

# Review of: "A unified drug–target interaction prediction framework based on knowledge graph and recommendation system"

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Potential competing interests: No potential competing interests to declare.

The authors present KGE\_NFM, a unified framework for Drug-Target Interaction (DTI) prediction that seamlessly integrates knowledge graph (KG) and recommendation system techniques. The model first learns low-dimensional representations of entities in the KG and subsequently employs the neural factorization machine (NFM) to integrate multimodal information. The evaluation against seven baseline methods on Yamanishi\_08's dataset and the BioKG dataset in three sample scenarios demonstrates the superior performance of KGE\_NFM. This comparison indicates that the model not only outperforms longstanding baselines but also offers valuable insights for integrating KG and recommendation system-based approaches into a unified framework for novel DTI discovery.

In addition to its application in DTI prediction, KGE\_NFM effectively extracts heterogeneous information from multi-omics data. By combining this information with traditional drug and protein characterizations through NFM, the model achieves accurate and robust predictions. The extensive validation on benchmark datasets, particularly in scenarios like the cold start for proteins, showcases the powerful predictive ability of KGE\_NFM. However, it is important to note that the model exhibits sensitivity to parameter adjustments, requiring careful consideration during the training procedure.

In summary, the authors have done an exemplary job in presenting a well-written paper that not only introduces a novel framework but also substantiates its effectiveness through rigorous experimentation. The model's success in DTI prediction and its versatility in handling multi-omics data make it a noteworthy contribution to the field. The mention of sensitivity to parameter adjustment provides valuable guidance for future users and researchers.