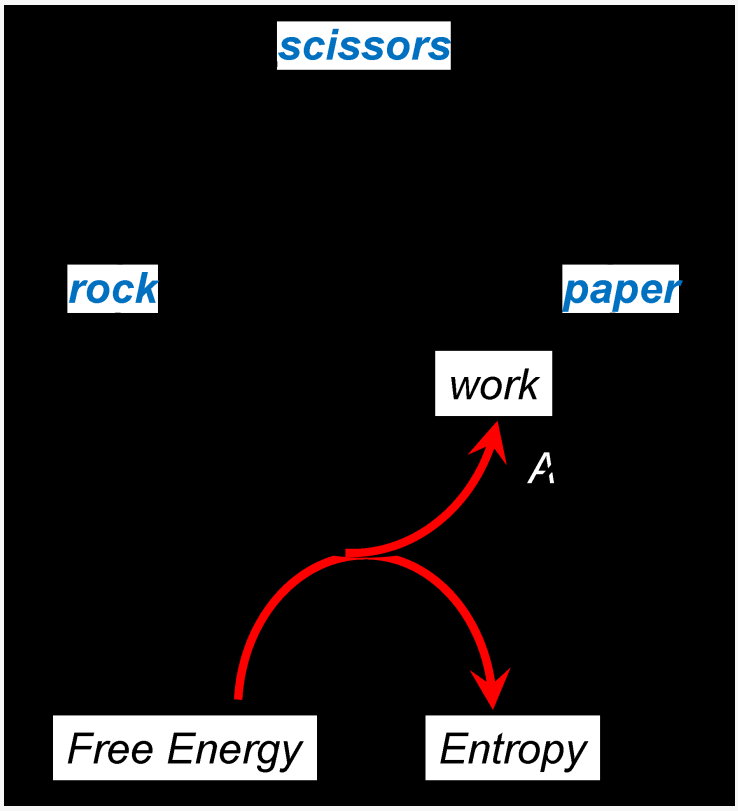
When the Genome Gets it Wrong, but Still Gets it Right

Current Computation Approaches do not model Biological Systems very well.

CHARLESTOWN, MA, UNITED STATES, November 18, 2023 /EINPresswire.com/ -- Dr. Alan Herbert from InsideOutBio describes how biological systems compute differently from our current generation of machines in a published online today by The International Journal of Molecular Science. The study focuses on the intransitive logic of biological systems that is enhanced by a genome full of junk DNA. Previously junk DNA was considered as an accumulation of genomic errors. Instead, the junk adds a level of programmability to the genome that was not previously appreciated.



The same play can either win or lose depending on what the other player does. The flow of information in biological systems is also directed. The different paths between nodes can then be coupled to produce unrelated outcomes. During the process, free ene

Intransitive logic is found in games like rock, paper, scissors where each choice can either win of lose the game depending on the other players' response. Here the rules are fixed, but the outcome is determined by the flow of the information. The rules establish when one play beats another. They are best described using a directed cycle (DC) (Figure 1). Of course, the game uses energy to power the play and involves losses through entropy.

Biological systems follow the same logic. The directed cycles ensure that the system regenerates itself. The different paths followed allows the cycle to drive different biochemical pathways. Those outcomes can be determined by natural selection that acts also to minimize energy losses through entropy. Unlike computational devices based on Turing machines, biological systems are not designed to arrive at an answer, then halt. Through their intransitive nature, DCs enable a cell to do a number of things current computational devices cannot do: regenerate, recalibrate,

reset, repair, rewrite, and reproduce themselves into the next generation.

The intransitive logic of directed cycles is also embedded in the genome through what has previously be called junk DNA. The name junk was given because these sequences are of low complexity and do not code for protein. They take up over 50% of the genome and are considered by many as evolutionary fluff. However, these repeat sequences have informational value because that act as flipons, adopting alternative conformations that localize cellular machinery to a genomic region. The response depends on whether flipons are in the right-handed Watson-Crick B-DNA conformation or are in an alternative structure like left-handed Z-DNA. By cycling between conformations, they act as binary switches, enabling different outcomes to be associated with each state. The repeat elements therefore increase the complexity of the genome and alter the readout of genetic information. The increased diversity they generate is subject to natural selection and provides an evolutionary advantage to individuals of a species.

The complexity of a genome can also be viewed from a programming perspective. The most complex program a genome can generate is equivalent to the complexity of the genome itself, an example of the theorem proposed by Andrey Kolmogorov. From this perspective, junk DNA is advantageous. Even though the junk sequences are simple and repetitive, they enable simple rules that, like the Conway Game of Life, can generate unexpected and diverse outcomes, some of which cycle between states.

The paper explores in depth both thermodynamic and informational entropies and provides examples of both, concluding by stating: “DCs offer the best way to survive in the midst of chaos, but they do not guarantee eternal life. DCs embrace intransitivity. They maximize informational entropy while avoiding thermodynamic equilibrium. DCs are not just the cycles of life, but they also embed the logic of life.”

The paper is entitled "The Intransitive Logic of Directed Cycles and Flipons Enhances the Evolution of Molecular Computers by Augmenting the Kolmogorov Complexity of Genomes”

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