

Analysis of complex protein structure through sequence extraction and visualization.

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Presentation Description:

Human Proteins structure are complex and many of their properties are still unknown. Our study focuses on discussing the implementing algorithms to find different protein sequencing and its associated properties. Using protein data from UniProt database, data and analytics tools were widely applied for finding the unknown functionalities of human protein structure.

Abstract:

Human protein are large and complex molecules contains amino acids which are linked by peptide bonds and form long chains. Protein plays critical role as they are part of cells and are responsible for structure and functionality of body tissues. The functionality of proteins depends on the 3-dimentional structure which includes amino acids, disulfide bonds and glycosylation, among others. Due to the presence of complex shapes many of the human protein functionalities are still unknown. Our study focuses on finding the unknown functionalities of Human protein using computer algorithms, data analytics and visualization tools. The purpose of our project is to identify different patterns of disulfide bonds, glycosylation, from finding patterns of the protein sequence and on examining how the two modifications affect the functionality of proteins. Using computer-aided methods, data processing tools have been applied to protein data downloaded from UniProt to envision protein structure. A score system algorithm also implemented for different scenarios depending upon the positions of disulfide pairs in proteins. Using this method, each protein score was calculated and visualized along with protein length, which helps in understanding the positions of these features. Our study provides useful insights for structures and functions of proteins and particularly to proteins with unknown structures.

References/Acknowledgments:

Dr. Bingyun Sun, Tanya Bakshi, David Pham