

Abstract

The structure-function paradigm of protein biology has been fundamentally changed in the last three decades by the discovery of intrinsically disordered proteins (IDPs) and regions (IDRs). These proteins have been identified as critical components in various cellular processes, including signaling, protein-protein interactions, and regulation.

While it is apparent that IDPs/IDRs are vital in the function of living organisms, the study of their structure has posed a great challenge. Despite recent advancements in NMR spectroscopy and deep learning algorithms for protein structure prediction, IDPs/IDRs remain a relatively unknown territory, with significant gaps in knowledge about their behavior and function in living systems.

Although IDPs are present in all life forms, their abundance reveals a correlation between organismal complexity and degree of protein disorder. Prokaryotic organisms exhibit a much lower prevalence of IDPs than eukaryotic. Notably, a substantial degree of disorder is observed in unicellular parasitic protists, implying, that IDPs are fundamental in pathogenesis and the progression of diseases like malaria and toxoplasmosis.

In humans, malfunctions in IDPs are linked to many conditions, including neurodegenerative diseases such as Parkinson's, Alzheimer's as well as various types of cancer. Understanding these proteins could significantly impact the development of therapeutic strategies for these conditions.

This thesis underscores the necessity of specialized computational tools for accurate prediction of IDPs/IDRs to fully understand their function and significance in living organisms.

Key words: Intrinsically disordered proteins, Protein structure prediction, structural biology, Deep Learning