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# DNA Pattern Analysis using FA, Mealy and Moore Machines

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## Abstract

Deoxyribonucleic Acid(DNA) is a series of genes made by the mixture of nucleotides. The adjustment in the succession of these nucleotides can alter the hereditary data that bring about numerous disarranges in living life forms. There are methods in theoretical computer science such as Finite Automata, Mealy machine and Moore machine to examine patterns of DNA and analyze any change in nucleotides to prevent various genetic disorders. In the present study, these three methods were combined to evaluate their performance. It was found that the Mealy machine is much better as compared to others because it has less states, and react faster to inputs don't need for clock.

**Keywords:** DNA, Finite Automata, Moore Machine, Mealy Machine, Pattern Analysis.

## Introduction:

DNA patterns are graphs of DNA or RNA sequences. It is an arrangement of qualities made of mix of nucleotides. The adjustment in the arrangement of these nucleotides can change the hereditary data that cause numerous issues in living creatures. So it is useful to find out such change in nucleotides to prevent such type of disorders and abnormalities. [1]

In genetic code of DNA, nucleotides in different sequences are used to form genetic information. Nucleotides in different sequences are utilized to frame hereditary data. These nucleotides are also called codons and combination of codons which helps in protein. For DNA pattern conversion there are four nucleotides that helps to understand pattern and transcribe into RNA pattern and then this RNA pattern translates into protein for finding any problem in pattern. The four important nucleotides are Cytosine (C), Adenine (A), Thymine (T) and Guanine (G).Pattern is very important for problem recognition in DNA. Identifying genes in DNA sequence is essential because pattern or sequence is known that any abnormality in gene can be detected. [1]

There are many methods to analyze the DNA pattern, especially in Computer Science to detect it from any change in the sequence of nucleotides. Finite Automata is used to analyze such patterns. We use NFA and DFA to analyze DNA pattern. The DNA is converted into a pre-mRNA then pre-mRNA is converted into mRNA and then mRNA converted into RNA which finally transformed into protein in final state. [1]This conversion in DNA is done by using enzymes. If some transitions are missing in the Finite Automata, the pattern is not completed. Next, for the sake of determining any pattern and DNA analysis by converting NFA into DFA, the other method used was the Mealy Machine Method. Mealy machine is a finite state machine whose output values are determined both by its current state and the current inputs. It is a deterministic finite state transducer, for each state and input, at most one transition is possible. Our last method, for analysis of pattern of DNA, it is Moore machine. A Moore machine is a finite-state machine whose output values are determined solely by its current state. This is in contrast to a Mealy machine, whose output values are determines both by its current state and by the values of its input.

## Related Work:

*Qura-Tul\_Ein*. [1] analyzed the DNA pattern that occurs in nucleotides to determine abnormalities. The problem is resolved by analyzing pattern of DNA through Finite Automata. The result if the genes combination not reached to final state or accepted it will be detect and resultant pattern is abnormal. The issue in paper was that in NFA, there are some states not properly ended in given pattern.

Different implementations of DNA limited state machines are contend, for example, Restriction Enzymes Finite State Machines, DNA enzymes Finite State Machines, and Finite State Machines with DNA Polymers in Eshra, A. (2013)[2]. Moreover, an assessment was made to clarify the favorable circumstances and burdens of every kind of DNA limited state machines. The issue that emerged was that the greater the machine turns into, the more execution time it costs..

The managing out capacities of DNA calculations from the flip side were by giving two sorts of executions to the limited state machine. A ligation-based methodology permits contribution of irregular length and can be eagerly executed with current biotechnology, yet requires ordered info encourage and distinctive atoms for various machines in Rose, J. (2010) [3].

In Wang, Z.- G. (2010) [4] the altered ideas of DNA machines (tweezers) to expect a catalyst free all-DNA robot. The considerable limited state machine uncovers a charming and conceivably helpful characteristic where the condition of the framework

is not just characterized by the setups of the atoms yet by the "history" of course of action of the example.

DNA pattern recognition for analyzing abnormality in genes is very important. The analysis of this type of pattern is done on Universal Turing machines. There will be some improvement of pattern for Turing machines in pattern analysis. *CH, S. (2011) [5].*

*Burks, C. (2010) [6].* In modeling a brief analysis of the dynamic characteristics of the DNA molecule is given. First, for non-biologists, an easily ripe introduction to the DNA molecule secondly, for both biologists and non-biologists, by as well as a synchronized conversion of properties of DNA into the language of automata theory also suggest approach for modeling DNA in terms of automata.

