EVERYTHING AS AN ALGORITHM-COMPUTATIONAL ANALYSIS AND MODEL FOR SPACE/TIME COMPLEXITY

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Author's Note

This paper is a revised edition of my "Quantum Framework For Our Mathematical Universe:Full Dissertation" paper and entirely reformatted".

ABSTRACT

Utilizing multiple theorems derived from and formulating the equation : $Z = \{\forall \Theta \in Z \rightarrow \exists s \in S \wedge \exists t \in T : \Theta = (s, t)\}$ and formulating the equation: $X = O + \sum \hat{H} + \frac{(n(\log)\Phi)}{P_{dx}}$, as well as some mathematical constraints and numerous implications in Quantum Physics, Classical Mechanics, and Algorithmic Quantization, we come up with a framework for mathematically representing our universe. These series of individualized papers make up a huge part of a dissertation on the subject matter of Quantum Similarity. Everything including how we view time itself and the origin point for our universe is explained in theoretical details throughout these papers.

Keywords Quantum Similarity · DNA · Molecular Biology · Metacodes · response variance · object set reference · Bioinformatics · Computational Physics · Computational Models · Mathematics · Probability · Statistics, Comparative Modeling · Biostatistics · Quantum Mechanics · Data Science · Algorithms · Quantum States · Nature · Theoretical Physics · Metaphysics · Mathematical Physics · Computer Science · Quantum Origin · Quantum Similarity · DNA Storage · Particle Physics · Classical Mechanics · Non-Relativistic Mechanics.

1 Quantum Similarity in our DNA, and in DNA Storage

Introduction

DNA is the building block of life, and to some extent acts like an algorithm. The way our DNA replicates information as some sort of communication ladder, isn't a coincidence. Everything, runs in sequences, including the strands of our own DNA. In some extent when cells are reproducing itself, it utilizes instructions that are placed in our DNA. The way this works is quite algorithmic and can be computationally modeled. Once you can encode and decode DNA, you can computationally compare it to other naturally occurring phenomena or even synthetically created bio-indicators. This leads us to create a probabilistic distribution on how DNA creates processes of data that give cells specific types of instructions. This analysis will then allow us to have a comparative model for the origin of life and even the statistical probability of us existing through intelligent means. The theoretical analysis and this proposal can accelerate our own understanding of life, the universe, and computational sciences as we know it.

This paper is an introduction to the object set references and recognizable mathematical patterns of DNA in terms of computational proofs, algorithmic nature, and mathematical representations or formations. This look on Quantum similarity, and approach to DNA informatics or DNA storage will provide a framework on the potential of the subjective nature of related research.

What is Quantum Similarity?

Quantum similarity is an extremely important concept in computational chemistry. Utilizing Quantum similarity allows us to look at different molecular response variances and the relationships between molecular sets¹ with recognizable patterns and descriptions, allow us to better understand the molecular composition of what we are observing. Some of these patterns can hence be mathematically analyzed and figure out missing links or response sequences that are difficult to see without using the concept of Quantum similarity. This utilizes advanced Quantum mechanical models that uses theoretical implications of Quantum mechanics and Quantum information to look at response variances, molecular position, states of polarity, chemical bonds, etc. We can then apply a geometric approach² to the observation of certain molecular structures and compounds. Utilizing this approach, we can recognize patterns mathematically or create some sort of computational algorithm that utilizes regression analysis or computer vision to do so for us.

Quantum Similarity in DNA

Quantum Similarity is an important aspect in the genomic analysis of our DNA. We utilize the principles of Quantum similarity to analyze the molecular composition, then we look at the geometrical modeling through Quantum similarity forth in our RNA systems. The decoding and encoding of expressions in genes can hence be computationally modeled and analyzed utilizing these said principals. The first thing to analyze computationally is structural analysis of the

¹ Carbo, R., & Calabuig, B. (1992, November). Quantum similarity measures, molecular cloud description, and structure-properties relationships. Retrieved October 22, 2018, from <https://pubs.acs.org/doi/abs/10.1021/ci00010a005>

² Pothos, E. M., Busemeyer, J. R., & Trueblood, J. S. (n.d.). *A quantum geometric model of similarity*. Retrieved October 22, 2018, from <http://www.psy.vanderbilt.edu/jdmlab/papers/QuantumSimilarity.pdf>

molecular composition, then we look at the geometrical modeling through Quantum similarity. After this, a preset optical flow model is formed. Having an optical flow model will then allow us to use advanced computational principles in data science to look at how our DNA mathematically performs and functions. For modeling we set up the tagged set:

$$Z = S * T \quad (1)$$

Where Z being the object you are computationally analyzing, I.e. (The DNA strand) S is the object set and T is the tagged set formation³

When looking at the Boolean tags,
we set:

$$Z = \{\forall \theta \in Z \rightarrow \exists s \in S \wedge \exists t \in T : \theta = (s, t)\} \quad (2)$$

This creates a matrix set for what we are mathematically modeling. You end up having a matrix tree where you start out with the analysis of Z (The DNA) strand and end up with the tagged and object set formation, which is the analysis of the DNA metacodes.

Utilizing this method allows you to prepare for the implementation of QSPR for your computational analysis.

Quantum Similarity in Molecular Biology and Molecular Geometry

Molecular Biology

When looking at Quantum Similarity, we are utilizing a numerical analysis. computational model for how molecular response variances “communicate” in our DNA systems. This is the origin point of our biological systems.

Figure 1: Structure of DNA.

