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REVIEWER'S REPORT

Manuscript No.: IJAR-50790 Date: 27-03-2025

Title: Optimization of feature extraction for the prediction of macromolecular interactions : OTE-24 Approach

Recommendation:
Accept as it is……**YES……**
Accept after minor revision……
Accept after major revision ……
Do not accept (*Reasons below*) ……

Rating	Excel.	Good	Fair	Poor
Originality	√			
Techn. Quality		√		
Clarity		√		
Significance			√	

Reviewer's Name: Mir Tanveer

Reviewer's Decision about Paper: **Recommended for Publication.**

Comments (*Use additional pages, if required*)
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Reviewer's Comment / Report

The study titled **"Optimization of Feature Extraction for the Prediction of Macromolecular Interactions: OTE-24 Approach"** provides a comprehensive analysis of computational feature extraction techniques for macromolecular interaction prediction. It presents a novel approach based on physicochemical property correlations, aiming to improve accuracy over existing methods.

Abstract

The abstract effectively outlines the significance of macromolecular interactions in molecular biology and highlights the limitations of traditional feature extraction techniques. It clearly establishes the necessity of computational approaches while addressing their current inefficiencies. The proposed method, which focuses on the correlation between hydrophobicity

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and hydrophilicity of amino acids, is well introduced. The improvement in accuracy by 2.58% compared to existing methods is a noteworthy contribution, reinforcing the study's relevance.

Introduction

The introduction provides a strong foundation by emphasizing the importance of macromolecular interactions in drug development, bioinformatics, and medical research. It systematically presents various high-throughput experimental techniques such as NMR, SPR, and ITC, effectively highlighting their advantages and limitations. The discussion transitions seamlessly into the necessity of computational models for large-scale interaction predictions, establishing the context for the study's contribution.

The historical overview of computational methods, ranging from gene fusion techniques to 3D structural data and gene ontology-based approaches, is well-articulated. The limitations of these approaches, particularly regarding data incompleteness, computational complexity, and the lack of fully resolved 3D protein structures, are effectively discussed. The study rightly emphasizes the scarcity of well-documented macromolecular interactions across species, reinforcing the challenges in current predictive models.

The rationale for focusing on amino acid properties is well-founded, given the wide availability of sequence data in biological databases. The transition from traditional approaches to the OTE-24 feature extraction method is clearly justified, setting the stage for a deeper analysis of its implementation and impact.

Overall Evaluation

The paper presents a well-structured and informative discussion on macromolecular interaction prediction. The literature review is extensive, providing a thorough background on existing techniques while clearly identifying their limitations. The introduction successfully establishes the need for an improved computational approach, and the proposed method appears to address these challenges effectively.

The study is well-written, engaging, and contributes valuable insights into the field of molecular biology and computational bioinformatics.

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