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Formulating DNA Chains Using Effective Calculability

Syed Atif Ali Shah[a*], Zafar Khan[b], Zubia Rauf[c], Syed Asif Ali Shah[d]

[a,b]*Northern University, Nowshera*
[c]*Qurtuba University, Peshawar*
[d]*Abasyn University, Peshawar*
[a]*Email: atif@northern.edu.pk*
[b]*Email: zafarkhan@northern.edu.pk*
[c]*Email: dboss009@yahoo.com*
[d]*Email: asifatsun@yahoo.com*

Abstract

Nearly all computational algorithms are modeled as 'Effective Calculability' i.e Finite State Model and Lambda Calculus. Effectively calculable function Comprise of three parts: the info, the yield, and the finite state function or transition function. It takes stream of data as input and translates to specific output, as defined by transition function [1]. The aftereffect of this conversion is another flood of information or the yield. Both i.e info and yield information streams comprise of arrangements of characters and are known as strings. DNA exhibits a property of being a pattern of strings. Automatic machines like automata and Lambda Calculus or simply the Effective Calculability [8] can be an efficient approach to study these patterns. By the introduction of Effective Calculability we can express the pattern of DNA in much better way. The transition function runs stepwise each character of the information string to produce the output string. The transformations achieved by the transition function are relatively simple in nature. Complex computations and operations can be affected by linking together several Effective Calculability switches so that the output string of one switch becomes the input string of another switch.

Keywords: DNA Chains; DNA Modeling; Effective Calculability; Lambda Calculus; Turing Machine.

1. Introduction

Advent of DNA molecules sequencing dramatically changed the biological sciences [9]. It has revolutionized our philosophy about biological evolution. Undeniably, it is one of the best examples of the power of reductionism.

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* Corresponding author.

Nonetheless, for difficult non-linear arrangements like DNA, there are limits to the reductionist approach: Knowledge of the way in which individual parts fit together ultimately fails to present a sufficient understanding of the system as a whole. These restrictions are currently obvious in that, even though over two million base pairs have been sequenced, the rate of understanding of these data is covering behind the rate of possession [2, 3]. Fig 1 illustrates the complex composition of DNA [10]. Even were we able to entirely sequence a cell's DNA and recognize all the details of the attendant biochemistry? It is not clear that we would automatically materialize with an understanding of the global software design principles underlying the functioning of the DNA molecule.

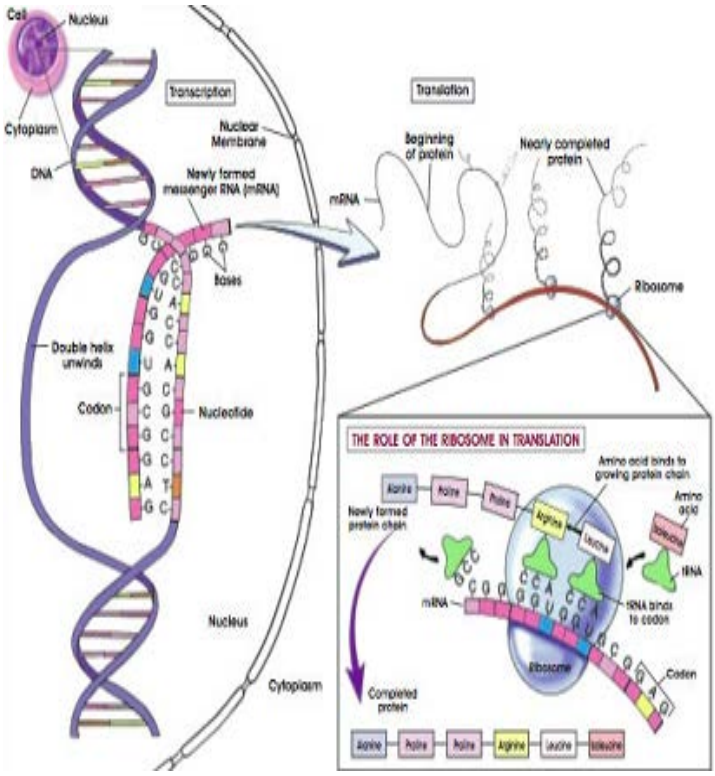

Figure1: A DNA Molecule

2. Effective Calculability

In computer discipline, and more particularly in Information Sciences, a model of computation is a model which portrays the relationship between given a set of inputs to a set of outputs [4]. This representation articulates how units of resources are being structured. The computational complication of a solution can be calculated using a given sculpt of computation. To emulate the concept of algorithm two models i.e Turing machines and Lambda Calculus are being used. An abstract model of Effective Calculability is represented in fig 2. Turing Machine is discovery of Allan Turing while Lambda calculus was invented by Church to perform computations with functions. Principally, each problem that is calculable by Lambda calculus is also calculable using Turing machine. Thus both are equivalent models of computation and both try to capture the power of any computation.