This will then allow us to create this representation of QSPR. Z represents the entire DNA strand. The tagged reference set T is the base pairs, S is the actual helix/chain holding the base pairs together. Now that you have the object set reference for DNA, you have the numerical representation of DNA with the set Boolean tags to perform

$$Z_{AB} = \iint \rho_A(r_1) \Omega(r_1, r_2) \rho_B(r_2, \Theta) dr_1 dr_2^4 \quad (3)$$

The equation above signifies QSPR when looking at the relationship of molecular descriptors. Our DNA has similar descriptors where we process information and biological instructions performing almost as a molecular data set. The mathematical and numerical characterization⁵ of our DNA allows us to utilize these equations and have a different perspective on how our DNA performs. It performs like sets of sequential data.

Molecular Geometry

Figure 2: Graph of a regression model

³ CARBÓ-DORCA, R., & GIRONÉS, X. (2014, August 13). *Foundation of Quantum Similarity Measures and Their...* Retrieved October 22, 2018, from <http://iqc.udg.es/articles/pdf/iqc417.pdf>

⁴ Robert, D., Besalu, E., Amat, L., Carbó, R., & Girones, X. (2000). *Molecular quantum similarity in QSAR and drug design*. Berlin, Springer.

⁵ Yu, H., & Huang, D. (2013). *Descriptors for DNA sequences based on joint diagonalization of their feature matrices from dinucleotide physio-chemical properties*. *Tsinghua Science and Technology*, 18(5), 446-453. doi:10.1109/tst.2013.6616518

$$y = a + b(x)$$

$$b_1 = \frac{\sum (x - \bar{x}) - (y - \bar{y})}{\sum (x - \bar{x})^2} \quad (4)$$

Figure 3: Harmonic pattern illustration using Wolfram Alpha's computational engine.

For molecular geometry, we utilize a regression model for analyzing object set references in dimensional data. This utilizes the above sequence. b_1 objectively being the first replicator set for transferring information obtained from regression analysis.

You have the summation of the first strand of molecular data minus its mean. That is, it is being subtracted from the secondary strand of data and its mean. You then divide the equation for the first strand to the second power. This small numerical a small piece of data for the reoccurring computational model for processed information.

DNA Storage

This is an example of QSPR being diagrammed for the response variances that happen in our DNA. Here, you have the origin and block for the beginning to end of the DNA strand. In our model, a reference to the response variances and molecular composition of our DNA is also being included. Sequentially, the DNA has these different response variances that communicate information to our cells and genetic makeup. These are the algorithmic sequences happening inside our DNA.

Figure 4: Optical flow model for molecular response variances communication.

1.1 Tunneling Algorithm

$$\Gamma = Z \sim (S, T) \quad (5)$$

This sample proof has the Euler–Mascheroni constant which sets the distributions for Z being the object set reference. This equation can be simplified as the following in relation to Quantum Tunneling and QSPR, and its implications:

$$\Gamma = \lim_{s \rightarrow z} \left(-\ln s + \sum_{t=1}^s \frac{1}{t} \right) \quad (6)$$

The limit is set for the strand and set sequence. The patterns are represented by the continuing base pairs. So for a tunneling algorithm,

$$\Gamma = \lim_{s \rightarrow z} \left(-\ln s + \sum_{t=1}^s \frac{1}{t} \right) \cap \lim_{s \rightarrow z} \rightarrow \infty \quad (7)$$

theoretically you can have this sequential pattern and combined set of elements formulating over and over again. This will be until no chemical information is being processed. The mathematical representation therefore represent the theoretical processing of information through DNA storage. Just as a computer, one does not have a set increment on the set time limit for the biochemical processing of information. Predictive analysis is not set for chemical response variances. These harmonic patterns therefore represent continuation of processing of biochemical information.

Elements of DNA

DNA has a double helix pair and nucleotide bases that store information for biological functions. What is fascinating in the field of computational sciences, is what DNA is theoretically capable of doing. According to *Science Magazine*⁶, one can store 215 petabytes worth of data into a single gram of DNA. The fact that DNA has these base pairs to form these computational-like functions that transfer data from one pair to another seem quite applicable on what understanding DNA can mean for the future of computing. The idea that one can have this synthetic algorithmic network that functions in any systematically similar capacity. It changes the way modern algorithms are designed in general.

Even Quantum Computing in essence will have to be put in an entirely different scale. When combining this with other theoretical technologies, the future seems almost limitless. Technologies such as interstellar communications, discovering nuclear fusion, or building space crafts traveling in light years would be considered child's play compared to standpoint. Even simulating Super String theory or M theory would not be as sophisticated as what this research can provide. Using the same type of sequential logic DNA uses, one can create custom algorithms for solving the unknown.

Implications of Quantum Similarity in Genomics

In terms of genetics, it can take about a day for some of the most advanced computational infrastructure to analyze the human genome. The Microsoft Azure cloud has made significant advances in lowering the cost of genomic analysis⁷. Even advanced mathematics and mathematical proof allow us to create algorithms that more advanced in the analysis of genomic sequencing. With the ability to recursively analyze processes in computing, and the trivial mathematical theorems, one can provide for forming large algorithmic proofs which expands the possibility of this research.

Quantum similarity and many other advanced concepts are also taking a large role. Advancements in modern medicine will be possible once people map out genomic data and computationally analyze it against case studies

or open bio-portals. An example of this is immunology or researching into cancer genomics.

Figure 5: Sample plot of genomic data[27].

