

# Modern Applications and Challenges of DNA Computing

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**Abstract:-** DNA computing is an exciting field that encompasses different scientific subjects and merges them with computer science. It is based on the theory, experiments, and applications of DNA to solve computer-related problems. This paper describes what DNA computing entails and also presents the research carried over the years in the field of DNA computing. Furthermore, some of the algorithms used for improvements are present as well as the drawbacks of this evolving field. This paper aims to keep researchers abreast of the current trend of this field thus informing their future research efforts.

**Keywords:-** DNA Computing, Nanotech, Computer Circuitry, Computer Architecture, Data Storage.

## I. INTRODUCTION

Every biological organism is made up of deoxyribonucleic acid otherwise known as DNA. DNA contains the genetic makeup of all organisms that are required for hereditary purposes. They are usually found in the organism's cell nucleus but others have been found to exist outside of the nucleus purposely for the conversion of food to energy that the cell can make use of for other purposes like developing and living. In other words, DNA contains instructions that guide an organism on how to carry out its life needed activities.

According to [14] the information contained in DNA are codified into four chemical bases namely adenine (A), guanine (G), cytosine (C), and thymine (T); and DNA bases pair up with each other, A with T and C with G, to form units called base pairs. Each base is also attached to a sugar molecule and a phosphate molecule. DNA can replicate its molecular structure to form new cells that can carry out the same task.

DNA computing, inspired by Leonard Adleman in 1994 is an evolving branch of computer science based on theory, experiments, and applications of DNA to solve computer-related problems inspired by the similarity between how DNA and the theoretical Turing machine works. It seeks to make computers mimic the workings of molecules in biological makeup. This is made possible because science continues to dig deeper and get a better understanding of our molecular structure which began with the work of Friedrich Miescher [15].

Given the vast amount of data being generated that needs to be processed, it is undeniably evident why the need for more elegant and lesser computing resources requirement methods is important. DNA contains data, so this study seeks to look at the applications of DNA computing and the challenges it faces in the modern world.

## II. DNA COMPUTING APPROACHES

The process of DNA computing can take either in vitro or in vivo methods. [1] posits that in vivo refers to work that's performed in a whole, living organism while in vitro is Latin for "within the glass." When something is performed in vitro, it happens outside of a living organism.

## III. DNA STRUCTURE

[3] described DNA as being made up of six smaller molecules – a five-carbon sugar called deoxyribose, a phosphate molecule, and four different nitrogenous bases (adenine, thymine, cytosine, and guanine). [5] show that of the four kinds of monomers (nucleotides) present in a DNA molecule, two types were always present in equal amounts and the remaining two types were also always present in equal amounts.

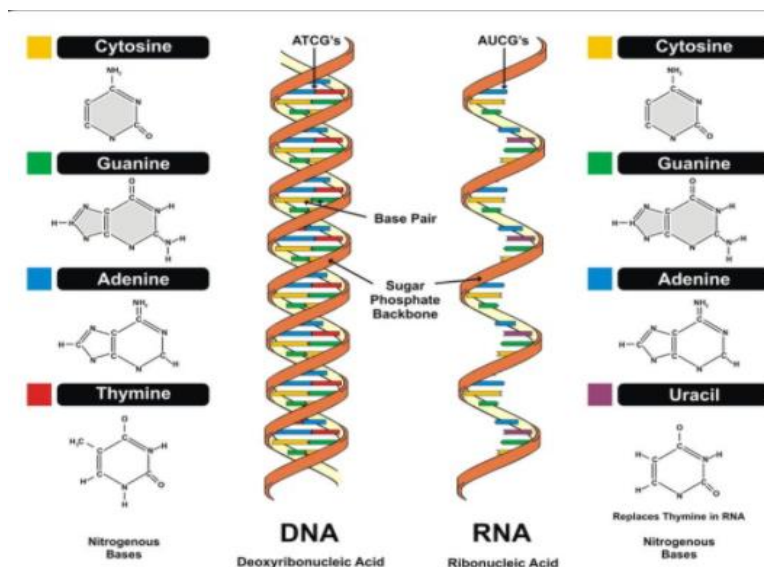


Fig 1:- Structure of DNA and RNA [17]