Most of the existing research to analyze the pattern of DNA through FA, and Turing Machines increases complexity, as there are many states which maybe difficult to analyze . In this research Mealy and Moore machines both were used which were proved to be easier with few states.

## Methodology:

### DNA pattern:

DNA sequence constitutes a combination of nucleotides. These nucleotides are also called as codons. In DNA consists of combinations of four Codons which are known as Cytosine (C), Adenine (A), Thymine (T) and Guanine (G). This DNA pattern converted into RNA with the help of different enzymes and Uracil (U) replaces the Thymine.

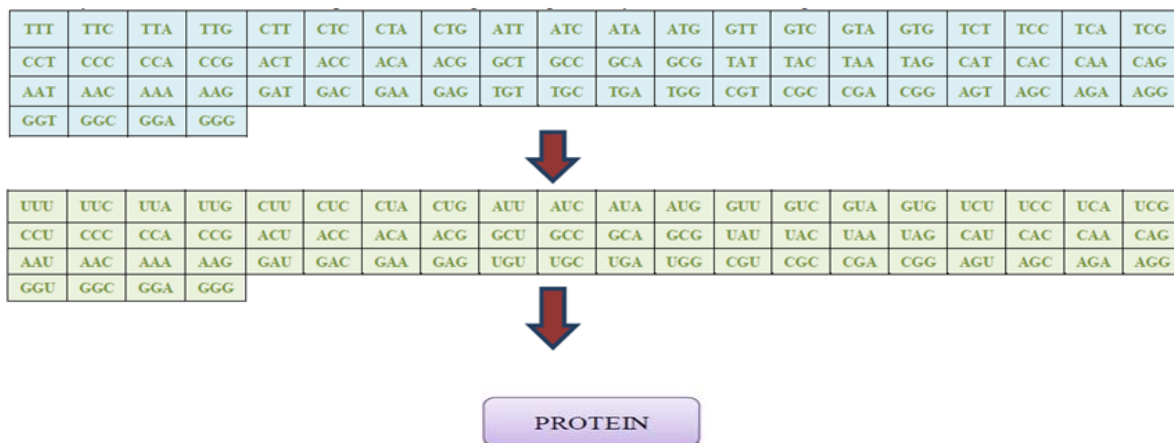


Fig. 1 DNA pattern

## 1) DNA Pattern Analysis with Finite Automata:

In the proposed model, eight states were used to analyze DNA normal and abnormal patterns using JFLAP.

$$Q = \{ 1,2,3,4,5,6,7,8 \}$$

$$\Sigma = \{ A,T,C,G \}$$

The 8 states of DNA pattern, in which on every state were checked for the inputs of DNA general pattern, if an input was accepted by given machine it was to be regarded as a normal pattern otherwise some abnormality in specific pattern was be assumed.