⁶ Service Mar, R. F., BlausteinOct, R., MervisOct, J., Voosen Oct, P., Waldman, S., & E News Oct. (2017, December 08). *DNA could store all of the world's data in one room*. Retrieved October 22, 2018, from <http://www.sciencemag.org/news/2017/03/dna-could-store-all-worlds-data-one-room>

⁷ Bergeson, T. (2018, June 15). *Power the democratization of genomics with the cloud*. Retrieved October 22, 2018, from <https://cloudblogs.microsoft.com/industry-blog/industry/health/power-the-democratization-of-genomics-with-the-clo>

The shrunk image above is take from an open source project I did⁸ utilizing RapidMiner studio and open portals for genomics data. This is just a small example of what is possible with genomic sequencing. Creating a small algorithm for regression analysis, one is genetic mutational views or complexities not easily viewed on open data. small fraction compared to the advanced processes that can be done computationally. Utilizing more advance computational proofs or constraints, will allow us to solve complexities that can modernize medicine. The usage of Quantum similarity and logic along with the usage of genomic sequencing, allow for us to form more accurate analysis. This is because once you know how DNA communicates, how it stores information, and have a generalized idea of the sequential processes of DNA, the accuracy of your models will be much more in depth.

Figure 6: Linear visualization of genomic data[27].

Also, this shrunk image above from my same project, utilize the same predictive analysis for applying regression analysis on these sample ids, genetic mutations, and case studies in a linear data visualization.

Being able to have set computational models or visualizations utilizing sequential processes and mapping allows you to get much more accurate data sets while consuming less storage. The computational data can sequentially be analyzed recursively in a similar manner to the logic of QSPR.

DNA's Data

Logic of DNA's Computational Data

DNA works logically with its object set references. One looks at the patterns that our DNA creates as fairly algorithmic. You have biological information being communicated through the chemical synthesis that happens in your DNA. As mentioned, this shows that DNA acts almost as its own computer. One can view a computer as having these halting sequences, or mathematical complexities such as Quasi-Polynomial time. There are numerous examples or reoccurring logical sequences that a computer takes its time to solve. The way our DNA transcribes information, functions in a similar but more advanced manner. You have set limits for these base pairs and in time complexity algorithms, exponential time is represented as $2^{poly(n)}$, you have some biochemical processes formulating slower than others. For Quasi polynomial proofs as $2^{poly(\log n)}$, one can look at naturally occurring time patterns through approximation. Although genetic algorithms or representations are represented through more linear processes, DNA transmits data almost through polynomial set references. You have these bases having object set references that follow recursive patterns and biologically transcribe instructions over and over again. Each one is sort of tagged and has this reference point for an advanced biochemical process. Some biochemical processes have constraints and others don't. They all follow a set reference that is still naturally algorithmic. Quantum Similarity represents these set reference happening in our molecular response variances and an overall metric that leans towards the mathematical representation of our DNA.

DNA's Metacodes

Metadata describes other data or information about information.⁹ If you look at our DNA in general, the chemical synthesis that happens transcribes instructions. The metacodes or data for that information is the chemical processes, combinations, and response variances that describe a certain biochemical process. Theoretically, one can say that every biochemical process follows a certain type of representative pattern at a representative time. Looking at QSPR and time complexity, one represents this process going on. Certain metacodes or descriptors of information are more unique than others. This is why sequencing allows us to look at certain complexities or unique describers. Just as advanced computers are analyzing certain complexities such as unknown mathematical proofs, the complexities in DNA are much

⁸ Kamal, A. M. (2016). *Data Mining Cancer Genomics Case Studies*. Retrieved October 22, 2018, from <https://devpost.com/software/data-mining-cancer-genomics-case-studies>

⁹ Metacode. (n.d.). Retrieved October 22, 2018, from <https://www.thefreedictionary.com/Metacode>

more advanced. One can theoretically represent a found complexity and utilize algorithmic designs or programs for formulating highly computational tasks. The knowledge unlocked in certain molecular descriptors are in essence what formulates certain building blocks or biochemical processes happening at certain times. Even micro-evolution, heredity, or genetic mutations follow a set object set reference pattern of transcribed biochemical code.

Science and Probability of the Means of Design

Next, we look at what this means in terms of the theoretical origin of things. As questioned in the “Evolution 2.0 Prize”,¹⁰ the information in knowing the algorithmic processes of our DNA changes the way we look at science in general. One can see that these objective set of mathematical laws formulate and govern the universe.¹¹ People question the objectivity of whether or not math in essence can prove the existence of intellectualism involved in the creation of the universe. However, the mathematical implications and patterns that go into our DNA can provide some usage of practical implications. Even human consciousness follows some sort of indicative pattern. As humans have free will, one can indicate that the patterns happening deeply in their neural thinking processing formulate at different times and time complexities.

The late Prof. Hawking¹² even argued that since the universe has fundamental laws of sciences, then a creator must be subject to these laws. However, the reverse logic of this argument is that it is theoretically feasible that before the existence of time itself something or someone fundamentally created set laws of origin. This is not an argument of pseudoscience because mathematics can universally exist independent of our own physical realities¹³. In comparison to how our DNA processes information and Quantum similarity in general, even biological processes are subject to the fundamental laws of mathematics. In theory one can argue that random genetic mutations are also indicative of a mathematical pattern. One can argue that the laws of mathematics existed since the beginning, however, the fundamental question lies that if math can lie outside our physical realities, it is indicative of some sort of intellectualism.

The set theories of mathematical laws is that even DNA has a higher proposed implication then what was once thought of. The theoretical analysis of how we look at our DNA could be quite intriguing to the fundamental unsolved problems of theoretical physics. Even looking at Quantum gravitational theory of atomism, one sees that theoretical physics can be in harmony together. Questions such as the average live of a proton or things physics is yet to determine, could all be looked at as time complexities or recursive sequences. This in essence shows that DNA is subject to similar fundamental mathematical laws as other occurring phenomena. The main difference is in the mathematical representation of these laws as well as their proofs and formation.