DNA works by storing information for the formation of proteins coupled with the performance of enzymes that are designed to interact with it. [12] posit that match between DNA structure and the activities of these enzymes is so effective and well-refined that DNA has become, over evolutionary time, the universal information-storage molecule for all forms of life. DNA can perform its function because its structure is based on a building block system. Nucleotide monomers or single molecules which perform specific functions combine to form polymers (DNA molecules). These monomers, namely A, C, T, G are made up of sugar, a phosphate group, and a nucleobase.

The goal of DNA computing is to make use of the algorithms embedded in DNA to solve problems by making and breaking new bonds in the fashion of a biological DNA structure answer.

#### IV. APPLICATIONS OF DNA COMPUTING

The advantage of DNA computing can be traced to the combination of the strengths of computer science and biological sciences and its applications are wide and evolving. It is geared towards nanotech, information processing & dissemination while drawing strength from human micro-level mechanics.

[4] show that in the early days of DNA computing, Adleman was able to use DNA computing to solve an instance of a 6-variable 11- clause 3-SAT problem on a gel-based DNA computer based on parallelism. Adleman made use of DNA molecules to solve computational problems because there had been speculation that molecular computers might be suitable for attacking problems that have resisted conventional methods. Using this method, he was able to solve the Hamiltonian path problem which was represented notationally as the travelling salesman problem.

[13] applied their knowledge of DNA and logic gates using an aqueous solution to develop nanoscopic agents that can be introduced into living organisms, which would detect pathologies and react. They did this using a simulated tic-tac-toe game environment by developing automata that play as noughts and crosses. The human player adds DNA strand solutions to indicate moves, and the DNA computer responds by illuminating the square he has chosen to take for the next turn.

[16] posited that biomolecular systems have been hypothesized to carry out neural network-like computations in vivo. Using a simple DNA gate architecture that allows experimental scale-up of multilayer digital circuits, they systematically transformed arbitrary linear threshold circuits (an artificial neural network model) into DNA strand displacement cascades that function as small neural networks. Their approach allowed for the implementation of a Hopfield associative memory with four fully connected artificial neurons that, after training in silico, remember four single-stranded DNA patterns and recall the most similar one when presented with an incomplete pattern. Their results suggest that DNA strand displacement cascades could be used to endow autonomous chemical systems with the capability of recognizing patterns of molecular events, making decisions, and responding to the environment.

[9], based on reviewing the principle of DNA computing and the development situation of DNA computing, the study analyzed some schemes with secret key searching and introduced the application of DNA computing in encryption, steganography, and authentication.

[6] showed that spatial organization of cells can be a similarly powerful design principle for overcoming limitations of speed and modularity in engineered molecular circuits. They created logic gates and signal transmission lines by spatially arranging reactive DNA hairpins on DNA origami. Signal propagation was demonstrated across transmission lines of different lengths and orientations and

logic gates were modularly combined into circuits that establish the universality of their approach. Their result showed that detailed computational models enable predictive circuit design and anticipate that their approach will motivate the use of spatial constraints for future molecular control circuit designs.

[8] posited that DNA-based neural networks have been limited to the recognition of a set of no more than four patterns, each composed of four distinct DNA molecules. Making use of winner-take-all computation which has been suggested as a potential strategy for enhancing the capability of DNA-based neural networks, the study was a systematic implementation of winner-take-all neural networks based on DNA-strand displacement. The writers made use of a preliminarily developed seesaw DNA gate motif extended to include a simple and robust element that facilitates the collaborative hybridization that's involved in the process of choosing a 'winner'. Their result showed that with this method, DNA- based neural networks can classify patterns into nine categories.

