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Review Article

Protein secondary structure prediction using neural networks and deep learning: A review

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ABSTRACT

Literature contains over fifty years of accumulated methods proposed by researchers for predicting the secondary structures of proteins in silico. A large part of this collection is comprised of artificial neural network-based approaches, a field of artificial intelligence and machine learning that is gaining increasing popularity in various application areas. The primary objective of this paper is to put together the summary of works that are important but sparse in time, to help new researchers have a clear view of the domain in a single place. An informative introduction to protein secondary structure and artificial neural networks is also included for context. This review will be valuable in designing future methods to improve protein secondary structure prediction accuracy. The various neural network methods found in this problem domain employ varying architectures and feature spaces, and a handful stand out due to significant improvements in prediction. Neural networks with larger feature scope and higher architecture complexity have been found to produce better protein secondary structure prediction. The current prediction accuracy lies around the 84% marks, leaving much room for further improvement in the prediction of secondary structures in silico. It was found that the estimated limit of 88% prediction accuracy has not been reached yet, hence further research is a timely demand.

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