A Comprehensive Model for Feature extraction of Proteomic Data as a Tool for more Accurate In-Silico Identification of Proteins

Proteins are an essential building block of all living beings. Nearly all of the biological functions in eukaryotes and prokaryotes are carried out with the help of Proteins. Proteins are responsible for all metabolic activities. They maintain the cell structure and also perform regulation of living tissues and organ. The Uniprot database lists millions of proteins out of which only few hundred thousands are categorized. Researchers are increasingly understanding the significance of in-Silico protein prediction models which greatly simplifies their task by providing a reliable result very quickly and inexpensively as compared to in-Vitro or in-Vivo determination. However, such models makes use of computational intelligence and devising such models is a challenging job. This study pertains to development of robust and convincingly accurate model for this purpose. A feature extraction model is proposed that deeply, effectively and efficiently extracts the obscure patterns within the primary structure of proteins to establish inferences regarding its properties. The work also produces assiduous and promising results as compared to other models for various proteomic classifications.