[10] compared trends in DNA circuits, they showed that some previous DNA - based circuits are use-once circuits since the gate motifs of the DNA circuits get permanently destroyed as a side effect of the computation, and hence can not respond rightly to posterior changes in inputs and other DNA - based circuits use a large reservoir of buffered gates to replace the working gates of the circuit and can be used to drive a limited number of computation cycles. They also showed that in numerous operations of DNA circuits, the inputs are innately asynchronous, and this necessitates that the DNA circuits be asynchronous: the output must always be correct irrespective of the differences in the arrival time of inputs. This work demonstrated that renewable DNA circuits, which can be manually returned to their original state by the addition of DNA strands, and time-responsive DNA circuits, where if the inputs change over time, the DNA circuit can recompute the output rightly based on the new inputs, that are manually added after the system has been reset.

[19] identified two limitations in DNA logic circuits which are: the slow computation speed, often requiring hours to compute a simple function and the high complexity of the circuits regarding the number of DNA strands. For this purpose, a DNA logic circuit architecture predicated on single-stranded logic gates that use strand-displacing DNA polymerase was introduced. The logic gates consist of only single DNA strands, which largely reduces leakage reactions and signal restoration steps such that the circuits are improved regarding both speed of computation and the number of DNA strands needed. Their result demonstrated a fast and compact logic circuit that computes the square-root function of four-bit input numbers.

[18] posited that Chemical Reaction Networks (CRNs) provide a powerful abstraction to formally represent complex biochemical processes. And showed in their work an alternative architecture that lies along the spectrum in between DNA-only systems and multienzyme DNA systems. Their architecture relied on only a strand displacing polymerase enzyme and DNA hybridization reactions for implementing CRNs. First, they briefly introduced the theory and DNA design of simple CRNs and then explored the fundamental properties of polymerase-based strand displacement systems. They then engineered a catalytic amplifier in vitro as a use-case of their framework since such amplifiers require the intricate design of DNA sequences and reaction conditions.

### V. DNA COMPUTING ALGORITHMS

#### A. The Molecular Learning Model

The hyper network shown by [2] is a graphical model with nodes and connections between two or more nodes called hyperedges. The connections between these nodes are strengthened or weakened through the process of weight update or error correction during learning.

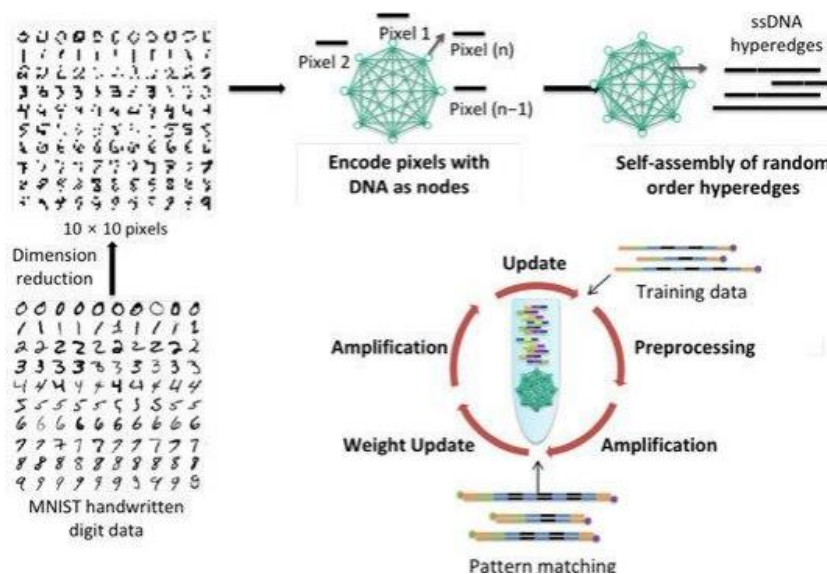


Fig 2:- Machine Learning Algorithm for DNA-Based Molecular Ligands [2]

**B. A DNA-based memory within vitro learning and associative recall**

The learning protocol stores the sequences to which it was exposed and memories are recalled by sequence content through DNA-to-DNA template annealing reactions. Experiments show that biological DNA could be learned and

that sequences similar to the training DNA are recalled correctly, and that unlike sequences were differentiated. Theoretically, the memory has a pattern separation capability that is very large and can learn long DNA sequences. The learning and recall protocols are massively parallel and simple, inexpensive, and quick.