According to Dr. Ali Binazir¹⁴, the odds of one existing is 1 in $10^{2,685,000}$ and this number expands as the human population expands exponentially. Even looking at just a sperm meeting an egg, the probability is still 1 in 400 trillion. However, in implications for genomics, the probability of humanity existing at all gets slimmer and slimmer. This is because the rarity of the computational patterns in our DNA happening the way that it is. These mathematical probability vs. possibilities have less to do on whether or not we look at the existence of the universe as unlikely, rather than the statistical nature of the laws of the universe being governed solely by math. Even randomization is impacted by the laws of logic. If math is in harmony with being outside of our physical realities, then the way we look at the fundamental building blocks of life is quite profound as mathematically subjective. The theoretical implications of what science believes governs these mathematical laws has even bigger implications then what one might realize. The creation of dark matter itself or the universe's origin point can then be computationally representative of the algorithmic nature of the universe. As fundamental physics must have invoking algorithmic representations and proofs to lead to major breakthroughs in Quantum Physics.

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¹⁰Marshall, P. (n.d.). *Artificial Intelligence Origin of Life Prize, \$5 Million USD*. Retrieved October 22, 2018, from <https://www.herox.com/evolution2.0>

¹¹Nelson, R. H. (2018, September 18). *Arguments why God (very probably) exists*. Retrieved October 22, 2018, from <http://theconversation.com/arguments-why-god-very-probably-exists-75451>

¹²Gabbatt, A. (2010, September 02). Stephen Hawking says universe not created by God. Retrieved October 22, 2018, from <https://www.theguardian.com/science/2010/sep/02/stephen-hawking-big-bang-creator>

¹³Nelson, R. H. (2018, September 18). *Arguments why God (very probably) exists*. Retrieved October 22, 2018, from <http://theconversation.com/arguments-why-god-very-probably-exists-75451>

¹⁴Spector, D. (2012, June 11). *The Odds Of You Being Alive Are Incredibly Small*. Retrieved October 22, 2018, from <https://www.businessinsider.com/infographic-the-odds-of-being-alive-2012-6>

Analysis of DNA

Constant of Information in DNA

Constants are non-altered values¹⁵ or information being processed in computer programming. Regular chemical synthesis and even genetic forms of mutation have constants in their values. Even when a mutation happens, a sequential flow also happens in the transfer of biochemical information. This sequential flow creates a trace of data in the nucleotides that store information about the chemical sub-processing going on. The idea of Quantum similarity and a certain set of object references for these chemical processes show more of an algorithmic sequencing than what one might realize.

Chemical synthesis seems to always be taking place but the rate, complexity, and time of a set process is deterministic on the nature of the instructions being transcribed. These recurring processes happen in different forms and sequences.

Decomposed Analysis of DNA Design

The way our DNA works seems almost computational in its natural form. You have these biological processes and mathematical thresholds demonstrating its chemical synthesis. Things such as the constraints showed previously, as well as the regressional transcribing of biochemical instructions formulate a base point on how the information is transmitted. The metacodes and what is being described as well as the non-altered values represent a logical flow of information. Just as neural networks propagates output layers or recursively transmits information, the same can be said about our DNA's base pairs.

Dynamic Phenotypes and Correctional Networks

The way one analyzes neural networks, is similar to the types of computational networks being analyzed in our DNA. Binary Neural Networks in particular, have this deterministic threshold for their functionality. A DBN or (Deterministic binary neuron) can hence be mathematically represented:

$$DBN(x) = 1_x > 10^{16} \quad (8)$$

This is similar, but not as advanced as the computational representation for the complexities of our DNA's processing of sequential and chemically synthetic information. Utilizing mathematical representations of biological networks and formations allow us to create indicators or advanced mathematical models for our algorithms to systematically optimize functions to better analyze complexities.

Regression Analysis of DNA

Using QSPR, genomic sequencing is important for the regression analysis of our DNA. As proposed earlier, mapping out the human genome and creating subsets of sequential patterns allow us to lead to further biomedical breakthroughs.

Figure 7: Data view from RapidMiner.

The figure above¹⁷ is another sample from my RapidMiner project. This is a view of ICGC donor data from that same data set.

One is able to view different data by donor, sample ID, and see the complexities in certain genome types or mutations. Things such as combinations of helper cells, or gene therapy or immune boosters are more feasible when you utilize genomic sequencing with large data sets and algorithmic proofs. This is yet another small example of the theoretical potential that is possible with the mathematical representation of our DNA, and the overall view of what genomic sequencing can provide. Hence, another reason on why mathematical formulations can be used to represent both biological or non-biological networks.

¹⁵(2018). *Constant*. Retrieved October 22, 2018, from <https://www.encyclopedia.com/science-and-technology/computers-and-electrical-engineering/computers-and-computing/constant>

¹⁶Dong, H., & Yang, Y. (2018). *Binary Neurons*. Retrieved October 22, 2018, from <https://salu133445.github.io/bmuseg>

¹⁷GDGC Data View [Personal figure screenshots from RapidMiner]. (2018).

Quantum Origin Boolean Tags

For object set references, one can represent Quantum similarity set references as well with Boolean tagging. The same Boolean tagging that can be used to represent Quantum information can be utilized in a representation for the states of sequential information being processed in our DNA. One set proof is the preliminary function $f : \{0, 1\}^n \rightarrow \{0, 1\}$ ¹⁸ where you are representing n variables. The same tags can be applied to object set references.

