

Angel Code

By Craig Paardekooper (23rd July 2023)

There is much evidence that living things are the product of intelligent design – which you can find here – [intelligent design](#). However, my intention is to go a step further – and look at the coding systems used by our putative creators. What you will see, described here, is Angel Code – numbering and counting systems employed by those entrusted with the creation of life on earth.

This knowledge may open doors to further understanding.

Boot-Camp

To begin with I must describe some concepts about DNA and the genetic code for those who are newbies. You can relax because the concepts are no more difficult to understand than using a recipe.

The Building Blocks : Amino-acids

Your body is made of amino-acid molecules, which are the building blocks of all living things. There are 20 different amino-acids, each one being different in size, weight and structure. So there are 20 different building blocks that “nature” uses to create you, or a giraffe or a sponge or a sparrow.

Stringing Them Together

These amino-acids must be strung together in a particular order to make the different organs and mechanisms of your body. When amino-acids are connected together into a string we call them proteins. So a protein is just a string of amino-acids.

It is important that the amino-acids are connected in the right order, otherwise the organs that are built from them will not function properly. The instructions for connecting the amino-acids in the correct order are found in your DNA and in the RNA derived from it.

So DNA is like a recipe – a list of instructions telling your body what amino-acids to make and the order in which to attach them.

Instructions : DNA

The instructions are in the form of DNA or RNA. These consist of a long string of letters. There are only 4 different letters in DNA – T, C, A, and G. Similarly there are only 4 different letters in RNA – U, C, A, and G. Here is an example of some DNA.

A machine in your body called a ribosome can read the instructions, and uses the information to connect amino-acids in the correct order to make proteins. It’s a bit like a factory – instructions enter at one end, the ribosome reads each group of 3 letters – gathers the corresponding amino-acid, and connects it to the growing string of amino-acids to make a protein.

The Genetic Code : Translating DNA or RNA into Amino acids

The genetic code is the system used by the ribosome to translate DNA or RNA into amino-acids.

Your RNA is made up of only 4 different letters – U, C, A, and G. Your ribosomes read your RNA in groups of 3 successive letters at a time. You can think of these groups of 3 letters as words, but technically they are called codons.

There are only 64 possible words or codons that can be made from 4 different letters ($4 \times 4 \times 4$), and each of these codons or words codes for a particular amino-acid.

The genetic code table is simply a table listing all of the 64 different 3-letter codes, and listing the amino-acid they code for. That's it. It's that simple. If you want to know which amino-acid will be produced you simply look at the 3 letters in the RNA, and use the genetic code to see which amino-acid is coded for by those 3 letters.

There are a total of 64 different 3-letter combinations that can be made from the 4 letters U, C, A, G. The genetic code table shows all 64 of the 3-letter combinations, and shows the amino-acid that is coded for by each one.

You probably noticed that not all of the 3-letter codes code for amino-acids – some of them code for a STOP signal, which tells the ribosome to stop adding amino-acids to a string.

The Nature of Code

A code is something that stands for more than what it is. It embodies information about something other than itself. For example, a book contains a story, but the story is not determined by the properties of the paper and ink upon which it is written – the story is about more than the medium that holds it.

In the same way, the story of your life is written by you, upon the medium of your physical existence, but not determined by it.

When the discrete masses of the amino-acids are combined in ways determined by the natural divisions within the Genetic Code Table, then they form unexpected patterns of balance and mathematical sequence. The amino-acids are just the ink – it's their arrangement in accord with the genetic code table that gives rise to unforeseen patterns – just as words manifest on paper when the ink is arranged in a certain way.

You will see that the arrangements of the amino-acids embody

- 1. Balance**
- 2. Multiples of 37**
- 3. Angel Numbers**
111, 222, 333, 444, 555, 666, 777, 888, 999, 1110

Angel Numbers

This is simply a term that is commonly used to refer to any three digit number where all the digits are the same. See [Angel Numbers - Google Search](#)

Patterns

Previously, Vernon Jenkins, discovered a mathematical pattern encoded within the Hebrew text of the Old Testament creation narratives. His work is displayed here –

[Vernon Jenkins](#)

I was impressed by the mathematical consistency of the patterns that Vernon discovered. The patterns in Genesis were quite clear and consistent, so I reasoned that these patterns were unlikely to be the product of chance, and so were probably put into the narrative deliberately by some intelligent agent – human or otherwise. I surmised that if God had encoded the patterns in the creation narrative, then perhaps the patterns would also manifest in the things that God supposedly created – i.e. in the living things He made.

