PROOF WE LIVE IN A SIMULATION
via a new, unifying concept in biology called:
SPACE. TIME. INFORMATION.

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Abstract: Space Time Information (a thought experiment) proves that protein evolution is the product of computation: possibly due to a simulation.

Introduction

Arguably, the top three scientific theories are: 1) general relativity, 2) quantum mechanics, and 3) Darwinian evolution. Evolution is a fact. However, mutations could be random or could be the result of computation. The resources of space (water content) and time limit information: protein creation. Protein evolution can have no more steps than historical ribosomal reads: which can be calculated.

The average protein length in single celled organisms is 247 amino acids. In bacteria it is 267 amino acids. In organisms having organelles with membranes it is 361 amino acids. And in humans it is 509 amino acids. The largest 1,050 human proteins average 2421 amino acids in length. To randomly guess 247 amino acid proteins would take, approximately, 20 to the power of 247 ribosomal reads.

The water content of the Earth is enormous compared to the size of a cell. And the age of the Earth is enormous: 4.59 billion years. This makes random mutation appear to be very plausible.

Methods

By dividing the volume of water on Earth by the ribosomal density, we obtain the maximum number of ribosomes that could ever be present on Earth. We then multiply this by the ribosomal read rate and the amount of time on Earth. The result is the number of ribosomal reads in the history of life.

Results

This calculation uses: 1) the age of the Earth or ~1.44E+17 seconds, 2) the volume of the average depth of the ocean or ~2.18E+45 cubic nanometers, 3) filled to a density of 10 million ribosomes per 2000 cubic micrometers, as per actual cells, and 4) 63 nucleotides are read per second, as per the actual ribosomal read rate. The calculation results in about 1E+59 ribosomal reads (see [1]).

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  2.18 E+45 NM^3 VOLUME OF WATER (OCEAN) CALCULATED
×    1 E+7  RIBOSOMES    PER 2E+12 NM^3
×   63      NUCLEOTIDES PER RIBOSOME PER SECOND
× 1.44 E+17 SECONDS (EARTH'S AGE)        CALCULATED
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RESULT = ~9.88E+58 NUCLEOTIDE READS
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Using logarithmic math, 1E+59 is 20 (the number of amino acids) raised to the power of 46. This is found by dividing 59 by the log of 20 (or 1.301). If mutations are random, the Earth can be expected to guess 46 amino acid proteins. At 62 amino acids larger, or 108, the chance of guessing that amino acid could be over 1 in 1E+80. This is worse odds than finding a single atom in the Universe.

Titin, the largest human protein, contains 34,350 amino acids. Raising 20 (different aminos) to the power of 34,350 results in ~1E+44,690 unique protein combinations. The dystrophin gene is 2.24 million base pairs long. Dystrophin is one of ~1E+971,435 unique nucleotide combinations.

Imagine filling the volume of the Universe with ribosomes. And these ribosomes are creating proteins for the entire age of the Universe. The result is ~1E+125 ribosomal reads or 96 amino acids.

Discussion

Evolution's mutations must be tied to some form of computation. Mutations are not random. Orgel's second rule (essentially "evolution is cleverer than you") requires computation. If mutations were random, no life would exist. Life's proteins cannot be arrived at by brute force. There are simply not enough random mutations in the history of life to account for proteins' complexity. Evolution is subject to the physical restrictions of the resources of: ribosomes, water, and time (see [1]).

Imagine making a 500-amino protein to cure cancer. There are 1E+650 unique protein combinations. If each unique sequence could be tested (in one clock cycle) on 1E+80 one-terahertz (1000 GHz) computers, it would take 1E+538 trillion years to find that cure via brute force. There are 50+ billion species: with unique DNA data that is equivalent to 2,300,000,000,000,000,000 bytes.

Conclusions

Imagine claiming that our cryptography could be cracked (solving the P versus NP conjecture) via "random mutation": but offering no mathematical proof. This would be unacceptable in physics or mathematics. Evolution must be elevated, via a formal math proof, to the same level as general relativity and quantum mechanics. There is a limit to space containing water; therefore, the maximum number of ribosomes is known. There is a limit to time; and ribosomes create proteins at a known rate. Therefore, there is limited biologic information available to any "random" evolutionary mechanism.

There are two natural conclusions to this work. The first being directed panspermia by Francis Crick: wherein the computation is located inside the cell itself. The second being the simulation hypothesis by Nick Bostrom: wherein the computation is external to our Universe. In biology, we see scarce evidence (see B. McClintock's and J. Shapiro's works) that the cell is directly performing computation that is changing its genome. Therefore, the conclusion is that we are likely living in a simulation. However, we cannot, today, rule out the possibility of a mechanism inside the cell.

This work leads to an experimental prediction. If a cell's genetics are physically altered, the cell may undergo rapid evolution. Because there is some form of computation behind evolution. We can determine how many steps are in evolution's mechanism by asking: How much data has passed through the ribosomes of life? In the end, the biology that we observe has precisely the properties we should expect if there is, at the bottom, biologic computation… and if we live in a simulation.

[1] Dr. Phillip M. Angelos "*Space Time Information*" Amazon © 2023