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*Application of efficiency based tools to explore the relationship of protein sequence and structure*

## **1. ABSTRACT**

The idea of this project is to study the protein structure and sequence relationship using the hidden markov model and artificial neural network. In this context we have assumed two hidden markov models. In first model we have taken protein secondary structures as hidden and protein sequences as observed. In second model we have taken protein sequences as hidden and protein structures as observed. The efficiencies for both the hidden markov models have been calculated. The results show that the efficiencies of first model is greater than the second one. These efficiencies are cross validated using artificial neural network. This signifies the importance of protein secondary structures as the main hidden controlling factors due to which we observe a particular amino acid sequence. This also signifies that protein secondary structure is more conserved in comparison to amino acid sequence.