Abstract

One of the critical issues in bioinformatics is the data structure used for representing the protein data; this representation is a base for the operations applied such as sequence alignment, structure alignment and motif finding. In this paper, a survey of different representations and well-known data structures used for protein data is presented from a computer science perspective. This work presents a survey and summarizes the efforts done for protein data representation and approximation. Hence, it could be a basic reference for research that is aiming to develop applications in the field of bioinformatics.

References

- V Sheth, "Visualization of protein 3D structures in reduced representation with simultaneous display of intra and inter-molecular interactions," phdthesis 2009.
- Fabian Schwarzer and Itay Lotan, "Approximation of Protein Structure for Fast Similarity measures," in Proceedings of the seventh annual international conference on
Protein Data Representation: A Survey


**Index Terms**

Computer Science

Information Systems

**Keywords**

Protein representation  Protein structure  Data structure  Data reduction  Protein structure approximation