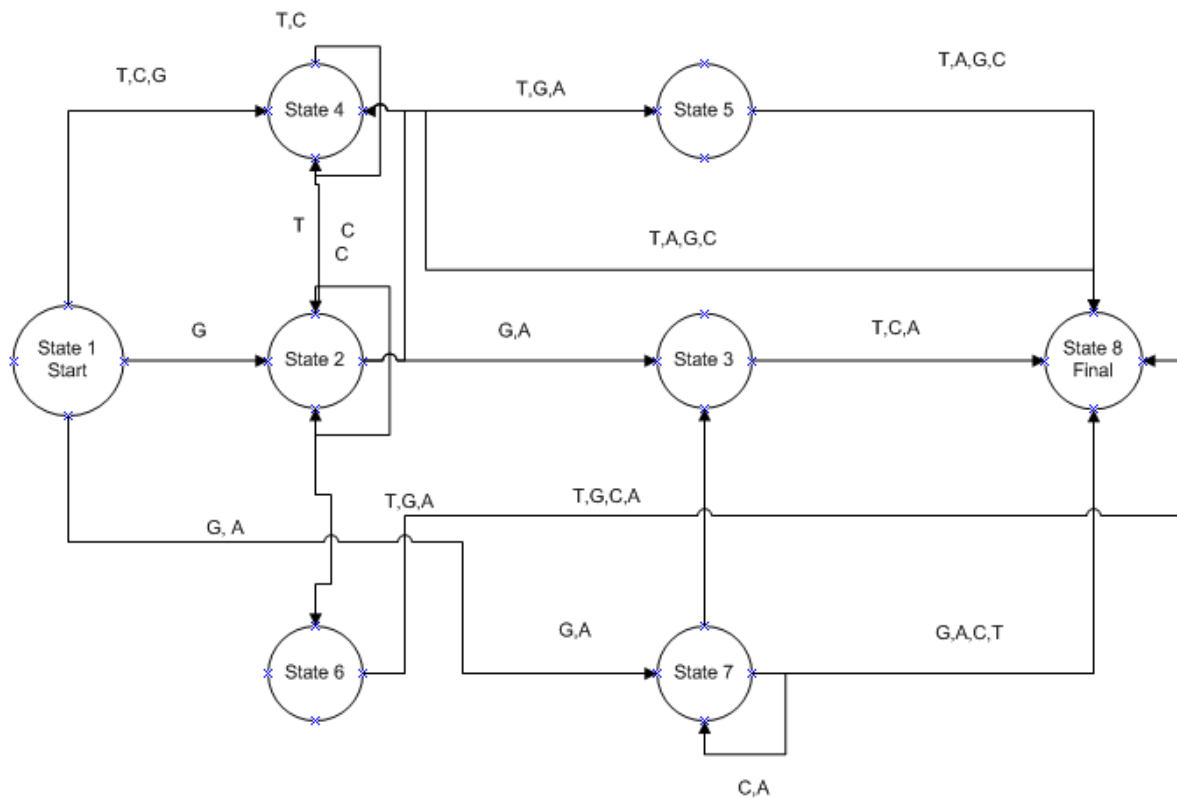


Fig. 2 FA of DNA pattern

## 2) DNA Pattern Analysis with Mealy Machines:

There are many inputs for DNA pattern, as mentioned above in Figure. 1. Random inputs were selected and checked for Mealy machines acceptance. In case the machine accepted the input on every stage, the DNA was normal otherwise it was abnormal. There is general model in which on every input check machine that is accepted or rejected.

Input (A, G, C, T)

There are five States.

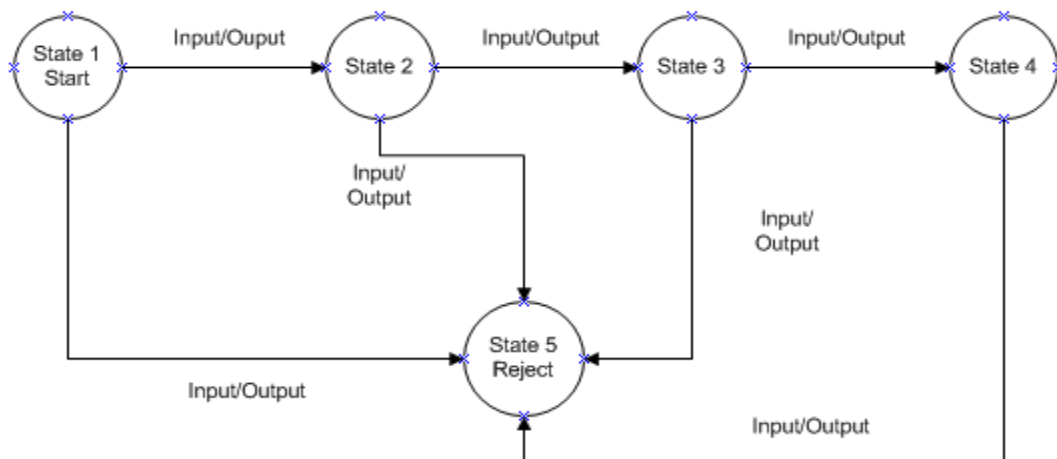


Fig. 3 General Model of Mealy Machine for every input.

The following model accepts TTT from DNA pattern.