Computational Proof Theory

One equation I want to reference is the Ramanujan- Δ -function: $\tau(n) = O(n2 + \varepsilon)$ for all $\varepsilon > 0$ ¹⁹. You have an indicative reference to space and functional complexities for viewing regressional complexities. If you utilize the same constraint as $\Gamma = Z \sim (S, T)$, and set its limit, you can apply a functional proof for representing recursive sequential data in chemical synthesis. The reference is $Z \sim (S, T) = O((S, T) + \varepsilon)$, ε utilizing the origin's point of the strand's object set reference instead of zero.

Conclusion

The usage of Quantum Similarity through the equation $Z = \{\forall \theta \in Z \rightarrow \exists s \in S \wedge \exists t \in T : \theta = (s, t)\}$, represents a way to analyze the way communication works in our DNA. Being able to create the object set reference for z being (s, t) in our DNA strands, we are able to set logical tags and representations of our DNA in a completely computational form. This will allow us to have a better understanding of the sequences that happen in our DNA. With this approach, we can also utilize mathematical formulas such as the Euler–Mascheroni constant, regression analysis, and computational proofs to answer important questions on Quantum biology, Quantum similarity, and Theoretical Physics.

The final response is a conclusion on these proofs. The view that DNA and biological life has an algorithmic design, among with the view of the mathematical representations regarding Quantum similarity, object set references, computational proof theory, and complexity algorithms lead to the introduction of Quantum Similarity Origin Point References or QSOPR theorem in general.

2 Utilizing Quantum Similarity for Mathematically Representing our Universe

Introduction

The first part of my paper is the explanation of how we view time. This is fairly important for coming up with an agreeable and unified view of our universe. Time is the beginning of the universe's origin point. It is when the universe as we know it have came into existence.

Anything before the beginning of time itself, or our universe's origin point, doesn't have to comply with the natural laws of our universe. Nor does anything before the origin point of our universe have to comply with the laws of mathematics, logic, or our understanding. This is an important note to point out, because once we agree that the universe has some sort of theoretical "origin point", we can begin explaining the unified laws that govern our universe. Now before we look at cosmic radiation, the composition of matter itself, or even dimensions and multiverses, we need to explain the theoretical. This is why we have string theory. The elementary particles we observe and even extremely light and small subatomic particles, make up these theoretical strings that are nearly the scale of Planck length. These strings that are nearly impossible for current technology to observe can theoretically create a metric for us to explain wavelengths, dimensions, and other important aspects in theoretical physics. Now we have this framework that can help us with the explanation of the very foundations of what makes up our universe as well as what science can't help us observe. Atoms represent the smallest constituent unit with constant properties.

¹⁸arXiv:0810.2435[quant-ph]

¹⁹Jannsen, U., Dr. (2016). *Deligne's Proof of the Weil-conjecture*. Retrieved October 22, 2018, from <http://www.mathematik.uni-regensburg.de/Jannsen/home/Weil-gesamt-eng.pdf>

However, these strings and extremely light subatomic particles are vastly smaller than atoms. These combination of strings formulate what begins to be the composition of matter. What is even more fascinating is one can look at the trivial ways these “strings” are connected and begin to start a journey on the mathematical representation of our universe. The whole universe then begins to look as some sort of algorithm with intact mathematically formulated laws that communicate with each other.

Looking at the universe through a purely mathematical and theoretical scope allows us to start explaining the unobservable. First let us start with describing the less explainable in this sort of “unobservable” circumstances. One of the most non-observable is different dimensions of the universe. We look at these different dimensions as having multiple universes with different set combinations. Think of parallel universes. Since, the universe is infinitely expanding, we have these different universes with different set of combinations that are possible. Universes systematically similar to ours could have beings similar to us doing slightly different things. What is fascinating is how we view the rules of logic is systematically similar for how we would view the rules of logic in their set universe.

Every universe follows a systematic combination. Just as how Quantum Similarity can function in our DNA, other naturally occurring phenomena can be explained mathematically. Every mathematical sequence follows certain patterns over and over again either recursively or at halt. The universe itself and the non-observable and observable can be described with these representations of mathematical randomizations. This means that since one can seemingly view the universe as being random, the fact that we have these infinitely expanding series and possibilities means it all could characteristically follow a recursive pattern.

Sample Natural Homomorphism:

$p : A\Gamma \rightarrow B(Hv)$, this is in relation to a question seen on MathOverflow in regards to Quantum cellular automata. This relation for Hv is in Hilbert spaces where $B(Hv)$ is its algebra bounded operators for its constraint. This is a small part of the overall equation I wanted use. We conclude that:

- ☐ Multi-dimensional space vectors can be implied in Hilbert spaces
- ☐ Natural Homomorphism occurs in group and ring link structures
- ☐ We live in a 3-dimensional space
- ☐ When looking at the algebraic constraints for hilbert spaces it is similar in mathematical formation for the constraints seen in object set references or Quantum similarity
- ☐ Thus the mathematical patterns for Quantum cellular automata try mimicking these same patterns.
- ☐ It is logical to conclude other dimensional spaces are under similar mathematical phenomena if all dimensions started at time’s “origin point”.
- ☐ A scientific challenge to propose is that all instances of the universe runs in different set sequences for the variances of its mathematical laws.

