



A Quantum Perspective Model to Genetic Codes Through Various Sciences

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ABSTRACT

The diversity of scientific disciplines is explored by many researchers. This article tries to search for the relationship between pi numbers and genetic codes. Twenty-two (22) seven (7) manual division, the result of the process after the comma is similar to the nucleotide base codes: As in fourteen (14) groups [Uracil (U), Thymine (T), Adenine (A)] forever. Written in reverse order, from UTA to ATU, as in the direction of reading gene expression between DNA and RNA (3' to 5' direction and vice versa). After searching this consequence in NCBI databases, some conceptual relationships were acquired regarding to living creatures. Because, the findings of NCBI (National Biotechnology Information Center) search result are similar to **ZEBRAFISH-DANIO RERIO**. It has been proved that Zebra fish genetic codes are very similar to human genetic codes. Additionally, these consequences are indicator of relationships between bases in biogenetics and other sciences. Secondly, not only are the maximum value number of the acid base ratio scale in chemistry fourteen but also, the number groups of each Pi are taken in math calculations related to nucleotide bases, fourteen too. Lastly, the chemical structures of bases include Carbon(C), Nitrogen (N), Oxygen (O) and Hydrogen (H). In sum, this resemblance may be the beginning of interrelationships of sciences on the basis of **quantum perspective model** at minor level systems. In other words, atoms with the smallest structures of bases can be taken as a small unit of analysis from the same point of view as math numbers. In sum, both 428571 serial numbers of pi and the whole nucleotide base atoms have a cycling periods, too. This paradigm may leads to "Interrelationships of Sciences".

Key Words: π numbers, genetic codes, Zebrafish-Danio Rerio, NCBI and Quantum Perspective Model

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Introduction

Diversity of Scientific Disciplines: The variety of scientific disciplines in which complex system examples can be found means that there are rich and varied frameworks, tools and modeling approaches. In addition to the cellular automata models of categorical systems, from genetic algorithms, neural networks, computer science, Lambda calculus to theoretical chemistry and evolutionary biology models based on combination optimization from evolutionary biology to mathematics. In particular, on the basis of modeling, this perspective had a

number of interesting conceptual connections with different sciences (Magure *et al.*, 1999, p.35-36). But this patterns extend not only *biochemistry and mathematics* at the macro level but also include *Pi number's sequences* and nucleotide sequences at the micro level (We will see on the next pages).

1.1. Fractals: Fractals are infinitely complex patterns resembling each other on different scales [1]. Fractals and Pi numbers have a peculiar form methods about mathematical calculations with specialties (Çambel, 1993; Devaney, 1989; Levinson, 1994). The calculation of **Pi (π) number is 22/7. Be careful to calculate that the mathematical process applies only with paper and pencil.** (Please, don't

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use a calculator). As a result of a division, the process is 3, 1428571428571...and so on. The interesting number is **428571**, repetitiously! Science has developed something undiscovered. Mostly, the definition of the “new science” among the systems is a set of limited terminology and concept only in their interests (Magure *et al.*, 1999, p.21).

1.2. Codon Capture Stage: The evolution of proteins encoded in nucleotide sequences began with the emergence of the triple code (Trifanov, 2000). The end of the evolution of the codon table is the period of the codon, which is still in progress. Besides, all of the 64 triples are already busy and each new amino acid codon must be captured from the established codon repertoires (Trifanov, 2004: p1-11). **When you search the sequence of pi number in genetic sequences or algorithms, can it be possible just like as in triplet's previous ones?** As seen in Pi numbers, fourteen groups sequence repeat, forever: “**UTA**” (Uracil, Thymine, and Adenine).

It has also been reported that there is an interesting connection between the nucleotide frequencies and the Fibonacci numbers in human single helix DNA (Beleza Yamagishi and Shimabukuro, 2008). In order to simplify relation between numbers and nucleotide bases, the only necessary thing may be a quantum perspective at micro levels. Such as, pi numbers and genetic codes? Similarly, Fibonacci numbers and DNA as mentioned above.

Quantum Perspective Model to Pi Numbers and Genetic Codes

The genetic code enables the conversion of genetic information from ribosome. Owing to experiments, the beginning of the (standard) genetic code used as an a new formula (Nirenberg *et al.*, 1965). The genetic code with many triplets of nucleotides, such as 20 amino acids and 3 stop codes defined as a degeneration (Tidjani Négadi, 2007). Known as the 21st and 22nd amino acids, both are encoded in the order of UGA and UAG codes which process like stop codes respectively (Please remember also pi: **22 /7**) (Tidjani Négadi, 2007). Then this similarity can be shown in the number of pi against genetic codes. With quantum perspectives as genetic codes of the Pi numbers, are likely to be modeled as UTA. Even, forever **UTA's**. In relation to this formulation of the genetic structure, it is perhaps referred to as a “**Quantum Perspective Model**” for fractals and nucleotide sequences. But, a universal “**Fractal Genome Code Law**” suggested by Perez, according

to frequency and situation of each of the 64 codons in the human genomics concerning about genetic bases (Perez, 2010).

2.1. Calculation of Pi Numbers and Genetic Codes

Pi number's fourteen groups can be shown as continuously **UTA, UTA...UTA**. As an instance:

The **first** fourteen group of pi after comma: $1+4+2+8+5+7+1+4+2+8+5+7+1+4=59$. Just like as in Uracil (**U**):58.

The **second** fourteen group of pi after comma: $2+8+5+7+1+4+2+8+5+7+1+4+2+8=64$. Thymine (**T**):66.

The **third** fourteen group of pi after comma: $5+7+1+4+2+8+5+7+1+4+2=68$. Just like as in Adenine (**A**).