In our generation we have become familiar with the genetic code as the repository of all the information and instructions necessary for life, so my attention turned to the genetic code to see if Vernon's patterns were found there.

Initially I sent out an email to Vernon, Iain Strachnan and Richard McGough asking them if they were aware of any occurrence of Vernon's patterns in the newly published human genome. Nothing came to light, and for a few months I allowed my thoughts about the subject to gather dust.

Then, as 2006 drew to an end, I decided to start looking myself. I soon discovered that over the last decade many scientists have begun exploring curious mathematical patterns found within DNA.

Vernon's pattern was intriguing, and it served as a key, guiding my search – a map, as it were, suggesting what I might find, and where to probe deeper....

January 2007 : In January of 2007 I came across the work of Shcherbak, a mathematician and geneticist. Shcherbak had written several papers on a recurring mathematical pattern that he had found in the genetic code. I obtained his papers at the British Library, and made a careful study of them - and produced a simplified booklet that I published online. You can find this linked to below. What was quite surprising was the resemblance between Shcherbak's genetic patterns and those found by Vernon in the creation narratives. Shcherbak's papers can be read here –

[Arithmetic Inside the Universal Genetic Code](#)

[Wow Signal](#)

I remember the moment I saw the similarity – the world appeared in a new light, and, as commonly happens with a paradigm shift, everything felt different.

I wrote a short booklet about Shcherbak's findings here –

[Genetic Patterns](#)

February 2007 : In February 2007 I created a website where I gathered a bibliography of current research on mathematical patterns within the genetic code, and sent this information to Vernon Jenkins, Richard McGough and Iain Strachnan. Vernon has since independently investigated and peer reviewed Shcherbak's findings. He has confirmed these resemblances and has created his own web page where the findings are clearly depicted -

[Revelation of a Biological Abacus](#)

February 2010 : Three years passed by, then in February 2010, prompted by Steve Coneglan to carry on searching, I made a study of the work of another geneticist - M. M. Rakocevic. The resemblances between Rakocevic's genetic patterns and those in the creation narratives was surprising. Rakocevic's paper can be read here –

[Rakocevic Paper](#)

[Rakocevic's Table](#)

December 2010 : In early December 2010, I became aware of the extraordinary research of Jean Claude Perez, a French geneticist and mathematician. He went beyond looking at the Genetic Code, and instead counted the frequency of each codon in the human genome. He found that there was an unexplained balance between the frequency of any codon and that of its mirror image.

[Perez's Paper](#)

[Jean Claude Perez and Balances in the Frequency of Codons](#) See also - [Perez](#)

I investigated Perez's findings, and confirmed that the mathematical balances occur. Using computer software, I fed the raw DNA into a computer algorithm that looped through each chromosome and counted the frequency of each codon in that chromosome. I found that the frequency of any codon was indeed the same as its reverse compliment (mirror). See here –

1. [Codon Balances in DNA](#)
2. [Mathematical Balances in DNA - Experiment 1](#)
3. [Mathematical Balances in DNA - Experiment 2](#)
4. [Mathematical Balances in DNA - Experiment 3](#)
5. [Mathematical Balances in DNA - Experiment 4](#)
6. [Software Code \(Vb.net\) for Counting Codons](#)

I also found that when the codons were arranged in accordance with the genetic code table, the frequencies of the codons belonging to opposite faces of the cube always summed to the same

7. [Genetic Code as a Rubik Cube of Codon Counts](#)
8. ["Rubik Cube Found in Human DNA](#)

March 4th 2011 : I received a copy of a paper written by Stephen Coneglan. Stephen had taken a deeper look at Rakocevic's table and had rearranged the amino acids by their chemical properties so that they are symmetrically placed. When Stephen did this he found that the numerical pattern that emerged possessed precise symmetry both vertically and horizontally. Here is a link to his paper –

- [Stephen Coneglan and the Table of Aminoacids](#)

An Expectation

Jean Claude Perez found a striking mathematical equality between the frequency of any codon (coding and non-coding) and its reverse compliment (mirror). I also found that the frequency of codons occupying opposite faces of a genetic code cube always sum to the same total, regardless of the genome being counted. So we have some grounds for expecting further mathematical anomalies pointing to an arithmetic precursor to life.