Next the Free Particle Equation:

- ☐ In non-relativistic mechanics we use $-\frac{\hbar^2}{2m}\nabla^2\varphi(r,t) = i\hbar\frac{\partial}{\partial t}\varphi(r,t)$ which is the Schrödinger equation for describing particle duality.
- ☐ For the Heisenberg Uncertainty, we reference $\Delta p_x\Delta x \geq \frac{\hbar}{2}$.
- ☐ In terms of relativistic vs. non-relativistic measurements let us look at the Ives-Stilwell experiment
  - ☐ When looking at the relativistic measurements it is best to make sure it is in harmony with classical measurements
    - ☐ This is true especially when testing the relativistic time dilation for the Doppler shift in light.
    - ☐ The way light travels, especially when testing the transverse doppler effect should be described accurately by classical mechanical measurements
  - ☐ There is different diversity in the way waves propagate.
    - ☐ This means since we have an understanding of these subsequent strings and what makes up what light is, then we can say the formations of waves can differ from time to time.
    - ☐ Classical mechanics and Quantum similarity can provide a universally applicable way for us to understand the universe through a mathematical and algorithmic thought process
    - ☐ Wavelengths are all a fundamental form of mathematical sequences all running at different time sequences. Just as we see how molecular compositions can be read as the same object set instances running at its own algorithmic and pattern based sequence, the same can be said about wavelengths.

- We can confer that what we are viewing as absolute the patterns as absolute but the time sequences of these patterns as randomized or relative all forming highly complex mathematical harmony with each other

Looking at classical Quantum mechanics, the universe has had some sort of mathematical formation bringing everything together. Even dark matter and the other vast cosmic areas of the universe that are harder to explain follow a mathematical pattern that is consistent in the way it performs. Everything acts as if its own instance following reference points and systematic mathematical patterns. Therefore, in all the areas of Theoretical physics equations related to Quantum similarity and classical mechanics can provide a more in depth understanding of the supposed theoretical nature of our universe.

Conclusion

Quantum Origin and many other important aspects of theoretical physics can go hand in hand with Quantum similarity and many of the unknown theories in regards to dark matter, the origin of time and the very laws that make up our universe. Utilizing many principles such as Classical Mechanics, Quantum Similarity, as well as the modern day brilliance of Edward Witten, Leonard Susskind, Halton Arp and the Heisenberg Uncertainty Principle, physics is unified. This is why we will look at some classic proofs such as Recession velocity, the Transverse Doppler effect, Quantum origin, and the mathematical nature of Quantum similarity. The classical free particle equation $P = MV$, and the constraint $\Gamma = Z \sim (S, T)$, will be used in part of my paper. This paper will also include natural homomorphism $\rho : A\Gamma \rightarrow B(Hv)$ and object set reference constraints to describe their unity with the subject matter of Quantum Similarity. This will help propose scientific proofs for analyzing the mathematical or computational representation of our universe, its formation, and a stepping stone towards a unified theorem for explaining most of dark matter, energy, and the universe.

3 Algorithmic Quantization for the Analysis of Wave Propagation, our Universe and Cosmic Origin

Our Universe 0 to ∞

EVERYTHING AS AN ALGORITHM-COMPUTATIONAL ANALYSIS AND MODEL FOR SPACE/TIME COMPLEXITY

What is everything

The best explanation of our universe is that we all know it has an origin point. As described in previous research, the beginning of time is when this hypothetical origin point started. This means that anything before the universe's origin point doesn't have to follow any of the laws of the universe or the principles that make the universe in harmony. There are likely two possibilities when looking at the universe. The universe is either entirely random or it is at harmony with these systematic patterns. In the structure of our universe, if it follows systematic patterns then this makes it easier to understand the very foundation of our universe and how it performs. Everything we look at including time itself will be explainable through simple mathematical variables and the complexities are already there for us to analyze. Our understanding of the universe is fairly limited, but it is quite obvious that the universe follows systematic and algorithmic patterns. Describing it in complex terms or even layman terms is but a struggle of modern day science. Once one accepts that the entire universe as we know it is mathematical, then we can begin having an overview of

our universe. However, one must also expect that before time itself, we as scientist can not conclude that prior to the origin point, mathematical laws existed. If the universe is created out of nothing, one can conclude it started at the point of origin. However, explaining the mathematical harmony of the universe would be exceedingly difficult, and likely impossible. If some randomized event or design happened before the origin point, than we can systematically look at the mathematical laws that govern our universe afterwards. However, scientist most realize either way the physical nature that we are observing is applicable towards after the universe's origin point. Pure theory alone can't explain the less explainable if we are limited to the mathematics after the universe's origin point. We must look at the sequences of nature, patterns, and statistical variances of what is going on.

Object-Set References

The algorithmic process seen above is basic recursion. This happens all throughout nature and even in simplest forms in Quantum Similarity, boolean logic, etc. For every sequence that happens either the information halts or continues. For our biomolecular sequences, once a process halts, there is usually still a continuation of another sequence. The most complex forms of recursion is best described with what happens in between. For example, besides this, what replicates information? What is the communication happening between and what is the randomized sequential data being transmitted? In the hierarchy of things, it is dependent on what is being analyzed. For DNA you have these replicators, and strand origin. For DNA, you have these sequential molecular response variances and what is described in QSPR. However, when looking at recursion for other set natural processes in the universe, the things happening in between utilize different data models with systematically similar mathematical patterns.

