31ˢᵗ Asia Pacific Biotechnology Congress

April 10-11, 2025 | Webinar

Computational analysis of protein-protein interactions for target identification in Biotechnology

Omar Faridi

Department of Computational Life Sciences, South Africa

In the field of biotechnology, identifying precise protein-protein interactions (PPIs) is essential for developing targeted therapeutics and biotechnological tools. This study presents a computational approach for modeling and analyzing PPIs within cellular systems to discover novel molecular targets relevant to industrial and medical biotechnology. A curated dataset of protein interactions from various human cell lines was processed to map signaling pathways and functional networks. Emphasis was placed on identifying hub proteins that play central regulatory roles in cell metabolism, growth, and immune response.

Advanced data mining techniques and machine learning algorithms were used to evaluate the strength and relevance of each interaction. Network topology analysis was integrated with biological significance scoring to filter out non-functional links. Statistical modeling, including Partial Least Squares (PLS) regression and logistic classification, was applied to predict potential intervention points in the PPI network. Several high-confidence candidate proteins—previously unannotated—were identified as prospective targets for therapeutic modulation or industrial enzyme engineering.

This computational framework provides an efficient strategy for uncovering functional protein interactions in complex biological systems. The ability to virtually screen and prioritize protein targets based on interaction strength and biological relevance can accelerate applications ranging from synthetic biology and metabolic engineering to vaccine design and precision therapeutics. The study demonstrates how integrative bioinformatics can streamline the early phases of biotechnology innovation by reducing experimental workload and increasing target discovery accuracy.

Biography

Dr. Omar Faridi is a researcher in computational life sciences with a decade of experience in systems biology, proteomics, and cancer data analysis. His work focuses on modeling cellular behavior and identifying biomarkers through machine learning and multivariate statistical methods. He has contributed to several interdisciplinary projects aiming to bridge biological data and clinical applications, and has published extensively in journals related to oncology and computational biology.