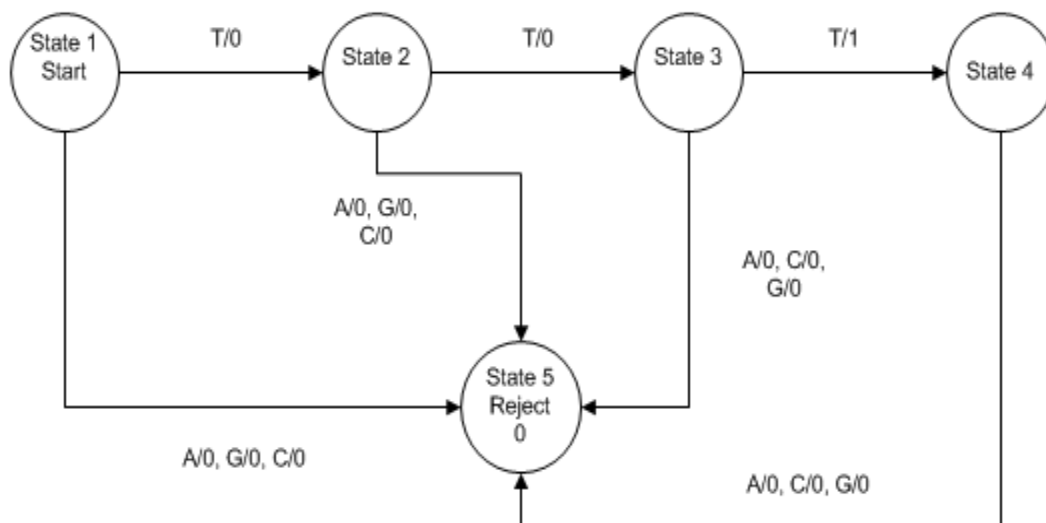


Fig. 4 Experiment Model of Mealy Machine for specific input.

## 2) DNA Pattern Analysis with Moore Machines:

There are many inputs for DNA pattern, as mentioned above in Figure. 1. So from that figure random inputs were selected and checked for every input that Moore machines acceptance . It was inferred that in case the machine accepted the input on every stage, the DNA will be normal otherwise it was proven to be abnormal. There is a general model through which various inputs can be checked for the acceptance and rejection by the machine.

Input (A, G, C, T)

There are five States.

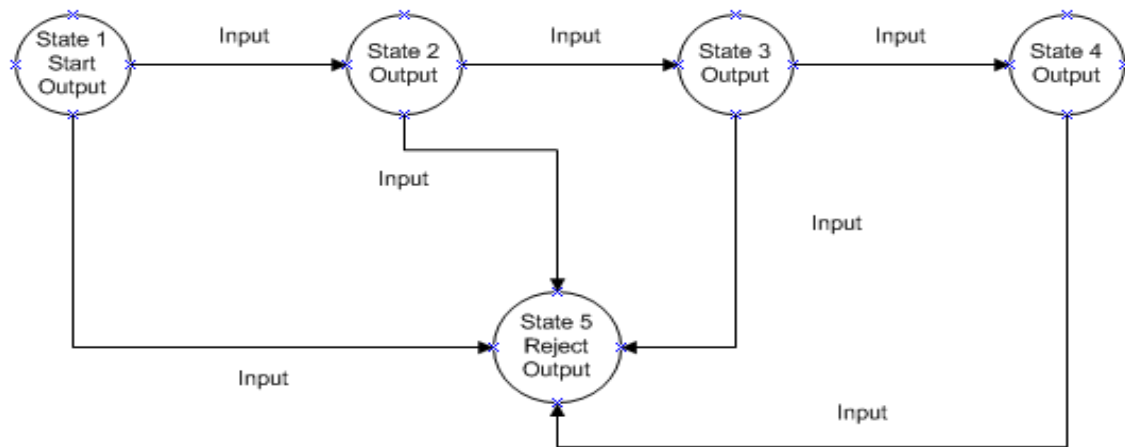


Fig. 5 General model of Moore Machine for every input.

The following model accepts TTT from DNA pattern.

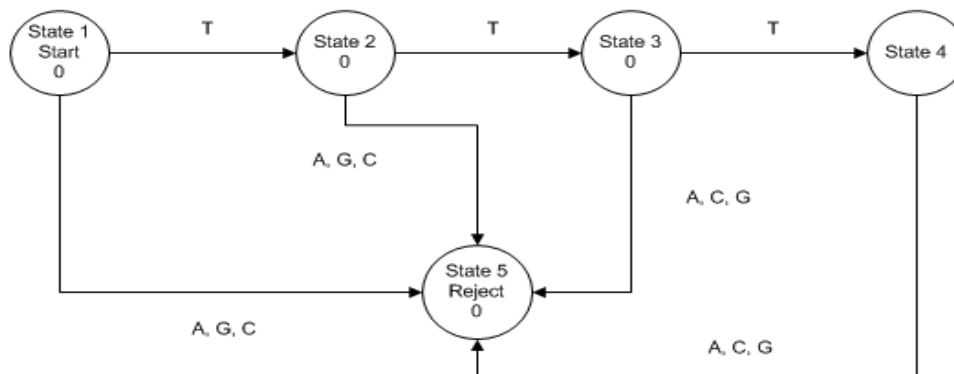


Fig. 6 Experiment model of Moore Machine for specific input.

