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.

References

- Fernanda Hembecker, Heitor Silvério Lopes (2010), “A Molecular Model for Representing Protein Structures and its Application to Protein Folding” IEEE.
- Jingjing Hu, Xiaolan Shen, Yu Shao, Chris Bystroff, Mohammed J. Zaki (2002), “Mining Protein Contact Maps”, In: Workshop on Data Mining in Bioinformatics
- Zafer Aydin, Yucel Altunbasak, and Hakan Erdogan (2011), “Bayesian Models and Algorithms for Protein B-Sheet Prediction”. In: Transactions on computational biology and bioinformatics, vol. 8, no. 2
- The Protein Data Bank,” http://www.rcsb.org/pdb, 2009
- Introduction to protein structure and structural bioinformatics, “secondary-structure.html”

Index Terms

Computer Science
Engineering and Technology
Keywords
Protein Structure Prediction  Amino Acids  Contact Map  Non-local Contact Map  2-Norm Distances