A Series of Keys that Unlock the Book of Life

Based on the patterns found by Shcherbak within the genetic code, we can hypothesise that DNA may also embody similar mathematical patterns. In order to investigate this, we must first list the parameters that give rise to Shcherbak's patterns –

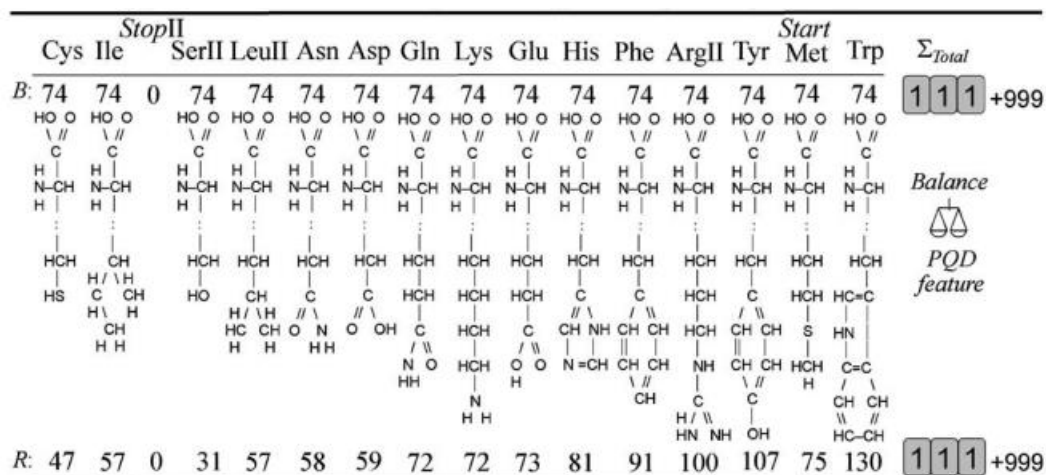
1. The patterns are mass sums of the unique parts of amino-acids
2. Mass sums are found within specific groups of amino-acids –
 - a. Group 1V Degeneracy vs Groups I, II, and III
 - b. Pyrimidines and Purines summed separately
 - c. Inner rows and inner columns as a single sum
 - d. Outer rows and outer columns as a single sum
 - e. Amino-acids with two identical bases as a single sum
 - f. Amino-acids with 3 identical bases and amino-acids with 3 unique bases as a single sum

These are the “conditions” that gave rise to Shcherbak's patterns. It follows that if we are to detect these patterns in raw DNA, we must apply the same “conditions”. What I am suggesting is that these “conditions” are like algorithms, or keys, and each key must be applied to unlock the book of life.

Between Start and Stop

A further condition is that the patterns may be confined to the coding regions of DNA, i.e. those regions coding for protein synthesis because -

1. Shcherbak's patterns are found within the genetic code – the primary purpose of which is protein synthesis.
2. Shcherbak's patterns relate to the combined masses of amino-acids – the building blocks of protein synthesis
3. One of Shcherbak's patterns appears to be a semantic message – an instruction



Read Semantically :

In the genetic code –

- the STOP signals are TAA, TGA, TAG
- the START signal is ATG

So our 222 sequence can be read as G - **STOP – STOP** - AAA – **START - START**

We know that the genetic code applies to coding regions, and coding regions always begin with a START signal and end with a STOP signal. Is this pattern instructing us – to only apply the code between START and STOP ?