## Experiments and Results:

## 1) DNA Pattern Analysis Using Finite Automata

**NFA:**

The following figure accepts DNA pattern which is mentioned above in Fig. 1.

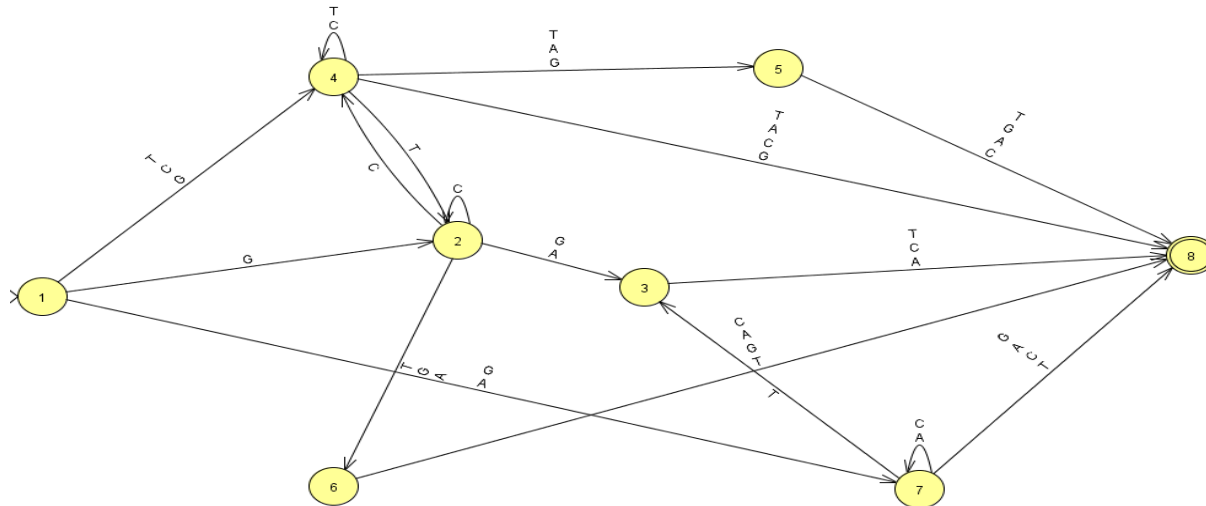


Fig. 7NFA of DNA pattern.

**DFA:**

The following figure accepts DNA pattern which is mentioned above in Fig. 1.

