

Beyond Binary: Biological Algorithms and the Code That Writes Life

Professor Somkiat Wattanasirichaigoon, M.D.

President, Thai Biomedical Engineering Association

Director, Center for Continuing Medical Education, Thai Medical Council

Information Technology Management, Faculty of Engineering, Mahidol University

somkiat.wat@mahidol.edu

Abstract— This article invites the reader into an immersive exploration of life's deepest computational layers. Whereas machines operate in binary—constrained to decisions of yes or no—living systems function within a spectrum of logic written in four molecular symbols: A, T, C, and G. Within this quaternary structure lies the foundation of biological intelligence—capable of memory, self-regulation, adaptation, and multidimensional decision-making. Biological algorithms transcend traditional logic gates, offering insights critical to future paradigms in medicine, artificial intelligence, and systems biology.

Index Terms—

I. INTRODUCTION

I.1 From Digital Dualism to the Biological Continuum

In the binary world of digital computation, operations are distilled into simple true/false logics. However, the realm of biology defies such reduction. Biological processes involve gradients, timing, spatial organization, and probabilistic outcomes. As such, while binary logic suffices for silicon machines, the wet, adaptive world of cells demands more. A neuron's decision to fire, a hormone's influence on a cell, or a gene's expression level are each context-sensitive, feedback-governed, and fundamentally analog in nature. These attributes necessitate a rethinking of what qualifies as an algorithm in living systems.

I.2 The Four-Letter Code of Life and Its Infinite Permutations

The genome is often described as a code—but unlike binary, it is composed of four symbols: A, T, C, and G. Codons, groups of three nucleotides, map to amino acids, which form the structural and functional units of cells: proteins. Yet the genome does not merely encode proteins; it also houses regulatory instructions, enhancers, silencers, and epigenetic marks. These features collectively allow the same genome to express thousands of cellular phenotypes. The power of four enables not only diversity but also robust error-checking and adaptability.

I.3 Beyond Logic Gates: Intelligence Emergent from Biology

While digital logic flows linearly through gates, biological systems exhibit emergent intelligence. Neurons integrate input in non-linear ways; immune cells refine their receptors over time; endocrine feedback loops calibrate based on need. These

systems demonstrate learning without programming and adaptation without rewriting code. Biological intelligence is not centralized, it is distributed, contextual, and resilient. It is algorithmic, but with properties more akin to deep reinforcement learning than classical programming.

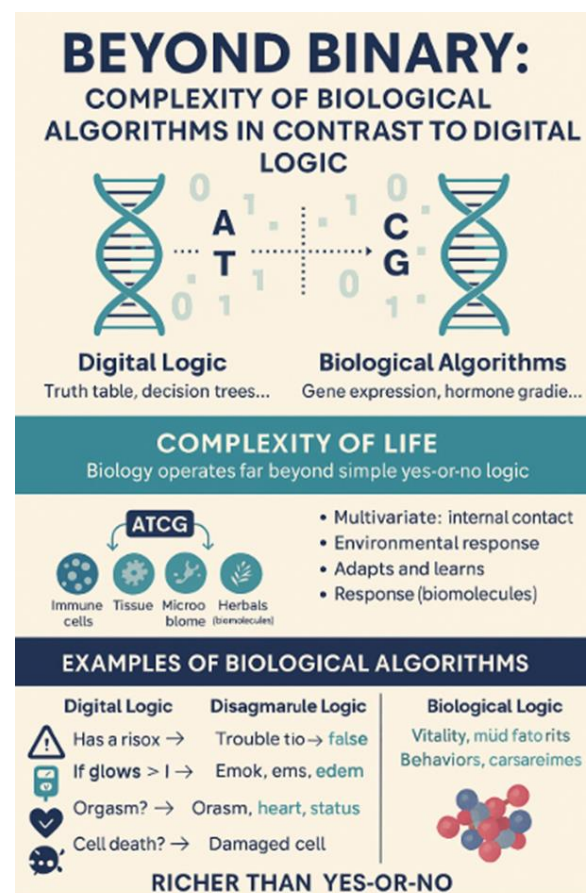


Fig 1

I.4 Hormonal Symphony: Messages Beyond Binary

Hormones serve as chemical messengers, yet their influence is anything but binary. Oxytocin can induce trust or caution depending on context; insulin's effect is modulated by circadian rhythms. This chemical signaling orchestrates a symphony of internal coordination. Hormonal cascades involve negative and positive feedback, receptor regulation, and gene expression changes. A single hormone may produce vastly different effects depending on receptor density, competing signals, or epigenetic state.

