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Prediction of All-Beta Protein Secondary Structure Using Garnier-Osguthorpe-Robson Method

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Abstract : Proteins are chained sequences of amino acids which are brought together by the peptide bonds. Many varying formations of the chains are possible due to multiple combinations of amino acids and rotation in numerous positions along the chain. Protein structure prediction is one of the crucial goals worked towards by the members of bioinformatics and theoretical chemistry backgrounds. Among the four different structure levels in proteins, we emphasize mainly the secondary level structure. Generally, the secondary protein basically comprises alpha-helix and beta-sheets. Multi-class classification problem of data with disparity is truly a challenge to overcome and has to be addressed for the beta strands. Imbalanced data distribution constitutes a couple of the classes of data having very limited training samples collated with other classes. The secondary structure data is extracted from the protein primary sequence, and the beta-strands are predicted using suitable machine learning algorithms.

Keywords : proteins, secondary structure elements, beta-sheets, beta-strands, alpha-helices, machine learning algorithms
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