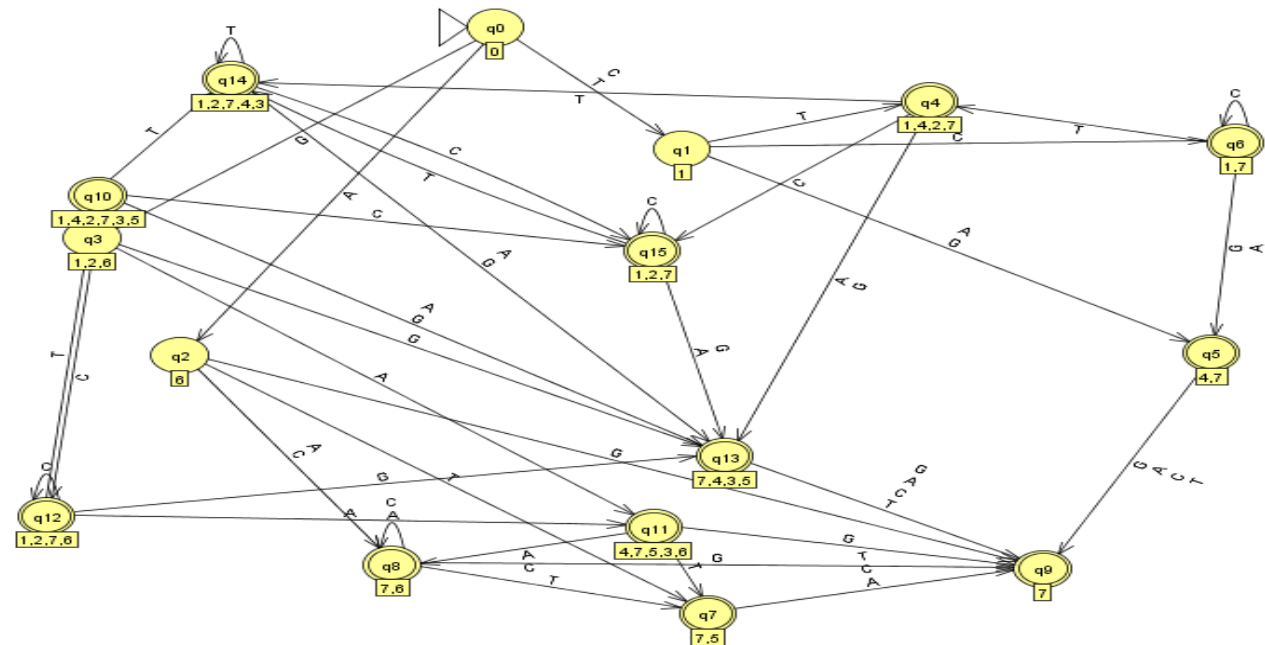


Fig. 8 DFA of DNA pattern.

### Results for DFA and NFA:

Input	Result
TTT	Accept
TCG	Accept
TAG	Accept
GTA	Accept
TCG	Accept
AAA	Accept
GGT	Accept
GGA	Accept
TCT	Accept
ACA	Accept
GGT	Accept
GGC	Accept
GGA	Accept
GGG	Accept
CGC	Accept
ATC	Accept
ATCG	Reject
GGTA	Reject

Table 1: Results of NFA and DFA

## 2.) DNA Pattern Analysis Using Mealy Machines

DNA pattern of Mealy Machine on some inputs (TTT, ATG, TAG, and CGA) are given as under:

### TTT

The following figure accepts DNA pattern for 'TTT'.

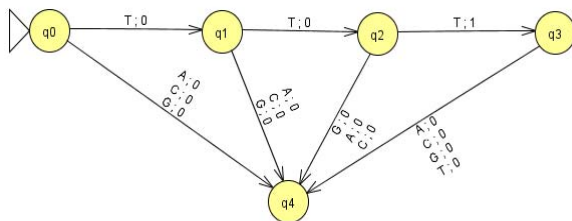


Fig. 9 'TTT' acceptance in Mealy Machines

### ATG

The following figure accepts DNA pattern for 'ATG'.

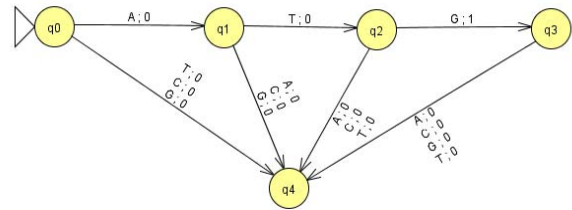


Fig. 10 'ATG' acceptance in Mealy Machines

### TAG

The following figure accepts DNA pattern for 'TAG'.

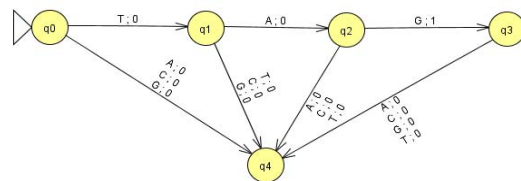


Fig. 11 'TAG' acceptance in Mealy Machines

### CGA

The following figure accepts DNA pattern for 'CGA'.



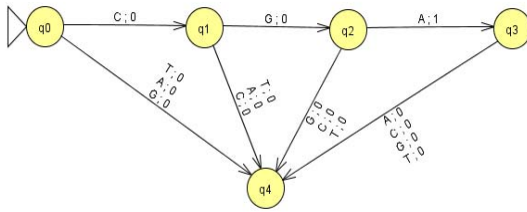


Fig. 12 'CGA' acceptance in Mealy Machines

### TTT result:

The following table shows result for acceptance DNA pattern for 'TTT'.