I.5 The Microbiome: Symbiotic Code and Dynamic Adaptation

The microbiome—our internal ecosystem of bacteria, fungi, and viruses—represents a parallel computational layer. These organisms produce metabolites that alter human gene expression, modulate immunity, and shape neurological states. The host-microbiome system is a co-evolved network. Its algorithm is not top-down, but mutualistic. Imbalances in this system have been linked to a wide range of NCDs including obesity, type 2 diabetes, and neuroinflammation.

I.6 Nature's Pharmacology: Herbal Intelligence in Systemic Rebalancing

Plants have long been used in traditional medicine, but only recently has their systemic bioactivity been appreciated. Compounds such as flavonoids and terpenoids act not on single pathways but on networks. They may modulate mitochondrial function, hormone receptors, and microbial populations simultaneously. For instance, black ginger enhances dopaminergic activity while regulating inflammatory markers. These polypharmacological effects suggest that plant molecules operate on biological networks using an evolved bio-intelligence.

I.7 Case Illustrations: Learning, Memory, Immunity, and Desire

Case studies bring theory to life: The lac operon in *E. coli* shows how gene regulation follows nutrient levels. Spike-timing-dependent plasticity reveals how neurons encode memory through patterns, not absolute values. Kinetic proofreading in T cells refines immune detection by temporal discrimination. Sexual arousal, mediated by dopamine and oxytocin, demonstrates how emotion and context intertwine with biology.

I.8 Toward Bio-Empathic Computation: The Role of AI and Quantum Systems

To simulate life, AI must move beyond IF-THEN logic. Deep learning begins to capture some of this, but limitations remain. Quantum computing holds promise in modeling probabilistic, entangled, multivariable systems. Future bio-computation will require hybrid models—drawing from systems biology, AI, and quantum logic—to emulate the complexity of life.

II. CONCLUSION

Life Computes in Paradox, Patterns, and Probabilities

The human body does not compute in zeros and ones. It computes in waves, gradients, probabilities, and paradoxes. Its logic is recursive, plastic, and deeply interdependent. To decode life, we must not reduce its complexity but embrace it. Our future—of AI, of medicine, and of meaning—may depend on learning to think as life does.

REFERENCES

- [1]. McKeithan, T. W. (1995). Kinetic proofreading in T-cell receptor signal transduction. *PNAS*, 92(11), 5042–5046.
- [2]. Raj, A., & van Oudenaarden, A. (2008). Stochastic gene expression and its consequences. *Cell*, 135(2), 216–226.
- [3]. Setty, Y., Mayo, A. E., Surette, M. G., & Alon, U. (2003). Map of a cis-regulatory input function. *PNAS*, 100(13), 7702–7707.
- [4]. Zadeh, L. A. (1965). Fuzzy sets. *Information and Control*, 8(3), 338–353.
- [5]. Alon, U. (2007). *An Introduction to Systems Biology*. Chapman & Hall/CRC.
- [6]. Bray, D. (2009). *Wetware: A Computer in Every Living Cell*. Yale University Press.
- [7]. Noble, D. (2006). *The Music of Life*. Oxford University Press.
- [8]. Gilbert, J. A. et al. (2018). Human microbiome. *Nature Medicine*, 24(4), 392–400.
- [9]. Tilg, H., & Moschen, A. R. (2014). Microbiota and diabetes. *Gut*, 63(9), 1513–1521.
- [10]. Williamson, E. M. (2001). Synergy in phytomedicines. *Phytomedicine*, 8(5), 401–409.