

## **International Journal of ChemTech Research**

CODEN (USA): IJCRGG, ISSN: 0974-4290, ISSN(Online):2455-9555 Vol.12 No.03, pp 227-232, 2019

ChemTech

## Introduction to Hidden Markov Model and its Biological Applications

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Abstract : Hidden Markov Model (HMM) is a stochastic model where all the states are hidden and emit outputs that are observable. HMM is intertwined with artificial intelligence that allows it to be applied to latest technologies like speech and handwriting recognition. It has proved to be an extremely valuable tool in the field of bioinformatics and has been extensively used in sequencing, alignment, homology prediction and protein secondary structure prediction. In order to understand HMM, we have used a simple problem based on land used for pigeon pea cultivation throughout years which has been illustrated using MATLAB and studied using matrix multiplication and probability concepts. This paper also outlines the technique used for studying gene prediction using HMM. It heavily draws content from the forward and backward recursions which were given by Ruslan L Stratonovichlt in 1960. It is a nexus of complicated ideas and calculations, including various algorithms like Viterbi and Forward algorithm which can be implemented using various programming languages such as C, C++ and tools like Matlab. Even though the concept is about 60 years old, it is one of the most detailed algorithms available to date. Due to ever increasing applications, it has become a constant in the curriculum for students of different backgrounds like computer science, electronics and bioinformatics.

**Keywords :** HMM, Markov chain, Transition diagram, Forward algorithm, Viterbi algorithm, Gene prediction.

S Narendra Kumar et al /International Journal of ChemTech Research, 2019,12(3): 227-232.

DOI= <u>http://dx.doi.org/10.20902/IJCTR.2019.120329</u>

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