Abstract

In this paper, we present a three-layered predictor, Profinder, for identification and analysis of protein enzyme ‘Protease’. This predictor is shaped by collecting the protease family domains represented by multiple sequence alignments and hidden markov modeling techniques. Present study here is an attempt to develop a specific algorithm for searching particular domains in the genome sequences of these protein enzymes. Therefore, it is important for both basic research and drug discovery to consider the following two problems. Given the sequence of a protein, determine whether the protein is a protease or not? And if so, then which class of proteases? It is only on the basis of their sequence analysis, one can identify their types and also can predict their secondary or tertiary structures. User can test their sequences in fasta format for identification of proteases domain and therefore can get some insights on their functions and secondary structures. Besides, analysis based on phylogenetic relation of these proteases by constructing their phylogenetic trees in the light of evolution can be done. Storing all the information extracted from these sequences in a new database is another perspective of this present in-silico study.

References

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Index Terms

Computer Science Applied Sciences
Keywords
Proteases  Motifs  Sequence Alignment  Protein Domains  Hidden Markov Model