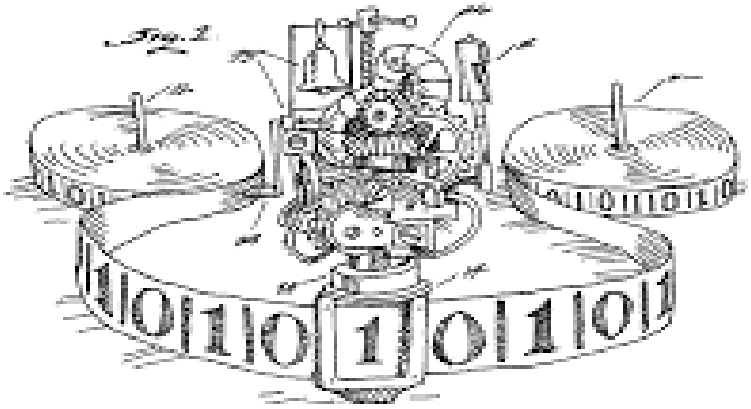

Figure 2: Abstract Machine

3. DNA Modeling Using Effective Calculability

The problem of understanding DNA might be associated to perceptive the functioning of a computer [5], for someone who has never seen one before. We now understand the basic philosophy of the underlying hardware, and through our acquaintance of the genetic code [11, 12], the basics of how the program is executing. Though we are closer to understanding the "microcode" of this program, but the crucial flow chart is still an unknown. In time we might hope to assemble a digital model of the DNA molecule and its attendant hardware, and thus actually execute a simulated "genetic program" [6]. The level of knowledge and the computation power that are nuts and bolts for this approach are likely to be some time in coming, however. One more reasonably different approach to this problem, exemplified by the work of Holland and Kauffman, is to study the generic chattels of models whose properties and size are simpler and smaller than those of the full DNA molecule [7]. If common sequences appear from these easy models, we can expect that they will also be present in more complex systems. Given the design limitation stated by organic chemistry, there may be a limited number of different solutions to a given problem. Moreover, the patterns of these solutions may not be exact to the particulars of organic chemistry, but rather only to the broad outlines [13].