Input	Result
TTT	001
TGA	00
AGT	0

Table 2: TTT acceptance in Mealy Machines

### 3.) DNA Pattern Analysis Using Moore Machines

DNA pattern of Mealy Machine on some inputs (TTT, ATG, TAG, and CGA)

#### TTT

The following figure accepts DNA pattern for 'TTT'.

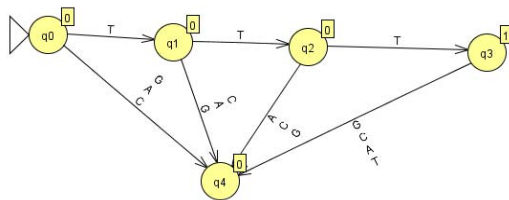


Fig. 13 'TTT' acceptance in Moore Machines

#### ATG

The following figure accepts DNA pattern for 'ATG'.

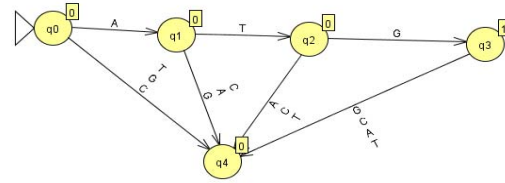


Fig. 14 'ATG' acceptance in Moore Machines

#### TAG

The following figure accepts DNA pattern for 'TAG'.

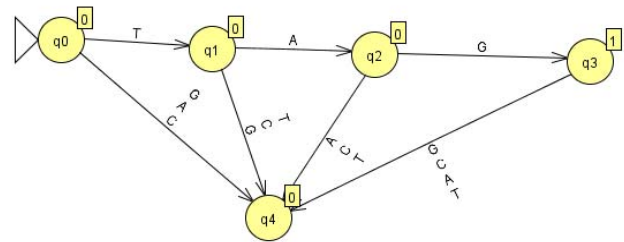


Fig. 15 'TAG' acceptance in Moore Machines

#### CGA

The following figure accepts DNA pattern for 'CGA'.

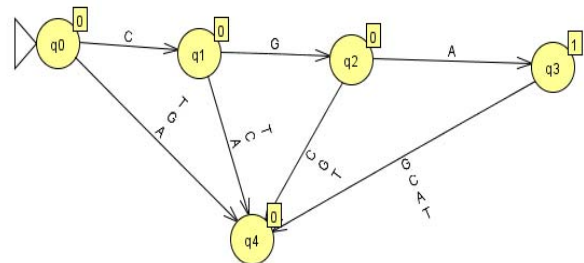


Fig. 16 'CGA' acceptance in Moore Machines

#### CGA Result:

The following Table shows the acceptance of DNA pattern for 'CGA'.

Input	Result
TTT	00
TGA	00
AGT	00
CGA	0001

Table 3: 'CGA' acceptance in Moore Machines

## Conclusion and Future Work:

Mealy machine is much better than Moore machine. The results show the performance of Mealy machines is better for analyzing the DNA pattern because the Output depends both upon present state and present input. Generally, it has fewer states than Moore Machine. Output changes at the clock edges. Mealy machines react faster to inputs. In future we work to analyze pattern of DNA through other computational models compare with these machines for performance.

## References

1. Qura-Tul-Ein, DNA Pattern Analysis using Finite Automata, International Research Journal of Computer Science (IRJCS), Vol. 2, No. 2, 2014, pp. 1-4.
- A.Name, and B. Name, "Journal Paper Title", Journal Name, Vol. X, No. X, Year, pp. xxx-xxx.
2. Abeer Eshra, Finite State Machines implementations using DNA Techniques, International Journal of Computing Science and Information Technology, Vol. 1, No. 1, 2013, pp. 1-7.
3. J. A. Rose, DNA Implementation of Finite-State Machines. International Research Journal of Computer Science, Vol. 1, No. 1, 2010, pp. 1-8.
4. Zhen-Gang Wang, All-DNA finite-state automata with finite memory, Proceedings of the National Academy of Sciences of the United States of America (PNAS), Vol. 1, No. 1, 2010, pp. 1-6.
5. Sumitha C.H, Implementation of DNA pattern recognition in Turing Machines, GSTF International Journal On Computing, Vol. 1, No. 2, 2011, pp. 1-6.
6. Christian Burks, Towards modeling DNA sequences as automata, Journal of High Energy Physics, Vol. 1, No. 1, 2010, pp. 1-11.