Institute of Biochemistry and Biophysics,
University of Tehran

Seminar Presentation

Predicting Metalloprotein Binding Sites: A Machine Learning Approach

Abstract

In the world of bioinformatics, proteins play a crucial role in areas like predicting structures, annotating functions, discovering drugs, and understanding diseases. About half of all proteins are classified as metalloproteins, and metal ions have a big say in how proteins interact with other molecules. These metal ions act like specific docking sites, affecting how proteins bind to things like peptides, ligands, and drugs. Lately, there's been a lot of interest in using machine learning to predict where these metal ions bind on proteins. Our study checks how well machine learning works compared to other ways of figuring this out. We're especially looking at the challenges posed by metal ions in binding sites and trying to bring together what we already know, highlight what's been achieved, and point out where we still need more answers. Our seminar aims to make things clearer for researchers by discussing machine learning methods, like Random Forest and Support Vector Machines, as the most successful ones in predicting metalloprotein binding sites. We'll also talk about some online tools used for this work. Finally, we'll break down the results of these methods and what they reveal about dealing with these tricky proteins.

Presenter
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Location (Physical and Online presentation)
Institute of Biochemistry and Biophysics. Amphitheater
https://join.skype.com/AOch5b2nahIw