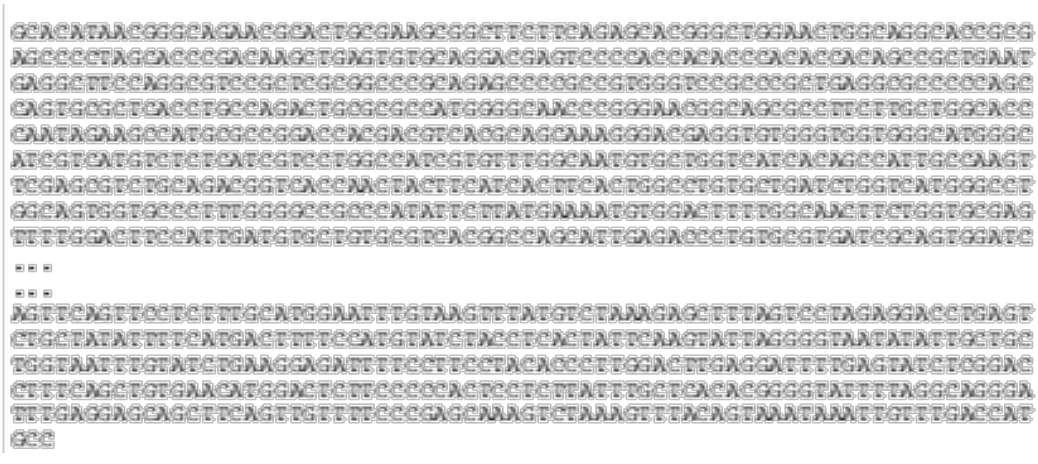

Figure 3: DNA String

As shown in the fig 2 the string of DNA is collected using the above mentioned technique, it contains a huge universe of information. Advanced level interpretation of DNA sequences may be explored using simple qualitative models based on DNA and it may give us insight and help illuminate the best methods [14]. And the vice versa, this knowledge will provide insight into high-quality designs for adaptive Effective Calculability. In order to employ a transformational or switching technique, we must be pledge of the capability and maturity of the agreed model [15]. Now a days and in near past there was a considerable growth seem in qualitative nature of Effective Calculability models. This encroachment was made by studying a diversity of simple models until patterns in their manners emerged, and then penetrating for these same patterns in investigational data generated by finite state machine. It straight away proposes that Effective Calculability might prove to be an imperative tool for the modeling of DNA.

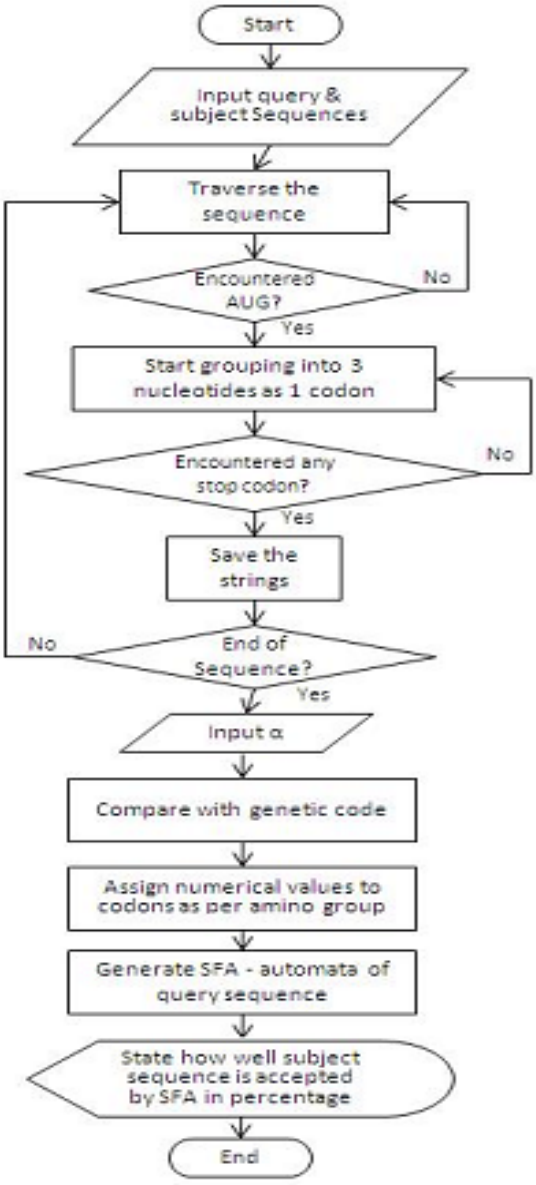

Figure 4: DNA Modeling Process

In fig 4 the basic algorithm is described, it's the simplest way to copy a sequence of DNA from nuclei to be

digitized for analysis and pattern matching objectives. It is important to realize that the DNA molecule is not just a linear string of base pairs; instead it has a variety of other systems for information storage. Moreover, for the majority purposes, the DNA molecule cannot be form in isolation; it is required to consider operation of the attendant biochemical mechanism [16]. All those who desire to explore simple models of DNA should be properly apprised of recent developments concerning the higher level structures present in DNA before they begin their explorations. We are presenting a brief review of the effervescent properties of the DNA in the framework of Effective Calculability. It not only present an easily digestible approach to the DNA molecule, described in non-technical terms; but also for both biologists and non-biologists, suggest strategies for modeling DNA in terms of Effective Calculability.

String 1: AUG GCG CCA AGA GCG CAG GCU CCA CAC GCC CCA AGG UGA

String 2: AUG AGA GUG UCA AAG CCA CUU UGU ACG UGG UGG UCU GGG AGG AAA UCC UUG CUG GCU UCC UUA UGG AUG CGG GAC GAU UGA

String 3: AUG AGG UCA AGG ACA UAA

String 4: AUG GCU GCA ACA GAU UGG AGA AUA UGU ACC GCA ACU GCC GUA CUA ACA CAC GGA GUA ACU UGU GUU CUU ACC CCC ACA AGA GUA UUA AUU AGA GAA GCA UGC UAU AAG AAA AAA UGA

Figure 5: Sample Information of DNA

Considering the string patterns as shown in the fig 5, these patterns have been collected in laboratory from various tissues.