Continuing Recursion Sample

The example image to the right shows what happens to simplified recursive patterns when you add a bit of logic and hierarchical learning. The sample simple xml chart we seen earlier is now much more complex. This is why the sequential patterns in nature have their own uniqueness for complexities based on the data model being followed. Us as a species rely on harmonized mathematics for the continuation of our universe. This is simply how the laws of nature works. Not only is logic itself algorithmic but fundamental sub-processes that happened after our universe's origin point all follow a harmonized mathematical pattern. Even when information itself halts or an end event happens, a continued process of data transmission or logic happens afterwards. Time in essence is all mathematical recursion. As the universe expands, the mathematical complexity of the universe becomes more and more in depth. Even us as a species become more and more improbable in our own existence, and the statistical order of the universe is in itself a harmonized pattern. All of mathematics is discrete, and every sub-process of that happens given a

certain event is a continued sequence of its own. Even random events or statistical outliers happen at recursion. Given the universe's expansion, these events are no longer

considered random. Even if the universe halted, the very statistical nature already is a profound harmony given what is observable in fundamental nature.

Geometric Symmetry

As we already know, our universe is observably three dimensional. Everything in our universe follows this systematic symmetry or mixed geometry. Even the human anatomy is its own unique symmetry. The fact is that the objective or dimensional views of the universe all follows a systematic pattern as well. Vectors and space as we know is fairly algorithmic and systematically point to point. One can not look at the universe as just set integrals but also as interconnected strings. Even different universes or what is non-observable follows some sort of characteristic pattern with expanding probabilities.

Quantum States

We also have different states of isolated quantum systems. These states are able to describe particle position, vector spaces, and an overall characteristic view that can be utilized in wave propagation. One can utilize Quantum states to have these different sets of linear combinations of time and vector spaces and create a probabilistic and statistical model. Let us say you have a randomized state, ϕ . Then let us say this state has different densities and positions for a set particle. The position can either be purely absolute or it can be relative as it is randomized and the set particle can form a string with another particle or break off on its own. The relative vs. absolute position and state the particle is in, is similar to the Schrödinger's cat analogy in which it is in an existent or now non-existent state and what happens in between.

Wave Algo

The above example is a simple diagram to illustrate the following point on waves:

1. Let A represent the starting point (Strand)
2. B and C are object set references
3. F is the wave composition
4. L is the continuation of the wave
5. N represents the end point

One can say all waves systematically represent an object-set reference. In terms of nature, what happens in recursion is that all created, simulated and represented waves are algorithmic. This is an example of the importance of mathematics in terms of the systematic nature of our universe.

$$\text{Point A} \longrightarrow (\text{Propagation}) \longrightarrow \text{Point B.}$$

The propagation in terms of “waves” is the data or what is being transmitted as set references. This is another way we can represent that nature is purely mathematical recursion.

Important Methodology

- QSOPR Theorem: Quantum Similarity Origin Point References Theorem
- The Ramanujan- Δ -function: $\tau(n) = O(n + \varepsilon)$ for all $\varepsilon > 0$ 19
- Set Constraint: $\Gamma = Z \sim (S, T)$.
- Objective instance: $Z \sim (S, T) = ()O(S, T) + \varepsilon$.
- Boolean Tagging: $f : \{0, 1\}^n \rightarrow \{0, 1\}$.
- Quasi-Polynomial Proofs: $2^{\text{Poly}(\log n)}$.
- Tunneling Algorithms

Our Universe

Our universe has its own set origin, but every multiverse that exists is part of the set origin. Since the beginning of time was the origin point of everything, then even as the universe constantly expands, they all follow everything after this set origin point. Mathematics fundamentally harmonizes everything in nature.

Natural Sequences

It is certain that:

- ☐ Patterns in nature are sequential.
- ☐ Patterns in what is non-observable after time are sequential.
- ☐ As the universe expands, recursion is happening.
- ☐ Mathematical recursion is the continuation of natural laws for the universe.
- ☐ The universe is mathematically constrained towards its own origin.

Event Randomization

It is also certain that:

- ☐ While the universe constantly expands, randomization is no longer random.
- ☐ Any "halting periods" in nature would mean that:
  - ☐ Randomization is only a thing at halt.
  - ☐ Event at halt:
    - ☐ Mathematical recursion was happening since origin to halt.
    - ☐ Therefore, everything was mathematically sequential regardless.
  - ☐ If the universe is algorithmic:
    - ☐ The only thing that can halt expansion of the universe most not follow the laws of the universe.
    - ☐ If nothing existed before origin, then we can't explain the unknown
      - ☐ If we can't explain the unknown, it is impossible to prove prior to origin existence
      - ☐ If the universe has its own set origin point then everything is randomized and hence nature isn't mathematical.

- ☐ Therefore, we come up with the following conclusion:
  - ☐ Intellectual Design
    - ☐ Prior to origin point no requirement of mathematical laws.
  - ☐ Randomized
    - ☐ Mathematical laws are random.
    - ☐ Therefore, the universe isn't systematic.
    - ☐ Fundamental laws are likely infinitely hypothetical.

FHB Galaxies

FHB galaxies as described earlier by astronomer Thomas Zolotor are defined as “Faint Hubble Bubble Galaxies”. They are so far that the hubble telescope sees it as faint. This is the maximum of our observation point. What we can possibly see is likely less than 0.00001 our known universe, and that number is actually very lenient in my guess. It is actually more and more closer to zero given the continuation of our universe and the cosmic activity that takes place. The interesting part is that our universe in essence is seemingly an infinitely expanding mathematical pattern. Even at a theoretical halt, (which is basically near impossible), it would all form a giant mathematical model. Cosmic activity in our universe adds to the algorithmic and recursive nature of the mathematical harmony that takes place. 100s of billions of galaxies can be made seconds by seconds with expanding probabilities following recursive mathematical patterns.