Guanine Cap and the Poly AAA Tail

When DNA is transcribed into RNA, two additional things are always added –

1. A Guanine Cap (G) is added to the START of the RNA
2. A poly-AAA tail is added to the END of the RNA

It is therefore curious that our sequence embodies these very two things, once again suggesting that the code is meant to be applied to coding regions – from its beginning to its end.

G TAG TAA AAA ATG ATG

Gcap – STOP – STOP - Poly-AAA-tail – START - START

The 5' cap is added to the first nucleotide in the transcript during transcription. The cap is a modified guanine (G) nucleotide, and it protects the transcript from being broken down. It also helps the ribosome attach to the mRNA and start reading it to make a protein.



How is the poly-A tail added? The 3' end of the RNA forms in kind of a bizarre way. When a sequence called a **polyadenylation signal** shows up in an RNA molecule during transcription, an enzyme chops the RNA in two at that site. Another enzyme adds about 100 - 200 adenine (A) nucleotides to the cut end, forming a **poly-A tail**. The tail makes the transcript more stable and helps it get exported from the nucleus to the cytosol.

[Eukaryotic pre-mRNA processing](#) | [RNA splicing \(article\)](#) | [Khan Academy](#)

- When we start transcription the first thing added is the G-Cap
- When we stop transcription, the last thing added is the poly-AAA-tail

Testing the Hypothesis

Therefore, the initial test will be to analyse the coding regions of DNA only, for the reasons specified above. Initially, I will define a coding sequence as any sequence that begins with a START signal (MET) and ends with a STOP signal.

A Method

I will create software that can loop through coding DNA, (any sequence that begins with a START SIGNAL and ends with a STOP SIGNAL), and sums the amino-acid masses for Pyrimidines, and separately sums the amino-acid masses for Purines.

As the software loops through the DNA and sums the masses, the occurrence of multiples of 37 and Angel Numbers will be recorded and their distribution will be examined.

I will do the same for non-coding regions, and compare the results for both.

Summary

The genetic code table, the amino-acid table, and raw DNA itself, each demonstrate a degree of mathematical balance and mathematical sequencing that is unexpected, given the supposed random origin of life.

These repeating patterns and balances seem to show that an agent/s possessing arithmetical ability played a part in the origins of life – even prior to the first cell.

The repeated manifestation of specific multiples of 37 and triple digit “Angel Numbers” suggest that these may also organise raw DNA. A computer analysis may reveal if this is the case. Computer science can help decipher this Angel-Code, which may lead to further discoveries in DNA..

Dear Craig,

thank for your longstanding interest to my research. You have attached two articles. Article by Stephen Coneglan updates 5x4 table of 20 canonical amino acids published by Miloje Rakocevic in JTB while your article gives geometrical interpretation to these results. I think that Miloje Rakocevic finding became even more brilliant due to your scrupulous research.

However, pure mathematical approach to the genetic code and its numerical parameters threatens to be the scholastic one. To avoid scholasticism I try, for example, to interpret my results as instruction on possible universal arithmetic grammar of genomes. By the way, I recommend you to pay attention to the second Chargaff's rule (see attached articles). This phenomenon and its total power may be a continuation of the genetic code arithmetical order, this time in genomes. Therefore we – I and my young colleague Maxim Makukov – are searching now for analogous numerical grammar in genomes.

There are two squared numbers of total sum $2 \times 37^2 = 2738$ in your articles. On the other hand there is equation $12^2 + 35^2 = 37^2$ among Pythagorean numbers. I would like to ask you and Stephen: is it possible to bisect regularly 5x4 table and its total sum producing the same equations $12^2 + 35^2 = 37^2$ and $12^2 + 35^2 = 37^2$? I ask this question because the genetic code has shown already the first Pythagorean number.

Yours sincerely

Vladimir Shcherbak

The articles attached to the letter relate to Chargaff's second rule – namely the enigmatic mirroring of the frequency of codons with their reverse compliments.

[Buelher Article](#)

[Okamura Article](#)

Chargaff's second rule is the same phenomenon highlighted by Jean Claude Perez. [Perez's Paper](#)

Shcherbak suggests that it is within this phenomenon that I might find an occurrence of his patterns - within the genomes of all living creatures.