecular information, so all discussions about molecular information and the genetic code are inherently meaningless today. The discussions originated on a false conclusion taken to be a valid premise. The conclusion was that molecular information is one-dimensional, and so the language and arguments are now non sequiturs based on our knowledge that this conclusion is indeed false. They no longer advance valid arguments; they simply and logically preclude them.

Principle 4:
Information depends on basic notions of logic, space and time.

This is a further expansion of Argument B. And it perhaps can be seen as a separate argument, one that is also essential to CCGI.

This principle is being universally ignored in Biochemistry today. The consequences are epistemically and pragmatically devastating. The simple logical fact is that molecular information can never be based solely on spatial components. Without a time component, all concepts of molecular information are incomplete, and arguments about them within the time context of their formation and function are meaningless. It is imperative that this be understood.

Virtually all concepts of molecular information in Biochemistry today lack a time component. For instance, ideas about protein formation via the codon table omit a time component. However, the codon table is translated on a time scale, and information about that scale is transferred through it. Additionally, the codon table was formed on a time scale, and molecular information in stored by it. The spatial component is equally important and similarly lacking.

General Relativity taught us convincingly that all concepts of space must include time. Molecules are no different. Essentially, any molecule is nothing but information that changes through time in space. Our idea about the atom is based on our understanding of information acting in space through time. That is what an atom is.

The definition of a molecule must include time and space, and the definition of molecular information must as well.

When we look specifically at the genetic code, it can only be understood in the context of space and time. That is the only way to understand what it is, where it came from, and how it functions.

Here is a simple example. I hold in my hand six identical bullets. I label each with a number, one to six. This information has limited meaning in only this context, but when I load the bullets sequentially into a revolver, the information is now made clear. The bullets all now have a spatial meaning relative to each other, and a meaning relative to something else – the revolver. Bullet number one will be the first to be fired *at some future time*. It is information that has meaning relative to some *potential* future event. Perhaps we could call this Information Potential. I can now spin the chamber, and the specific information will change, but the relative meaning between bullets and bullets, bullets and revolver, bullets and time all remain unchanged. Relative information is unchanged, but information potential is changed.

The molecular information contained within the genetic code is precisely this kind of information. The genetic code contains large amounts of accumulated information, and this is represented in large part by its information potential.

The information contained in the genetic code is complex and diverse. It is related to many different things, and must be viewed relative to time, space, and relative to other things – other molecules. There was a time course to the formation of this code, and this too imparts information within and without. There is a time course to the execution of this code, and this too imparts information within and without. There is a spatial component to all of this - always. All of these things can only be taken in the context of the things being operated on, operated with, as well as all of those other things that contain their own information by virtue of having undergone previous operations of this nature.

The information is complex and layered in both time and space. It is complex because it never merely reflects a simple relationship between two sets of things, but sets of relationships between sets of things. **When these types of complexities are missed, so too are the qualities and quantities of information.**

This is a fundamentally simple principle. It is imperative that it is taken into account, but it has been explicitly ignored in all prior discussions and descriptions of molecular information. Those things are inherently flawed and meaningless as a result. They simply lead to meaningless tautologies.

Principle 5:
Concepts contained within CCGI depend on Natural Selection.

Quite simply, Natural Selection is the animating principle of life on Earth, and it is the animating principle of genetic information. It is even the animating principle of molecular information.

Everybody has a basic understanding of Natural Selection. For the purposes of this explanation and the arguments contained herein I will give a precise definition of Natural Selection that can be used in all cases here.

Life is both a thing and a process. Life is both a collection of information and a process for generating and organizing information in both space and time. Natural Selection is the process or logic for generating information and organizing it in space and time.

If I have ten fish and select one of those fish for breeding, then I have created information about these fish. This information will then serve as a basis for future choices, and therefore the basis of future information. This is an iterative process where the same logic becomes

layered in the information of both time and space. This is a competitive process where information competes to become the basis of future information.

Learning is the word we use to describe any process of generating, obtaining and organizing information in time and space. Therefore, Natural Selection is a process of learning. Molecules learn. It is a competitive learning. Life simply must have a way to generate choices, make choices, and record the choices made in the perpetuation of this iterative competitive learning process.

Molecules are subject to the competitive learning process of Natural Selection. They have ways of generating, making and recording choices for the purpose of perpetuating the process. The net result is an increase in quantity and complexity of molecular information in space through time.

There is a common, mistaken view of Natural Selection that it is a linear process. I understand the essence of this view, and it is useful in a very limited sense, but I reject the entirety of this simple notion. Natural Selection proceeds "linearly" in time, as all processes must, but it is an inherently non-linear process.

There is an overly simplistic view that life began as a single organism, a cell perhaps, and all subsequent life is a branching tree growing from this primordial genitor. I prefer to view primordial life as a system of crystals competing within a competing set of crystal systems.

In this simplistic sense, life today is merely an extension of a single one of those systems. However, by the time anything as complex as what we know as a cell today could be formed, there was an enormous amount of accumulated molecular information within and between the competing systems. The molecular information contained in that same system today is decidedly non-linear, and it is functioning in decidedly non-linear ways - in every meaningful use of the concept of linearity.

Our view of genetic information in general and the genetic code in particular must fully embrace the animating principle of Natural Selection if they are to be properly understood.

Principle 6:
Concepts within CCGI depend on concepts of Biochemistry, which are necessary, but they are currently not adequate for these purposes.

This is simply an elaboration of Arguments A, B, C, D and E.

We cannot properly understand the general concept of genetic information and the specific concept of the genetic code if we try to use the language and ideas of Biochemistry today. The

ideas and language as they exist today must evolve to match our evolving understanding of these concepts.

Some of the existing ideas and language are still valid and useful. **All of the existing data is valid and useful.** We simply must start a logical process of sorting wheat from chaff, and then begin rebuilding from the ground up. The genetic code is the ideal place to start that process.

The existing ideas and language were born of the discovery of the double helix. That brought with it the ideas and language of linearity. These quickly led to discovery of the genetic code, which adopted in their entirety the ideas and language of the double helix. These ideas and language could take us only so far before they began failing in simple and obvious ways. They are now failing at alarming rates and in intractable ways. They are precluding all meaningful discussion of all meaningful empiric observations.