Now it’s feasible to analyze these patterns with an automated machine or model.

This machine/model can process an ocean of organic molecules in a test-tube.

The tape will be made from a huge polymer of linked-up molecules where each individual molecule corresponds to a symbol on the tape.

The read/write head will be a sort of molecular "reaction vessel" which fits over the part of the polymer subsequent to the current symbol being processed. The overall state of system will be encoded by "transition" molecules, which bind to the current symbol molecule. There'll be a unique transition molecule for every possible state the system can be in. As for programming the "mechanism", this will be done by determining the possible chemical reactions between transition molecule and symbol pairings.

String 1: 0 0 0 3 0 1 0 0 3 0 0 3 -1

String 2: 0 3 0 1 3 0 0 1 1 0 0 1 1 3 3 1 0 0 0 1 0 0 0 3
1 1 -1

String 3: 0 3 1 3 1 -1

String 4: 0 0 0 1 1 0 3 0 1 1 0 1 0 0 0 1 3 1 0 1 1 0 0 1
0 1 3 0 0 0 3 2 0 1 1 3 3 3 -1

Figure 6: Transformed DNA

The very 1st step will produce a new pattern in digital form, a sample is depicted in fig 6. There are some other stags as well but we are only interested in transition and manipulation of the strings, which can be used in variety of applications for number of purposes [17]. To express the system for storing information in the patterns of DNA sequences can be fairly multifaceted, and should be incorporated as adaption of any simple model of the evolution of DNA sequences. We conclude with some remarks concerning approaches to modeling, including a summary of the type of information collected in the nucleic acid sequence database at Los Alamos, and a review of current approaches to searching for and comparing patterns in DNA sequences [18].

4. Literature Review

4.1. Alternative Methods for DNA Representation

The study of DNA string for discovery patterns in the series as replication of nucleotides, to find vital characteristic sites such as the Tbox, and evaluation the DNA strings with each other for evolutionary results have been done from a long time. It was one of the very momentous research field bioinformatics. Several techniques have been developed in this regard. Few of them are mentioned below.

4.2. 3D Technique of DNA Pattern Matching

When the textual DNA is compared with other strings, there were many deficiencies found in finding the attributes data about the species [16]. It clearly states that the DNA is rather more than just the series of characters; they are found in the cells in form of double helical structure, where hydrogen bonds are responsible for their build. Thus 3D model of the DNAs is considered and compared to solve the problem. The dimensions and the double helix structure of DNA sequences are compared. Here biological studies for the species behavioral characteristics as included in protein folding are performed.

4.3. DNA Pattern Matching using FPGA

Field Programmable Gate Arrays or FPGAs are used to investigate DNA series and for pattern matching. Though this technique is faster due to direct usage of hardware it becomes quite expensive. It converts the matching into Boolean format and then designs a circuit. Due to the limitation is of the DNA size, meaning the

string capacity that FPGAs support [20].

5. Conclusion

Given the design constraint avowed by macrobiotic chemistry, there may be a limited number of different solutions to a given problem. The patterns of these solutions may not be exact to the particulars of organic chemistry, rather only to the broad outlines. It is essential to understand that the DNA fragment [19] is not just a linear string of base pairs; instead it has a variety of other systems for information storage. All those who desire to explore simple models of DNA should be properly apprised of recent developments concerning the higher level structures present in DNA before they begin their explorations. This paper is self-effacing in objective with the purpose stated above in mind. Here we presented a concise review of the vibrant properties of the DNA molecule, discussed in the framework of Effective Calculability. it not only provide an easily digestible overture to the DNA molecule, described in non-technical terms; but also for both biologists and non-biologists, by including a concurrent transformation of property of DNA into the language of automaton theory, we hope to suggest strategies for modeling DNA in terms of Effective Calculability. Advanced level interpretation of DNA sequences may be explored using simple qualitative models based on effective calculability and it may give us insight and help illuminate the best methods. It straight away proposes that Effective Calculability might prove to be an imperative tool for the modeling of DNA.

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