

Received: 2017.08.03 Accepted: 2017.08.03 Published: 2017.08.14 e-ISSN 1643-3750 © Med Sci Monit, 2017; 23: 3923-3924 DOI: 10.12659/MSM.906498

Artificial Intelligence, DNA Mimicry, and Human Health

- 1,2 George B. Stefano
- 1 Richard M. Kream

1 Department of Psychiatry, Charles University, Center for Molecular and Cognitive Neuroscience, Prague, Czech Republic

2 Executive Vice President International Scientific Information, Melville, NY LLS A

Corresponding Author: George B. Stefano, e-mail: gbstefano@yahoo.com

The molecular evolution of genomic DNA across diverse plant and animal phyla involved dynamic registrations of sequence modifications to maintain existential homeostasis to increasingly complex patterns of environmental stressors. As an essential corollary, driver effects of positive evolutionary pressure are hypothesized to effect concerted modifications of genomic DNA sequences to meet expanded platforms of regulatory controls for successful implementation of advanced physiological requirements. It is also clearly apparent that preservation of updated registries of advantageous modifications of genomic DNA sequences requires coordinate expansion of convergent cellular proofreading/error correction mechanisms that are encoded by reciprocally modified genomic DNA. Computational expansion of operationally defined DNA memory extends to coordinate modification of coding and previously under-emphasized noncoding regions that now appear to represent essential reservoirs of untapped genetic information amenable to evolutionary driven recruitment into the realm of biologically active domains. Additionally, expansion of DNA memory potential via chemical modification and activation of noncoding sequences is targeted to vertical augmentation and integration of an expanded cadre of transcriptional and epigenetic regulatory factors affecting linear coding of protein amino acid sequences within open reading frames.

The burgeoning Artificial Intelligence (AI) discipline of biomolecular and DNA computing incorporates core operational machinery that includes input and output devices, memory, and biomolecular logic gates in order to utilize the potentially inexhaustible information technology (IT) capacity of genomic DNA [1]. Contextually, the dual application of DNA/RNA/protein complexed microcircuits to model AI deep learning and recurrent neural network paradigms carries the potential to significantly expand IT based strategies to effectively address a broad array of environmental challenges. Translational criteria to achieve effective augmentation of quality of life and life span require preemptive approaches to treat major disease states afflicting human populations from the perspective of personalized medicine that utilize reciprocally interactive genomic DNA databases [2,3]. To effectively advance these endeavors, the development of higher order AI-based bioinformatics based on complex cognitive processes linked to computational speed and accuracy may rely on evolutionary defined genomic DNA mimicry. The developmental elegance and critical biological importance of genomic DNA as a self-contained AI machine, crafted over the course of millions of years, establishes its primacy as the gold standard for design of higher order bioinformatics tools targeting human health processes. In summary, AI is not really artificial.

MeSH Keywords: Artificial Intelligence - Classification • DNA Methylation - Genetics • Longevity - Genetics

Full-text PDF: http://www.medscimonit.com/abstract/index/idArt/906498

■2 375 **■**2 **■**2 **■**2



References:

- 1. Miyamoto T, Razavi S, DeRose R, Inoue T: Synthesizing biomolecule-based Boolean logic gates. ACS Synth Biol, 2013; 2(2): 72–82
- Stefano GB, Fernandez EA: Biosensors: Enhancing the natural ability to sense and their dependence on bioinformatics. Med Sci Monit, 2017; 23: 3168–69
- Stefano GB, Kream RM, Personalized- and one- medicine: bioinformatics foundation in health and its economic feasibility. Med Sci Monit, 2015; 21: 201–4