I have catalogued and complained about the failure of current Biochemistry elsewhere. I will not do so again here. It should be obvious that we are currently on the wrong path, and it is equally obvious why that is true. It is time to simply acknowledge the mistake and begin trying to fix it in the simplest, most logical way. I believe that the genetic code and CCGI clearly point the way.

Principle 7:
Concepts within CCGI depend on concepts of Geochemistry, which are necessary, but they are currently not adequate for these purposes.

This is an elaboration of Arguments A, B, C, D and E. It argues from the end opposite of Principle 6, and brings the argument full circle.

It is a little known fact that the organizing principles of Geochemistry are at once simpler and more complex than the organizing principles of Biochemistry. Why should that be true? After all, Biochemistry is logically many orders of magnitude more complex than Geochemistry, and Biochemistry is a logical subset of it.

There are two good reasons for this paradox. Geochemists rarely concern themselves with Biochemistry, and Biochemists rarely concern themselves with Geochemistry. This leads to the creation and reinforcement of a wide conceptual gap between the two.

Geochemists address the gap by explicitly stating that Biochemistry is formally beyond their official purview. This is a non sequitur of the first order. Not only do bio-molecules produce and represent geochemicals, but Life is a mineral - based on the formal definition of a mineral. As a mineral, it covers much of the Earth's surface. How is this logically beyond the purview of geochemistry?

Biochemists address the gap by explicitly stating that they are rulers of their own kingdom, and geochemistry simply isn't one of their subjects. Geochemistry simply has nothing of meaning to offer to the study and understanding of current biochemistry.

What they both mean is that the problem is simply too complex for either to properly handle, and so they both remain willfully ignorant of the problem.

They both are clearly wrong. Biochemistry is a subset of Geochemistry, and Geochemistry has much to offer to modern Biochemistry. CCGI is intended to bridge this gap, but it must be built from the bottom up, taking from each and giving to both. Perhaps an entirely new discipline will be required to accomplish this task. We might call it Crystal Information Science, or CIS for short.

Principle 8:
Atoms "compete" within crystals.

This is a further elaboration of Principle 7.

If we are to bridge the gap between crystals and Life, we will first need to understand both and recognize the similarities. It is much simpler conceptually to understand the molecules of life and recognize how they behave like crystals than it is to understand the atoms of crystals and how they behave like Life. If a bridge is to be built, eventually, the two will meet in the middle.

This Principle is conceptually difficult for several reasons. The study of how atoms participate in the formation of crystals is called Mineralogy, which is conceptually difficult since our understanding of it is based on principles that are also conceptually difficult. Crystals form via a dynamic process. This basic idea will come as a surprise to most people, since crystals always appear to be static things. This dynamic process is based on many interacting physical factors. The formation of any crystal is entirely contingent upon the interaction and resolution of these dynamic factors in space and time.

Life is a dynamic process of dynamic crystal formation, so it is first important to understand the dynamic process of crystal formation, and second to understand how the dynamic process of Life can and does drive that process. Life is an iterative process of competitive learning, so we must see how atoms can and do "compete" within and between crystals, and how crystal systems differ.

The word 'compete' connotes a motivation where none is intended. That is why I have been using scare quotes when using it. I just can't think of a better word to use here. Atoms compete for their places in the utter absence of knowledge of that competition, and 'compete' connotes volition where none is required.

Full understanding of this general principle would require a basic understanding of Chemistry and Mineralogy. That clearly lies beyond the scope of this explanation. It is helpful, however, to know some of the simpler principles.

An atom is an anion or a cation within the structure of a crystal. This relates to whether the atom needs to add or lose an electron to make a full outer shell of electrons. This distinction depends on the atom, its current electron configuration in its outer shell of electrons, and the status of all other atoms in the environment of crystal formation. This simple distinction of the physical state of each atom and between atoms sets up a dynamic tension between anions and anions, cations and cations, anions and cations, as well as all participating atoms and the spatial systems in which they will form. It is the total resolution of all tensions that determines the nature of the crystal.

The resolution of this dynamic process is recorded in time and space in the actual crystal structure.

One can now recognize the conceptual difficulties within the organizing principles of this "simple" academic discipline. One can also begin to imagine in what general sense an atom can be thought to compete within the formation of any particular crystal.

The dynamic crystal system of life doesn't play the game once and quit; it contains crystal forms that are themselves dynamic, poised on the razor edge between solid and liquid, constantly forming and reforming, and ever building larger, more complex crystals with the ones previously built. This, of course, requires a water environment, controlled ranges of temperature, pressure and concentration, all of which it has learned to make portable and modular to allow continued grow of not only the crystals, but of the crystal system.

Principle 9:
Past crystal behavior determines future crystal behavior.

This further elaborates on Principle 8.

Although it is conceptually difficult to imagine competition between atoms, it is more difficult to conceptualize the logical nature of that competition and its consequences. The key concept here is that not only does Natural Selection have the ability to animate the process at the level of the atom, it can also animate it on a systemic level too, and once animated, the crystal has logical ways to record the process for future iterations of the process. This creates information not only in atomic relationships, but in the systems of their organization as well. This is the key conceptual bridge between ordinary crystals and the crystals of Life.

Both Biochemistry and Geochemistry lack the fundamental concepts to bridge the gap between the two. They both contain organizing and animating concepts. The basic organizing concepts of Geochemistry are better suited to the task, but it lacks the key animating and scaling

concepts. The animating concepts exist in Biochemistry, but the organizing concepts are woefully lacking. So the organizing concepts must be moved up to Biochemistry and the animating concepts down to Geochemistry. And then several scaling concepts must be added in order to bridge the conceptual gap. This Principle is an explanation of how this conceptual trick might possibly be done.

We can begin understanding this by using carbon as an example. It has six protons in its nucleus. It has two electrons in its inner shell, and four electrons in its outer shell, which needs eight electrons to be filled. This means that carbon either has four too many or four too few electrons in its outer shell. There are a variety of options to resolve this, and carbon can participate in many crystal structures, as well as many kinds of crystal structures. Carbon is an extremely versatile atom, and that versatility is the key to its central position within Life.

