**Abstract**

Efficient approach are based on probabilistic models, such as the Hidden Markov Models (HMMs), which currently represent one of the most popular techniques for multiple sequence alignment. In order to use an HMM method for MSA, one has to perform the parameter learning that is, to find the best set of state transition and output probabilities for an HMM with a given set of output sequences. In previous system, inspired by the free electron model in metal conductors placed in an external electric field here propose a novel variant of the PSO algorithm, called the random drift particle swarm optimization with diversity-guided search (RDPSO-DGS), and apply it to HMM training for MSA. In proposed system the two novel algorithms such that random drift firefly with diversity-guided search (RDFF- DGS) and random drift bat optimization with diversity-guided search (RDBO- DGS). It has fine adjustment of the parameters in this algorithm. In proposed algorithms are well effective than the existing system in terms of efficiency rate and computation cost of the system. That the HMMs learned by the RDFF and RDBO are able to generate better alignments. The experimental results show the RDBO-DGS gives the high accuracy 95% comparing to other algorithms for the herpes virus DNA data set it implement in MATLAB R2012a.. 100 data items are used for this research work, further can also use any Virus DNA for this alignment. It gives corresponding accuracy based on the data set. The remaining paper is organized as follows; Section 1. Describes introduction about the multiple sequence alignment. Section 2. Covers HIDDEN MARKOV MODELS FOR MSA. Section 3. Converse the related works behind in multiple sequence prediction. Section 4. Focus on experimental results comparison. Finally, Section 5. Discuss about the conclusion and feature work.