The **forth** fourteen group of pi after comma: $8+5+7+1+4+2+8+5+7+1+4+2+8+5=59$. Just like as in Uracil (**U**):58.

The **fifth** fourteen group of pi after comma: $7+1+4+2+8+5+7+1+4+2+8+5+7+1=61$. Just like as in Thymine (**T**):66.

The **sixth** fourteen group of pi after comma: $4+2+8+5+7+1+4+2+8+5+7+1+4+2=68$. Just like as in Adenine (**A**):70.

The **seventh** fourteen group of pi after comma: $8+5+7+1+4+2+8+5+7+1+4+2+8+5=59$. Just like as in Uracil (**U**):58.

The rest of the fourteen groups are the same as the previous groups. For example, the similarity of them is the **eighth** group of pi is equal to the **fifth** group of pi; the **ninth** group of pi is equal to the **sixth** group of pi; the **tenth** group of pi is equal to the **seventh** group of pi and so on... etc. It can be meaning of Pi sequence fourteen groups are “**UTA's**” forever. Let me try to explain this “**Quantum Perspective Model**”

The history of amino acid, sorted up with 20 amino acids by growing atomic numbers related to carbon, nitrogen and oxygen but not hydrogen. (Tidjani Négadi, 2002). Also, Perez stated a base code system referring to three significant integer numbers [golden ratio, 1(one) and 2(two)] (Perez, 2013).

The chemical structures of bases are **A, T, C, G and U**. The chemical structure of them: (**A**) Adenine:C₅H₅N₅:**70**; (**T**) Thymine:C₅H₆N₂O₂:**66**; (**C**) Cytosine:C₄H₅N₃O₁:**64**; (**G**) Guanine:C₅H₅N₅O₁:**78**,



(U) Uracil:C₄H₄N₂O₂:**58** (Lodish and *et al.*, 2018). The atomic numbers of them: Carbon(C):6, Nitrogen (N):7, Oxygen (O):8, Hydrogen (H):1 (Wieser and *et al.*, 2013).

The minor difference in Pi number fourteen (14) groups opposed to bases (A, T, C, G, U) related to **Quantum Perspective Model**. As seen in Uracil (U):58 versus to 59; Adenine (A):70 versus to 68, Thymine (T):66 versus to 64...etc. It may be possible to derive deviation reasons from molecular biology. In insignificant calculation of fourteen groups of Pi numbers due to this quantum difference. (Ester bonds, Glycoside bonds, Point mutations, Nucleotide substitutions and especially **Hydrogen bonds** H: 1). Hydrogen bonds can easily be removed For example; DNA bases, **Adenine (A)** pairs with Thymine by **two hydrogen bonds**, but modified AA-T complexes (**three-hydrogen bonds**) [3].

Tidjani stressed the Fibonacci sequence and genetic code is not only very suitable for the definition of mathematical structure (codon number, degeneration, characteristic patterns), but also classified according to its own increases in the classification of twenty canonical amino acids in agreement with *Non-hydrogen atoms numbers* (Tidjani Négadi, 2007).

Conclusion

Generally, models are mixed with chemical composition of the genetic codes and amino acids. Helix Nautilus is modeled with mathematical number sequences such as the Fibonacci sequence (Tidjani Négadi, 2007). However, in this example, unlike the Fibonacci sequence, Pi numbers sequences are likely to be similar to genetic codes. Because there are two result for sampling. One of them is the similarity of fourteen group of pi numbers are almost **428571**. This numbers **CYCLIC Number** (Sakai, 2007) or **Narcissistic Number** is called. Also, the numbers of Pi includes cyclic numbers "428571". Summarily, not only Pi numbers return, but also the genetic codes return, too [just like as respectively Uracil, Thymine, Adenine (UTA) revolves (ATU)]. Looking from correlative perspective between cyclic number and **gene expression**, RNA polymerase can only read the DNA strand in the 3' to 5' direction and synthesizes the DNA strand in the 5' to 3' direction [4] According to that mutual reversal perspective in biogenetics, The digits of Pi numbers expressed in triple genetic codes can also be reversed between (UTA) and (ATU). The meaning of this triplet is also significant and valid in

The National Center for Biotechnology Information (NCBI). If you take Pi numbers fourteen sequences as a genetic code "ATU" for a hundred times. The output of this nucleotide blast is similar to **ZEBRAFISH-DANIO RERIO**. It is an excellent favorite sample for many experiments about biology, gene sequences, nervous systems and brain disorders [5]. So, the other result is also meaningful in basic nucleotide databases (NCBI: *The National Center for Biotechnology*). Additionally, it is proved to be similar to human being genetic codes (NCBI Blast) [6]. As a result, the question of why do you take Pi number as a fourteen groups? The answer is future researches of **ACID-BASE RATIO (ph: 14) FOURTEEN!** By itself, the acid-base balance is not chaotic and meaningless, but it is also complex as seen only in Fractals, Pi numbers, genetic codes, chemical elements and scientific disciplines. At first glance it seems unrelated. But in reality, macro-level rotating systems, micro-rotating quantum physics systems and biogenic double-helix strands are related to bioinformatics. Not only were the previous sciences mentioned, but also other scientific systems associated with the quantum perspective model correlated. In mathematics, especially Pi numbers, Fibonacci numbers and the Golden Ratio, chemistry (element structure), physics (speed of Light number) and biology (genetic algorithms). etc. A broad application of the science relations between mathematics and biochemistry has also been determined in NeuroQuantology. The cause of this similarity may be the root of biotechnologies due to the smallest fractals of particles or quantum. As in the numbers of mathematics and the nucleotide base codes of biochemistry. Finally, the result of all these implications is "**Interrelationships of Sciences**".

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