When there is an environment of pure carbon, there are two kinds of crystal structure that it generally might form. The first one, the most common one, is called graphite. The "Coordination Number" of a carbon atom is 3. This means that, all things being equal, carbon will seek three partners for bonding in a crystal structure. This is what it does in graphite, where the only available bonding partner is carbon, so it bonds with three other carbon atoms. This forms planar sheets of hexagonal carbon rings. These sheets then form much weaker bonds between stacked sheets. The sheets are strong, but the bonds between them are not. This gives graphite its physical properties. Light bounces off of the sheets, so it is opaque and sparkly. The sheets easily cleave off, so it is greasy, and leaves a trail on paper.

Contrast that with the crystal that forms in an environment of pure carbon, as well as high heat and high pressure. This crystal is called diamond. It requires high heat and pressure because it takes energy to force carbon from the hexagonal planar structure into the tetrahedral lattice structure, one in which each carbon shares one electron with four other carbon atoms. This structure is much more stable. It is so stable, in fact, that diamond is the strongest mineral structure on Earth. It is harder to get carbon into this structure, and it is harder to get carbon out of this structure, and this structure accounts for the physical properties of diamond. Diamond is clear because there are no internal structures for light to bounce off. Yet, it cleaves in perfect planes because its internal structure is perfectly symmetrical. This seems to be a paradox, but it is not. Diamond is simply hard precisely because its structure is so intensely symmetrical and therefore intensely stable.

Contrast that with the kinds of "crystals" that carbon forms in Life. Of course this is far from a pure carbon environment. Carbon forms rings and lattices in Life, but it mostly forms chains between two other carbons. It generally has four bonding partners, and these partners are most often carbon and hydrogen. That is why Organic Chemistry is the study of carbon chemistry, and biomolecules are often referred to as hydrocarbons. This form of carbon is conceptually a hybrid of graphite and diamond at the crystal structural level. The properties of these crystals are determined by how the chains form spatial shapes, how the chains interact with other chains, and how the shapes interact with other shapes. But the key property is that

all of these things are dynamic in time and space. It is a competitive system of crystals for forming competitive crystals.

This is a cursory explanation of this Principle, and is well beyond the scope of this piece to be much more specific than this. The point is that crystal formation is a dynamic process. It is not a process that happens once and for all – old crystals eventually get re-processed into new crystals. The crystals themselves keep a record of events. So this is a clear form of information creation, storage, and processing. The process involves choices of atoms and choices of systems, both are recorded and later processed.

One of the reasons geochemistry currently has for disregarding Life as a crystal system is that it is not consistent with any known crystal system. This is not a good reason; it is an abdication of responsibility. Just because we don't know what it is doesn't mean that it isn't a legitimate subject of the larger discipline. We clearly don't know what it is simply because it is too complex in scales of time and space, and it is too dynamic on both of those scales.

There are no known crystal systems that scale in those dimensions. Yet.

We can get a better handle on the difficulties presented here merely by controlling those dimensions in our mind. A thought experiment, so to speak. We can imagine that we are roughly ten times the size of an atom, and we can slow down time however we like. We can now go into any crystal and watch it form. We can see the process of crystal formation as atoms move about, collide, and organize themselves into a clear and repeating pattern. When it is over, we can easily identify the precise locations of trillions of trillions of atoms, no matter how elaborate the pattern. The atomic information is recorded in the crystal structure. We can locate these atoms in time and space in all directions based on simple, universal principles of time and space.

Now let's do this same exercise in a human lung at the point where a red blood cell can find oxygen atoms. Again, we can slow down time to the point that we can pinpoint the precise location of trillions of atoms.

Within this thought experiment there are individual molecules called hemoglobin that each contains thousands of atoms, but we know the precise location of each of those atoms because this information has been obtained by and recorded in this crystal system.

And we can watch as this molecule adds atoms one at a time in the form of oxygen. Additionally, we can step into another area of the body and watch these molecules actually being built, one atom at a time, so to speak. Except, they are built roughly nineteen atoms at a time, and yet they require millions of atoms to do this. Still, we can watch as these massive collections of atoms collide in the exact way that the atoms in the simple crystal did. It is a much bigger process in the scale of time and space, but it is the same process. Atoms making crystals, molecules making molecules, crystals making crystals, at bottom it is conceptually all the exact same thing in time and space; only the scales differ.

The "unit cell" of the simple crystal structure is simple, and it repeats simply. That is a founding principle of Mineralogy. That is the principle that allows us to precisely locate individual atoms within a much larger crystal stricter.

This same principle holds true in the more complex crystal structures of Life. But in these more complex crystals there are still unit cells, but there are many more of them, they are larger, much more complex, and we would need to go back billions of years to see them forming in their original simplicity. They are the same processes, but the complex one is scaled much broader in time and space. The atoms do not change, but the structures do. The complexity is infinitely greater because the structures are built from the structures of prior structures. The crystals themselves are keeping the record of these structures in both time and space.

This is the essence of a competitive molecular learning environment.

There is a basic concept in Mineralogy called a Solid Substitution Solution. What this means is that a crystal framework is somehow first determined, and then components can be substituted within that framework in multiple ways. Life is just this, but we don't know the framework, and we don't know the scale, and we don't know the limitless scope of the possible substitutions. The system is far too complex for us to know these things at this time, but we can know that they are there.

Principle 10:
Paleo-chemistry illuminates contemporary biochemistry.

This is an elaboration of Arguments A, B, C, D and E, and an extension of Principles 9 and 10. By the very nature of the Principle, it involves much pure speculation, but it adds to these concepts in general.

We can imagine the dynamic crystal forming process of Life today, but we must somehow extend this back in time to the beginning to see how it could be first built and then successively built upon. To do this, we need to imagine what this process might be, and what kinds of atoms might participate.

We know exactly what the atoms are now, and we can assume that they are more or less the same now as they were in the beginning. The system selected these atoms. They are carbon, nitrogen, oxygen and hydrogen. In the periodic table these are 6, 7, 8 and 1. Why these atoms?