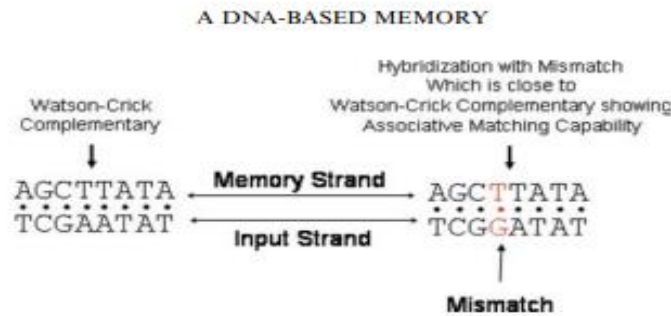


Fig 3:- A DNA based memory [7]

**C. QPSO-Based Adaptive DNA Computing Algorithm**

This new approach aims to perform a DNA computing algorithm with adaptive parameters towards the desired goal using quantum-behaved particle swarm optimization (QPSO). Some contributions provided by the proposed QPSO based on adaptive DNA computing algorithm are as follows: (1) parameters of population size, crossover rate, the

maximum number of operations, enzyme and virus mutation rate, and fitness function of DNA computing algorithm are simultaneously tuned for adaptive process, (2) adaptive algorithm is performed using QPSO algorithm for goal-driven progress, faster operation, and flexibility in data, and (3) numerical realization of DNA computing algorithm with proposed approach is implemented in system identification.

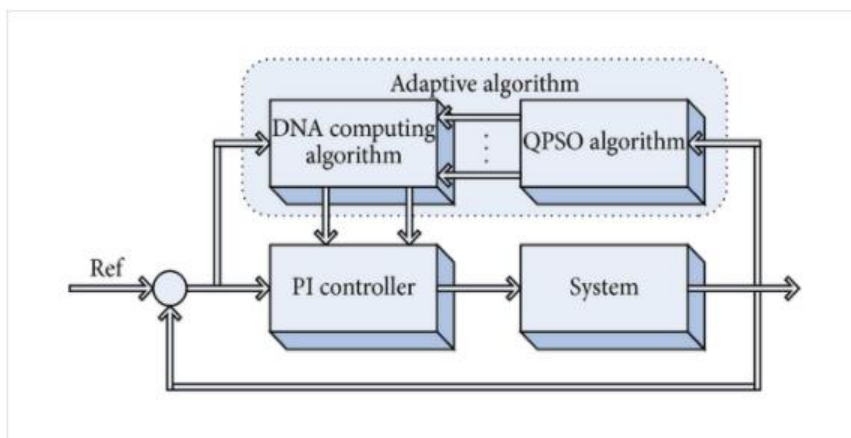


Fig 4:- QPSO-Based Adaptive DNA Computing model [11]

**VI. CHALLENGES OF DNA COMPUTING**

DNA computing has some problems in its application in real-world computing. First, a majority of its application has to do with trial and error and some cases cannot be explained in-depth. A difference between silicon-based and DNA computing is that DNA computing lack control which is a fundamental part of Neumann’s architecture. This can be confusing and computationally expensive in the larger spectrum of computations. DNA strands can replicate themselves, biologically, many times over but some paradigms show that DNA logic circuitry can be used only once.

**VII. CONCLUSION**

This work looked into DNA computing and its applications. Research shows that evolving fields throws up new problems as the field gets larger. Its implementation in some cases seems far-fetched and maybe misconstrued, however, it is a promising field that aims to improve computational abilities from 10<sup>12</sup> to 10<sup>20</sup>. The drawback to this field would most likely come from its invasive tendencies and how quickly other technologies will catch up to its potential.



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