Abstract

In this paper, we present a three-layered predictor, Profinder, for identification and analysis of protein enzyme &apos;Protease&apos;. 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

- A. J. Barrett, J. K. McDonald, Nomenclature: protease, proteinase and peptidase,
Computational Analysis of Proteases Domains using Hidden Markov Model

- Identification of proteases and their types by Hong-Bin Shen, Kuo-Chen Chou
- ProtIdent: A web server for identifying proteases and their types by fusing functional
domain and sequential evolution information by Kuo-Chen Chou, Hong-Bin Shen, Published by
- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ: Basic local alignment search tool.
- Pearson WR, Lipman DJ: Improved Tools for Biological Sequence Comparison. Proc
BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids
Thompson, J. D. , Higgins, D. G. and Gibson, T. J. (1994) CLUSTAL W: improving the
sensitivity of progressive multiple sequence alignment through sequence weighting, position
specific gap penalties and weight matrix choice. Nucleic Acids Research, 22(22), 4673-4680.
- Finn,R. D. , Tate,J. , Mistry,J. , Coggill,P. C. , Sammut,S. J. , Hotz,H. R. , Ceric,G. ,
- HMMER user’s guide: biological sequence analysis using profile hidden Markov
- Eddy SR: HMMER: Profile hidden Markov models for biological sequence analysis.
1998 [http://hmm.janelia.org/].
- Puente XS, Sanchez LM, Overall CM, Lopez-Otin C: Human and mouse proteases: a
- Barrett A. J. , Rawlings ND, Woessner JF. The Handbook of Proteolytic Enzymes, 2nd

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