The structure of Earth can be seen as consisting of a core, mantle, crust and atmosphere. The interface between the crust and atmosphere can be called the surface. The surface of Earth is 70% water. Earth is 5 billion years old. We can pick a time 4.5 billion years ago and compare

Earth then and now. The structure has not changed much, but the compositions of its parts have.

Of the 116 naturally occurring elements, only 15 of them appear in commonly formed minerals of Earth's crust. Carbon is a trace element, in other words, it is not common in Earth's crustal minerals. Carbon accounts for 0.02 percent of the crust. Compared to silicon - it's big sister that accounts for 26.7 percent - it is more than 1300 times rarer. Nitrogen is ten times rarer than carbon; it only accounts for 0.002 percent, so it too is a trace element in Earth's crust. Hydrogen is a trace element at 0.14 percent. (Note, these are by weight.) Oxygen is 46.6 percent of the crustal minerals, which obviously makes it the most common. Water is hydrogen and oxygen. Earth's water also contains considerable sodium and chloride, but very little nitrogen and carbon.

Earth's atmosphere now contains 21% oxygen and 78% nitrogen. The rest, obviously, are trace elements. Again, carbon and hydrogen are trace elements of the atmosphere.

There are two large differences between Earth now and then. Oxygen was a trace element of the atmosphere then. And the surface now has Life, which is merely a very large crystal that is virtually all oxygen, nitrogen, hydrogen and carbon. Carbon is clearly the base atom in this crystal.

So we can know that something drove a lot of nitrogen out of the atmosphere onto the surface, and a lot of oxygen out of the crust into the atmosphere, and a lot of carbon from scarce sources in the crust into a central role of abundance in an elaborate, complex and dynamic crystal system at the surface.

What did this, how, and why?

Obviously, Life did this.

How and why must remain a mystery, but we can know that it did this via Natural Selection, and it did it because this is how crystals grow, when they can. We can't absolutely know the specific answers, but wondering about simple, important questions here can provide insight to the processes of today. Surely, the processes now contain fingerprints from then.

Stipulating all of the above, we can begin asking good questions right away.

What are the obvious conceptual lines, and where shall we now draw them?

When and where does Natural Selection enter the picture? Is there a logical place or time that Natural Selection begins or ends?

I think there is not on both counts. I think it needs to be symmetrical in both space and time.

When do atoms in this system become a crystal, and when do they stop being a crystal?

Again, I believe it must be symmetrical in both space and time.

What are the atoms, and why were they selected? What is the crystal, what is its system, and why was it selected? What is the best way to go about understanding these questions and their possible answers?

I think the only way to think about these questions now is by turning to what we already know about Mineralogy. I think we can already know that Mineralogy cannot give us the important answers that we need – the Case is too unique, too dynamic, and too complex – but it is the logical, perhaps the only place to start.

When we look at this in just these terms we are looking at a Solid Substitution Solution on massive scales of time, space and complexity. The only possible way to attack it is by breaking it down into simpler parts. For these smaller parts we first need two basic parts. We need atoms, and we need a lattice.

The lattice selected the atoms, and the atoms selected the lattice. The atoms became molecules, and the molecules began evolving.

The lattice evolved with them.

This is what a crystal code is when it starts evolving. We are quite familiar with the atoms, but the lattice is something unknown to man. So let's start with the atoms.

In this light, the atoms are perhaps selected based on their abilities to substitute. On this score, carbon is the clear winner. It is perfectly built for substitution in terms of atoms, space and time. By simply adding hydrogen to the mix, carbon becomes any and all things within the system. It is a proverbial four-bladed Swiss army knife of atomic substitution, cation, anion, both, neither.

Interestingly, I think the numbers actually suggest that Life on Earth first selected oxygen. In other words, perhaps oxygen is the key atom toward formation of Life on Earth. The abundance of oxygen made it the defacto winner. Carbon's position relative to oxygen in the periodic table made it the coat tails runner up, one that eventually ascended the throne.

So that brings us to the curious question of silicon. Why carbon instead of silicon? There are three possible simple answers. Carbon is bigger than nitrogen which is bigger than oxygen. This is the nature of the information in space and time that is an atom. There are more parts in oxygen, but there is more volume in carbon. Silicon is much bigger than carbon, more than twice as big as oxygen. This size difference is probably the key. But perhaps silicon's being less electro-negative than carbon makes it an ill-suited partner for oxygen. Perhaps silicon's abundance was a detriment to the process.

In this light, perhaps silicon by virtue of its abundance and similarity to carbon was perhaps the first partner – a founding partner – with oxygen, and together they laid the necessary foundation for carbon's ensuing coup. Who knows? How could we ever decide?

Nitrogen is now the obvious, logical bridge between carbon and oxygen. We can see these things simply as three variations of the same thing. One has four electron holes, one has three electron holes, and one has two electron holes. Hydrogen is the clear and obvious choice of universal stray hole-plugger. This is what hydrogen is and what hydrogen does – it plugs electron holes. Perhaps a system such as this crystal system of Life will always require three contiguous partners in the periodic table. Perhaps there are other ways to arrange the table that might shed better light on questions of this nature. Who knows?

Regardless, having now answered questions about the atoms, we can shift focus to the much more difficult questions of the lattice. These questions are considerably more difficult. We can begin to have a general understanding of these questions, but a full understanding must await development of an entirely new branch of mathematics. There's just no way around it at this time.

A lattice traditionally is a static thing. That clearly can never be the case here. This lattice must be dynamic on all scales of time - the very short and the very long. It is conceptually very difficult to do this. The first thing we need to recognize is that we need more than one lattice, and more than one kind of lattice.

The first, most obvious lattice is a static tetrahedron. This is the obvious place to start in a system such as this with clearly known atoms.

This particular lattice shares the same spatial relations as diamond and water. The fact that water is an extremely dynamic lattice on short time scales is extremely helpful. In fact, water is so dynamic that it is not even a mineral, which is okay. When water becomes a mineral – ice – it switches to hexagonal rings, which is why it expands. This is also why Life exists in the form of water and not ice.

It is curious that carbon and water seem to reverse poles with respect to their latti, from tetrahedral to hexagonal. But this is also critical to the concept of coordination number, which clearly in this case is now 4. Therefore, the logical base of this crystal system is 4, and it defines the dynamic tetrahedral lattice of water while it is in solution, and water is the base solution of the Solid Substitution Solution of this crystal system. Water represents a dynamic tetrahedral lattice within this crystal system. This is the base system for all future crystal formation.

