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Abstract

Bioinformatics is a field which uses technology and is rapidly growing, to solve the problem related to biological area. Study of protein, predicting its structure to know its function is an important field in bioinformatics. Protein unit that is twenty amino acids have total information for converting linear sequences of amino acid into its unique and globular structures. Protein folding problem is process to determine that protein is folding into its exact tertiary structure. Protein folds into matter of seconds to its stable 3-D structure; once it is stable it may perform proper functions. Contact map is an intermediate step for converting 1-d structure to 3-d structure. Contact map is the representative graphical view, how the protein folds into its proper

structure. Here, 6 parameters are set, which consider 2-norm distances for generating the contact map. It will consider the co-ordinate data, only of the residue having alpha carbon as contact type and map the contact as 1 if differences is greater than threshold value or -1 if less than threshold value.

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Index Terms

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Keywords

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2-Norm Distances