PROTEIN SECONDARY STRUCTURE PREDICTION BY A MEASURE OF ARTIFICIAL NEURAL TECHNIQUE

M.GUNASEKARAN

DEPT. OF MATHEMATICS,
SRI SUBRAMANIA SWAMY GOVT. ARTS COLLEGE,
TIRUTTANI,

ABSTRACT
Some protein sequences have distinct amino acid motifs that always form a characteristic structure. Prediction of these structures from sequence is quite achievable using presently available methods and information. For most proteins, the accuracy of secondary structure prediction is approximately 70-75%. The need for such an effort is revealed by the rapid increases in the number of protein sequences and structures. In this paper, at the end of each iteration of learning, the network is evaluated with the test patterns. The network reaches a minimum of 80% SSP in 188,000 iterations with MSE as 0.0072. The % SSP oscillates slightly and increases.

KEYWORDS: Protein sequences, secondary structure prediction, accuracy, back propagation.