This is fundamentally why Life is a base 4 system of molecular information.

The next lattice that we consider will need to start as static, but this too presents multiple problems with no obvious solutions. At this point we are probably talking about a lattice that

exists in nature, but does not exist in human language. If it does, I am unaware of what it is. I strongly believe that it will require an entirely new branch of mathematics, and I have described that elsewhere. Needless to say, this is where simple concepts become extremely difficult to comprehend and assimilate, yet we have no choice.

The obvious starting point is to look at carbon. In Life, carbon exhibits clear coordinating numbers of 2, 3, and 4, and that's just for starters. After a few, simple atomic combinations, it exhibits coordination numbers of 6, 8, 12, as well as 20, and 60, and perhaps yet more. Who knows? In other words, in Life carbon exhibits all known coordination numbers and many unknown coordination numbers. This is one helluva problem. The only conceptual way to resolve this is to recognize that as the molecules evolve, the lattice evolves with it.

Still, we must construct a lattice somewhere, and we must have a place to start. We can start with carbon, and note that it is a base 4 atom. This atom forms chains, sheets, three-dimensional structures, three-dimensional latti, and all possible combinations of these things. I believe that ultimately we will need a base 4 mathematical language to build this lattice, and we do not have one. When we do, it will not build this lattice from points but from spatial structures. My bias is towards sheets that define points and structures, but I will not go into that here. It goes well beyond the scope of this explanation.

However, if we somehow start with the six planes of a perfect dodecahedron, a three-dimensional lattice can actually be built simply, but the mathematical properties of that structure are too bizarre for me to fully comprehend in its entirety. Regardless, this is precisely the kind of spatial structure needed here. It can begin statically in time and space, and evolve in both. This will fully retain the base 4 language of life, while being fully capable of building and retaining the molecular properties required for its formation and execution.

Principle 11:
The genetic code represents at least two entirely different things.

This explanation elaborates on all Arguments and all prior Principles.

Empiric facts:

- DNA is a molecular set of four common nucleotides.
- These four nucleotides have a logical relationship in time and space that leads to the fundamental logic of sequential DNA replication.
- Protein is made from a common set of twenty amino acids.
- The nucleotides in DNA are sequentially transcribed and translated by sets of three into sequences of amino acids.
- There are commonly sixty-four of these three-nucleotide sequences.

- All of these common nucleotides are based on five-carbon rings.
- The common amino acids are based on central carbon tetrahedrons.

Numeric facts:

- A perfect dodecahedron is a set of twenty points, five planar points define a face, and three faces define a point.
- Five sets of eight points of a cube can be simultaneously defined within the twenty points of a dodecahedron, such that all permutations of the points of a dodecahedron can ultimately define two hundred and forty unique cubes.
- Every cube can be defined as two complementary tetrahedrons.
- All permutations of the points of a dodecahedron can define two hundred and forty unique tetrahedrons.
- Four colors can be used to define the faces of a dodecahedron in such a way that all permutations of any three contiguous faces can generate sixty-four unique identifiers for the twenty points in a dodecahedron.
- It is a logical conclusion that every one of these point identifiers defines a unique tetrahedron within the points of a dodecahedron.
- Every ordered set of four points in a dodecahedron that represents a specific tetrahedron shares exactly one point with four other sets of ordered points that also represent a unique tetrahedron
- Any one ordered set of a tetrahedron is then logically and sequentially related to the one hundred and nineteen other ordered sets.
- A logical map can be made between all tetrahedrons in a dodecahedron and their shared points.
- Any sequence of shared points will generate a logical sequence of base 4.
- It is a practical matter that a base 4 sequential language exists that specifies any sequence of tetrahedrons in space when interpreted within the context of a dodecahedron.
- This logically means that a base 4 language exists that relates the transposition of tetrahedrons in space through time.

Numeric coincidences:

- The four nucleotides in DNA are consistent with the four unique face Identifiers of a dodecahedron, the four points of a tetrahedron, and the base-four language of sequential tetrahedrons in space through time, when taken in the context of a dodecahedron.
- The logical sequential replication of DNA in space through time is consistent with the dual tetrahedrons in a cube.

- There are three sequential nucleotides in translation of DNA to protein and the identification of a point on a dodecahedron by the sequential identity of its three contiguous faces.
- There are twenty common amino acids and twenty points in a dodecahedron.
- There are sixty-four common sequences of the four common nucleotides taken by threes and sixty-four unique point identifiers in a four-color dodecahedron.
- Five carbons in the base of common nucleotides are consistent with five planar points in a dodecahedron.
- The tetrahedral base of common amino acids is consistent with any four points of a tetrahedron in a dodecahedron.
- The numerical relationships in these particular biomolecules are precisely coincident with those of a dodecahedron in number, member, language, space and time.

Logical facts:

- Numeric coincidences can exist between two different things.
- Numeric coincidences can either represent cause and effect, or no logical relationship whatsoever. Numeric coincidences can be pure coincidence, or they can represent some form of cause and effect.
- The above noted numeric relationships between the elements of a dodecahedron are forced by the logic of space through time.
- The numeric relationships between the sets of biomolecules might not represent any forced logical relationships.
- They could equally well have been any other set of numerical relationships, in fact, they could be totally arbitrary.
- The above coincidences could represent either cause and effect or pure coincidence.
- The dodecahedron could cause this coincidence, but the biomolecules could not. In other words, a dodecahedron is what it is, and no amount of molecules will change ever that. It is logically true that this might be pure numeric coincidence
- ***If there is cause and effect, the dodecahedron must be the cause and the biomolecules must be the effect.***

We must carefully look at all of these things and sort fact from coincidence.

It is conceptually imperative that we decide cause and effect here. There is ample circumstantial evidence that cause and effect exists here. Sometimes circumstantial evidence is the best evidence. In a question such as this, circumstantial evidence is the only evidence we can ever have. It is impossible to recreate the genetic code empirically. There are many coincidences, and they are perfectly related in time and space. And the coincidences merely begin to pile up yet further when larger and smaller scales of time and space are taken into

consideration. The genetic code appears to be built from below, and is now still building above, based on these sets of logical spatial relationships through time.

