PhectorMatch: Contrastive Learning Enables Fast Virtual Screening

with 3D Pharmacophore Models

Daniel Rose^{1,2,3}, Oliver Wieder^{1,2}, Thomas Seidel^{1,2}, Thierry Langer^{1,2}

¹Department of Pharmaceutical Sciences, Division of Pharmaceutical Chemistry, Faculty of Life Sciences, University of Vienna, Josef-Holaubek-Platz 2, 1090 Vienna, Austria. ²Christian Doppler Laboratory for Molecular Informatics in the Biosciences, Department for Pharmaceutical Sciences, University of Vienna, Josef-Holaubek-Platz 2, 1090 Vienna, Austria

³Vienna Doctoral School of Pharmaceutical, Nutritional and Sport Sciences (PhaNuSpo), University of Vienna, Josef-Holaubek-Platz 2, 1090 Vienna, Austria

3D pharmacophore-based virtual screening is an established method in drug discovery^[1] but its applicability to massive datasets is limited due to the computationally expensive alignment of query pharmacophores to database ligands. We propose a novel approach inspired by neural subgraph matching^[2] that formulates alignment as approximate subgraph matching within an order embedding space^[3]. Pharmacophores are encoded into vector representations using a graph neural network, enabling efficient querying of pre-encoded conformational databases via the order embedding space, thereby bypassing traditional alignment (Figure 1). This significantly accelerates virtual screening, demonstrating promising results for the screening of massive datasets.

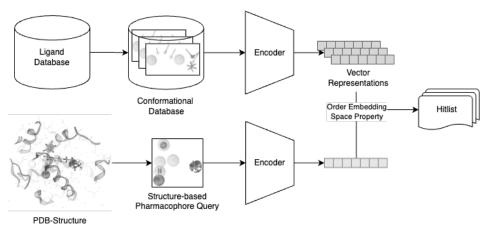


Figure 1: Schematic overview of the proposed method.

Bibliography :

[1] Wolber, G., & Langer, T. (2005). LigandScout: 3-D pharmacophores derived from protein-bound ligands and their use as virtual screening filters. *Journal of chemical information and modeling*, *45*(1), 160-169.

[2] Lou, Z., You, J., Wen, C., Canedo, A., & Leskovec, J. (2020). Neural subgraph matching. *arXiv* preprint arXiv:2007.03092.

[3] Vendrov, I., Kiros, R., Fidler, S., & Urtasun, R. (2015). Order-embeddings of images and language. *arXiv preprint arXiv:1511.06361*.