Conclusion

This paper has utilized advanced computational mathematics and Quantum statistics for an algorithmic view on our universe. We will look at the theoretical nature of wave propagation, different Quantum states and propose a mathematical analysis for how it ties all together. Sequential equations applicable to nature and a utilization of Quantum similarity as proposed in my previous papers will also be used. The purpose of this paper is to provide a new approach to algorithmic Quantization in terms of describing the biggest complexities in Quantum Mechanics.

The non-observable universe or what science is far from telling us will never be computationally modeled as much as computationally represented. We can say that the universe is the expanding algorithm with set origin point references. However, we can only model the beginning from time to the continued expansion. It is therefore systematically inaccurate to come up with a view or illustration for all of our universe unless you utilize the basis of an algorithmic system for an overview of your model. This is why all of theoretical physics is modeled as the cosmic origin point and beyond. As seen in the third figure of this paper, what is happening during the continuation of time is the nature of our “universe”.

4 The Infinite Quantum Loop Series: Multi-Dimensional Quantum Breakpoint Theorem

$$X = O + \sum \check{H} + \frac{(n(\log)\check{Y})^2}{Pd}$$

$O + \sum \check{H} + \frac{(n(\log)\check{Y})^2}{Pd}$ → Expanding universe and expanding objects in time.

$\check{H}$ = Quantum State

$\sum \check{H} \approx$ the sum of all Quantum States.

X - means before the origin point of time.

$\check{Y}$ - means unknown n states.

Pd - means fake known states.

$n(\log) \approx$ natural logs representing sequential patterns in nature

Relative points that formulate planes in space are represented as dimensions. Each of these so called points or coordinates all started from the same theoretical origin in time. That origin is known as the origin point of all things. Before time itself existed, you had nothing, once time existed, then the physical realms that make up our expanding universe have formulated. Amongst the existence of the multiple dimensions comes Quantum states, fundamentally sequential patterns in nature (Quantum Similarity present), and the laws of mathematical logic that formulate the universe we are in. Multiverses also unknown of our current reality would still follow the origin point for the existence of time itself. As the logic is fundamentally the same for a unified definition of time. This is why when formulating the logistics of what the universe came to be, we must accept that the very foundation of our universe has an origin point.

Let us now look at how we view mattresses in space and time, extremely light subatomic particles or antimatter in the theorem for everything. First off, we have relativistic measurements for what we know, even though there is the experimental flaw in the Ives-Stilwell experiment. The things that is unknown or false positives in physics can't be explained by pure relativistic theory. As though some aspects derived from relativity view how we see light traveling or the formulation of energy, it doesn't provide a grand and unified theorem for everything. For example, no physicist should be able to claim that energy and mass are interchangeable, or even what energy is actually equal to. The fundamental reason is that one would have to accept that all energy in the universe is exactly the same, including in undiscovered multiverses or unknown states of matter.

Technology can one day find an offset of energy that changes the rules. What if energy is formulating a new state of matter, or what if you find an infinite source of energy in an unknown universe formulated from subatomic particles that are faster than the speed of light. Isn't there a theoretical potential that some subatomic particles are already faster than the speed of light? What about the slight inaccuracies in the "Global Positioning System". Relativity is just what scientist have formulated as the best we have, but our deeper understanding of time, energy and the universe is actually further explained by Quantum Physics.

Quantum Physics goes further beyond the speed of light and is able to articulately describe the patterns in nature. The fact that everything follows an origin point and that origin point is the beginning of time itself, and it can all be unified in by Quantum theorems and advanced mathematical frameworks gives us a lot to expand upon. Our view on the very foundations of the physical manifestations that make up our universe is then changed, and we have a much broader understanding to expand upon. When looking at a grand unified theorem for everything, and our universe then we can see that these multiple dimensions have there set of sequential patterns that follow origin point strands and that the different geometrical patterns and states of nature still follow a logistical pattern.

Even looking at Quantum based computational systems, they still follow a Qubit based processing design that is formulated as a physical representation of a two-state Quantum-Mechanical based system. If Quantum Computing becomes further researched and more portable (as with what I am doing in the field), it can have highly advanced breakthroughs. However, this small representation meant to be one of the biggest engineering challenges of the 21st century is a minuscule representation of nature. The biggest engineering challenge of our era along with other problems such as Nuclear Fusion doesn't even make up 1/1000th of a percent the complexity of our physical reality. You have a series of Quantum states, you have unknown states in matter, and you even have things that can't be physically represented. The complexity of these patterns of nature are what formulates some of the greatest laws that make up our universe.

Let us explain an unknown state: We have beyond unknown states of matter, and even beyond Quantum states. We look at what is an unknown "body" or unexplained "anomaly" of physics. This is different then a false positive. You having an idea of an unknown allows you to formulate a standard for creating more expansions to theorems or ideas in physics. In the grand theorem of everything, all of physics including unknown is described as being derived from the origin point of time itself. This goes hand in hand with Quantum Similarity Origin Point References or QSOPR Theorem. Classical Mechanics can then be unified with Quantum Similarity and you having subjects such as Quantum mechanics allow you to take it a step further and explain the aspects that derive our universe.

Conclusion

I derived the equation $X = O + \sum \hat{H} + \frac{(n(\log)\Phi)}{Pd_x}$ for the representation of our universe under the origin point and dilation of time, t . This theorem will be one of the biggest of our understanding of the universe and what Quantum Origin as well as Quantum States symbolizes in terms of mathematically representing the universe as we know it. Following the same rational and logic with Quantum Similarity we have a much bigger picture of the mathematical framework that our universes is under. This will henceforth be one of the main papers in a series of others that explains our universe through Quantum physics and infinitely expanding loops and ripples in time.

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