There seems to be only one reasonable conclusion: **There exist at least two related but distinctly different things.**

There is a set of logical relationships based on spatial symmetries through time, and there is a set of biomolecules that represents a molecular code. The latter perfectly reflects the former, the former is surely the product of the latter. But now the biomolecules represent a different thing entirely. It is a molecular code that is both incredibly specific and incredibly complex. It is a product of the codes below it and a generator of the codes above it.

Determination of cause and effect here has significant practical consequences as well.

As a practical matter, we need to decide if the numeric relationships in the codon table are arbitrary or objective. If they are objective, then we need to pick the object. If they are arbitrary, we need to subjectively decide the best way to view them so that they can be fully explained and debated. In other words, *pick your very best codon table, and let's finally have at it.*

Current concepts of Biochemistry hold that the genetic code is a linear arrangement of molecular information.

The numeric relationships here are, for all intents and purposes, arbitrary. It is purely a subjective matter of taste how we graphically arrange this information. The table holds only one dimension of information, and that information can be equally and completely captured by an infinite number of graphical representations. No one way is objectively better than any other. Figure 1 is one such graphical representation.

CCGI holds that the genetic code is an objective molecular code.

A perfect dodecahedron is the primary object on which this concept is based, but there is yet a more complex object on which it can also be based. It is not linear information; there are many dimensions of information. There are dimensions of sequence, member, language, space, time – and scale.

The molecular information of concern here – nucleotides and amino acids - is best graphically portrayed in the broadest possible sense on the surface features of an icosidodecahedron, where the twelve pentagonal faces represent twelve different pentagonal nucleotides, and the twenty hexagonal faces represent two-hundred and forty possible tetrahedral amino acid assignments. I call this the G-Ball.

There are a very large number of ways to arrange twelve nucleotides of just four kinds on the surface of the G-Ball, but only two will generate all sixty-four unique permutations of three

contiguous nucleotides, and these two ways are stereoisomers. I arbitrarily chose one of them, so we can call this one G-Ball$_1$ and the other one G-Ball$_2$. I actually inadvertently switch between the two from time to time, because my brain struggles to see the difference. The rest of the possible configurations can be sequentially numbered, but I haven't bothered to come up with a system for doing that.

Figure 2 is a schematic of the G-Ball, and Figure 3 is a series of pictures that shows the G-Ball with color codes for nucleotides and amino acids that use a rainbow scale to color the molecules according to water affinity: Blue is hydrophyllic and red is hydrophobic.

It is conceptually imperative to recognize that Figure 1 and Figure 2 are not two different ways to do the same thing; they are two different things entirely.

Figure 1 is a codon table; Figure 2 is not. It is a nucleotide table that represents four concentric sets of relationships between nucleotides - the relationship between individual nucleotides, the set of all permutaions of three contiguous nucleotides, which might be called codons, the set of all relationships between codons, the set of all nucleotide sequences. Likewise, it is an amino acid table that perfectly complements all of these nucleotide sets.

Figure 1 is a single line of information that assigns one amino acid to each of sixty-four codons. It is merely one of many possible arbitrary arrangements of that line of information. It is used like a die stamper where amino acids are stamped into a line from a line of DNA. There is no time component and there is no spatial component. It is purely subjective, since there is no object on which it is based – other than a line, of course.

The G-Ball is not a codon table, it is not subjective, and it is not the full object of concern here. The codon table is merely a very small subset of the G-Ball. The full object is a perfect dodecahedron with a tetrahedron superimposed on it. I call this Code World.

Figure 4 shows the full object on the left, Code World on the right, and the G-Ball superimposed on the object. Figure 5 shows that the tetrahedron of Code World is functionally equivalent to a cube. We can call these Code World$_T$ and Code World$_C$.

To begin to understand the conceptual differences between the codon table and Code World, we first need to have some empiric facts about Biochemistry.

Codons are not molecules. A codon is both a molecular superset and a molecular subset. Codons don't specify amino acids; they specify anti-codons. There are more anti-codons than codons. Anti-codons don't specify amino acids; they specify tRNA. The tRNA molecule is much larger than a codon or an amino acid. It is shaped like a wedge of a dodecahedron. In other words, If you put a fair number of tRNA on all the points of a dodecahedron, they would make a much larger dodecahedron.

There are sets of codons that are assigned to the same amino acid, and we call these synonymous codons. When a mutation of a codon results in a synonymous codon, we call this a silent mutation. Proteins can fold in many different ways. When a protein folds entirely in the "wrong" way, we call this a prion. Prions teach other proteins the wrong way to fold. Prions are devastating when they occur in life. Silent mutations cause changes in the rate, volume and folding of protein formation. Proteins can and do fold in many ways for many reasons.

Nucleotide sequences are often shifted, spliced, repeated, complemented and inverted. We call these things sequence transformations. There are known instances where the same nucleotide sequence has been transformed to be translated as two separate proteins in the same organism.

We can now see that the codon table is not built to handle these empiric facts; Code World is.

When we first start to look at Code World and the G-Ball we need to think differently. It's just that simple. We cannot apply our old way of thinking to something that is entirely different and requires a different way of thinking. The G-Ball is not a die stamper; it is a crystal ball. It reflects events in time and space – big and small, past, present and future. It contains a vast amount of accumulated molecular information, and a vast amount of information potential.

The genetic code is not a linear cipher, it is a molecular code built upon sets of relationships in space and time. When we look at it, we need to try to understand the sets, the relationships, space and time simultaneously. More than dictating events, the genetic code records them and predicts them.

There are two primary sets of molecules on the G-Ball – nucleotides and amino acids. There are twelve different nucleotides of four kinds. We need to see them as a set of twelve because they have been assigned according to a harmonic scale with twelve different notes.

The first assignment of nucleotides is their relationships to other nucleotides. The first key relationship is that each nucleotide has a complementary pair. The next key relationship is between any nucleotide and two other contiguous nucleotides, what we might call a codon. **But we still don't know what a codon actually is, because there is another set of relationships between codons, and yet another between a set of all possible codon relationships.** It is only when we understand this set of nucleotides, and all the sets of relationships above and below it, that we can even begin to understand their assignments to amino acids.

The G-Ball is not a codon table; it is a matrix of molecular information that only has meaning in the fullness of time and space.

The set of twenty amino acids represent twenty molecules that only have meaning with respect to their physical properties, their relationships to each other, and all possible relationships within all possible chains of amino acids.

The two seemingly key properties of all of these amino acids lay their ability to form structural properties in a chain, and their ability to attract or repel water. There are two in particular that have unique chain forming properties, proline and glycine, and they represent opposite ends of the chain-forming spectrum. They also represent complementarity with regard to pairs on this scale; consequently, they generally travel in pairs, and they are strongly assigned to complementary pairs in the middle of this particular assignment spectrum.

We need to recognize that Life ultimately did not make its codon assignments based on codons and amino acids; it made them based on full sequences. It made them based on all possible assignments to all possible sequences. A codon is not assigned an amino acid - a set of codons is assigned a set of amino acids. The genetic code does not translate a chain of codons into a chain of amino acids; it translates all possible transformations of a sequence of nucleotides into all viable structures of protein, in the fullness of time and space.

When we look at the genetic code, we need to realize that it is the code that ultimately translates the set of all possible DNA structures into the set of all possible protein structures. It is also the code that determines all possible DNA structures. This is a key difference. It is only then that we can begin to appreciate the full meaning of the sets and all their relationships in time and space.

Even the simple codon table, when properly viewed, is unfathomably complex.

We can see that nucleotides relate to amino acids on much larger harmonic scales than just codons and amino acids. One scale is on water affinity. The total set of assignments has a rainbow with a beginning, middle and end on this scale. But this scale is made up of smaller logical sets of codons which also reflect rainbows. So it's not merely a rainbow; it is a harmonic rainbow of rainbows. The chain forming properties form a similar scale with proline and glycine as its center.

When we start to imagine why it would be useful for the genetic code to do this, it becomes obvious that the genetic code must perform many functions on many scales in space and time. It is not only a product of Natural Selection; it is the primary engine for Natural Selection. For Natural Selection to do its work here, it not only must build structures, but it must find new and useful structures to build.

The genetic code is both an operating system and a search engine.

The best place to search for new and useful structures is by using the useful structures already at hand. So by using simple, common sequence transformations and the harmonic assignments of the genetic code, Natural Selection has a ready stock of new and useful structures at hand.

As we recognize that the codon table is a small subset of the G-Ball and the G-Ball is a subset of Code World, we can now also finally recognize the utility of being able to relate space to space

through time. The simple base-four language of DNA replication is captured by Code World$_C$, and the simple base-four language of translation of DNA into protein is emulated by Code World$_T$. The former is actually a logical subset of the latter. Go figure.

The first decision that now must be made is whether the genetic code is one thing or more than one thing.

The next decision we must make is whether it is objective or arbitrary, and if it is objective, we must search for the object. I think Code World is the best place to start searching. Perhaps there are better, but I've yet to find them.

Principle 12:
The genetic code illuminates past, present and future biochemistry.

This explanation elaborates on all Arguments and all prior Principles.

We have come to a fork in the road with two paths from which to choose. We can either stick with the current path or choose a different path. The first way offers continued folly, and the second has an embarrassment of riches, but it also demands an awful lot of hard work.

We might now see this as two competing models of the genetic code, one of them a simple particle and the other a complex wave. The first is based on the simple premise that the genetic code is a linear arrangement of molecular information. The second is based on the simple premise that the genetic code is a set of logical relationships based in spatial symmetries through time.

Before we decide which model is best, let's see the implications of each.

The particle model has much to offer. The key feature is simplicity, but that brings its own set of limitations. Concepts are easy to understand, but they might not have much explanatory power. There are plenty of known facts that cannot be explained, so they must simply be taken as exceptions to the general rule. So we now have one simple, general rule with lots of difficult exceptions, and the exceptions are growing in number and importance.

At some point the simplicity becomes more of a liability than an asset.

The particle model was accepted from the beginning. The consequences of this are severe. The entire language of Biochemistry has grown up around this, and now the language merely fortifies the model. It perfectly insulates and perpetuates it.

Unfortunately, the model failed to predict or anticipate empiric findings, and now those findings are being forced into an ill-suited model. The entire logic of the model is internally

inconsistent - and it always ways. Our acceptance of simplicity over explanatory power is now exacting a huge price from our understanding of Biochemistry. What should have been its conceptual center – the genetic code – is now displaced to the periphery, and it is causing more problems than it solves.

The wave model is now a viable alternative, and it should ultimately be accepted. I can't even imagine why it wouldn't, but for ten long years it has not. The particle model is merely a small and imperfect subset of the wave model. The wave model can do everything the particle model does, plus a great deal more. The empiric evidence no longer represents exceptions to the rule; they are proof of the general rule. These are simply things that are predicted by the model.

The wave model even explains why the particle model seemed so appealing in the first place. In other words, it explains why the genetic code would want to appear to be one-dimensional. In more other words, the appearance of one-dimensionality was not a starting point in its evolution but an evolutionary advantage that was only achieved after much evolution. The genetic code, at its beginning, did not have any appearance of one-dimensionality.

Once we accept the fact that the genetic code is not a single, simple thing but a large number of related complex things, we can finally begin to imagine what these things might be.

The foundation is a code that logically relates space to space in time. That generates a code that relates atoms to molecules, then molecules to molecules in space through time. That generates a code that relates genes to polypeptides, another that relates DNA to protein and protein to DNA, ultimately all DNA to all protein. Then we can imagine more complex codes that relate cells to cells, cells to bodies, bodies to bodies until it encompasses all Life on Earth.

This is the essence of genetic information, and this is the essence of the Crystal Concept of Genetic Information. This does not logically limit us to this space in this time, this expands to all scales of space and on all scales of time.

Ultimately, it provides a logical bridge between Life at first, Life at present, and Life in future.

The consequences of finally accepting this model are numerous and important. It will mean that what we thought we knew, we really did not know. It will mean that we now know that there is much more that we don't know than what we do. It will mean that we must start all over from the beginning. We will need to rip out the old model from its roots and discard it along with the pernicious language it carries. That language is the single largest obstacle to building any new model.

An entirely new language will need to be built from scratch.

The new language will need to start in logic and move quickly to mathematics. I believe it requires an entirely new branch of mathematics, and I've described that elsewhere. From there it will depend heavily upon information science as it moves through chemistry and into

Geochemistry. It will be heavily dependent on linguistics, semantics and semiotics. It will draw from bioinformatics. This will take an awfully long time, and will be awfully difficult, but there seems to be no alternative, save for keeping the current model, which has clearly failed.

We can now point to Code World, the G-Ball, and the codon table, and say of each – this is the genetic code. But we need to be careful with our meaning. We need to be clear about what each one is, what it represents, how it instructs our understanding, and how it is related to the other things. We need to also clearly know that there is yet an entirely different thing – a real set of things – that is the genetic code, and none of these things we have pointed to is it. We need to recognize that the genetic code is at first and at once many different things that can be seen in many different ways.

Code World is a working model of simple spatial relationships through time. It shows us how space is related to space through operations on space through time. It shows us how this relationship forms the logical foundation of a base 4 language of spatial translation through time. It shows us that this language forms the logic of both DNA replication and protein synthesis.

The G-Ball shows us how spatial relationships can have a layered complexity such that each set of relationships forms the logical basis for higher sets of relationships. It can show us the specific sets of molecules that were formed by and operate on those relationships. It can enlighten us about the complexity of those molecules, their relationships to each other, and the nature of the information they contain.

The codon table is a tiny subset of the information contained in the G-Ball. It can show us one simple relationship within that subset. It is a logical fallacy and a grievous error to assume that this relationship reflects the very nature of that information.

The real thing that is the genetic code, the sets of molecules in nature and the sets of their relationships is perhaps the most complex thing in the known universe. It seemingly has no logical bottom and no logical top within the total sets of molecules we know as Life. It is the logical center, and it extends backward and forward, up and down in scales of both time and space. There is no "water's edge" when it comes to the genetic code and the role it plays in Life. It represents the origin and evolution of Life itself. It is actively operating today at the very core of all living things.

The single, simple idea that entirely drives this difficult concept is this: **Code World is the genetic code, and Life is playing Code World.**

The genetic code should become the very center of intense study by virtually all academic disciplines. It not only provides the single best clue to the origin of Life, it explains the function of Life at the very core. It will require all academic disciplines to finally be understood, and once properly understood, it will give back to all.

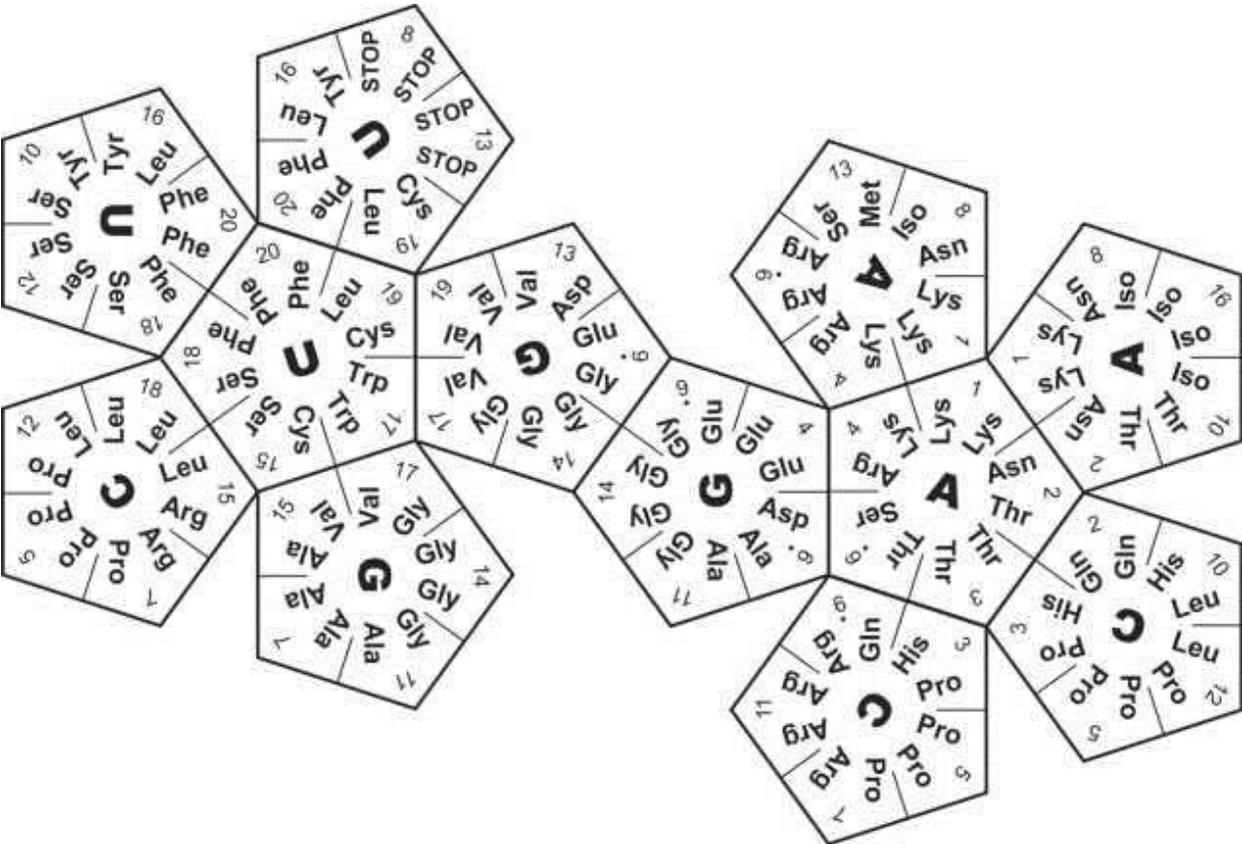|	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	STOP	STOP	A
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C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

Figure 1.

Figure 2.

Figure 3.

Figure 4.

Figure 5.

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