

Comparison of pharmacophore-based and ML approach to finding inhibitors of Sars-Cov-2 Nsp-13 helicase

Maria Bochenek, Tomasz Cheda, Mateusz Janduła,
Agnieszka Kowalewska, Joanna Krawczyk

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1 Introduction

The project's task was to identify potential Sars-Cov-2 Nsp-13 helicase inhibitors using virtual screening, docking simulations, and/or ML-based approaches. At the beginning of the course, we were given 5 resolved protein structures and an example of a database of small molecules to perform virtual screening on ([4]). Our pipeline is based on two alternative approaches of virtual screening - pharmacophore-based and DiffDock-based [2].

We built the first approach based on article [1]. We initially explored both ligand-based and receptor-based methods of constructing a pharmacophore, however, we chose the second one. Then, we screened the bioactives subdatabase from [4]. For this purpose (pharmacophore model construction and virtual screening), we used Schrödinger Maestro Phase software [3]. Our project workflow is presented in Fig. 1. We describe it in more detail in the section Materials & Methods.

In the project, we were paired with the **second team from Sorbonne University (S2)**.

1.1 Project workflow description

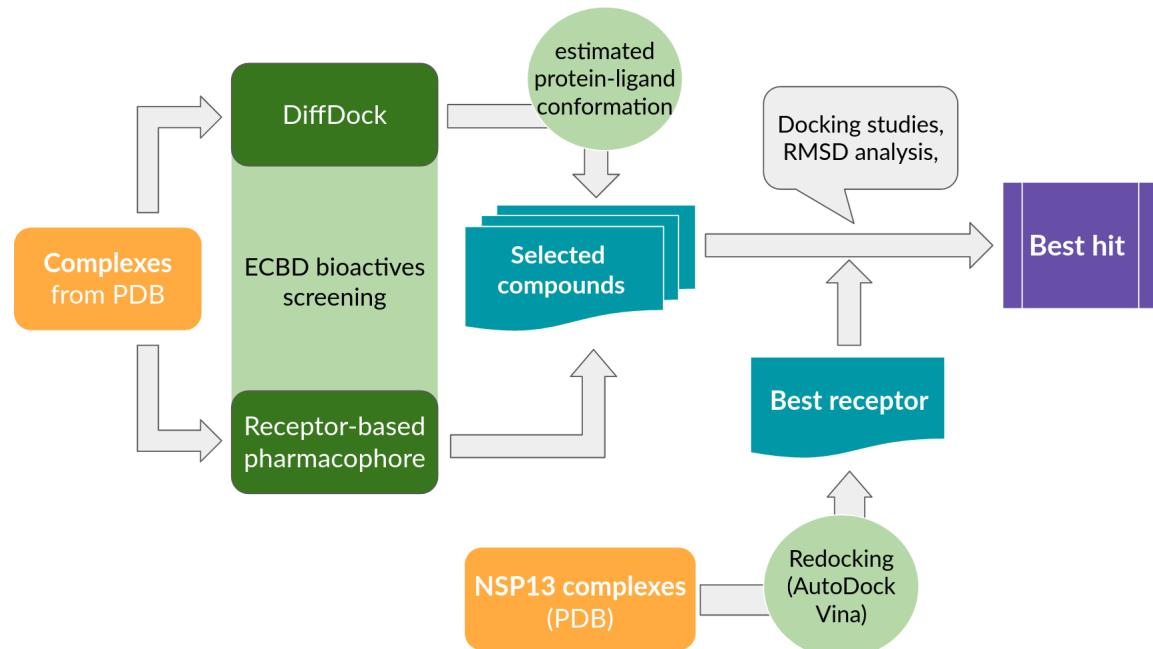


Figure 1: Workflow figure

2 Materials & Methods

2.1 Pharmacophore-based approach

In order to create a pharmacophore model, we have selected and downloaded 55 Nsp-13 complexes with ligands other than simple ions or ADP from the PDB database. Then, we selected one Nsp-13 complex with ADP (PDB 7KRN, chain E) as a reference structure. Consecutively, using PyMol, we have superposed the reference and query structures to check, if the ligand is located in the receptor's ADP binding site. After the visual analysis, we have preselected 15 complexes (5RL7, 5RL9, 5RLI, 5RLJ, 5RM2, 5RM7, 5RLN, 5RLO, 5RLR, 5RLS, 5RLW, 5RLV, 5RLY, 7NN0, 7NNG) to perform redocking using MGLtools [5] (also used for ligand and docking box preparation) and Autodock Vina [6, 7]. As redocking we define removing a ligand (native ligand) from a complex and docking it again in the same complex. Redocking can help us select a receptor for further docking. We define the ADP binding site of Nsp-13 after [1]: ASP374, GLU375, SER377, ASP401, GLN404, ARG443, LYS288, SER289, ARG567, and GLY538.

Based on the redocking score (binding affinity), we have selected a reference structure for docking - 7NN0 (based on binding affinity and visual analysis in PyMol and MGLtools). The comparison between the position of the native ligand and the predicted conformation is presented in Fig. 2. The best hits are presented in Table 1. It is worth mentioning that all the ligands except 7NN0 were docked far away from the native ligand (the two molecules were not overlapping).

PDB code	Binding affinity (kcal/mol)
7NN0	-10.7
5RL7	-7.2
5RLS	-7.2
7NNG	-7.1
5RLN	-6.9
5RM7	-6.9
5RM2	-6.7

Table 1: Best AutoDock Vina affinity binding scores for redocked ligands.

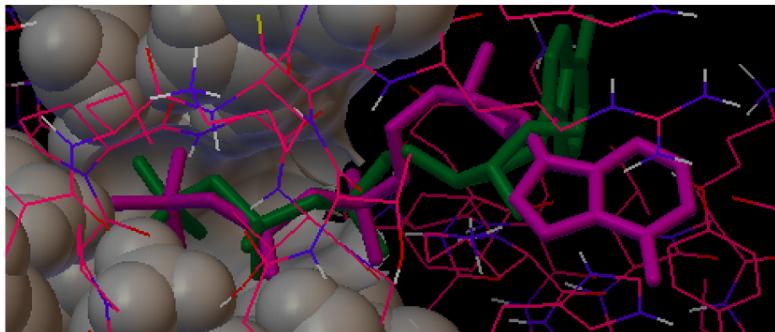


Figure 2: Redocking for complex 7NN0 visualised in MGLTools [?]. The native ligand is marked in magenta. The redocking output - in green. The binding site surface is marked in gray.

We have tried multiple approaches to creating a pharmacophore model. Initially, we wanted to construct a ligand-based pharmacophore using Python libraries - RDKit and CMapper. Unfortunately, we were not able to succeed on this path, since the Ligand Expo database, that we wanted was out of order for the entire month (January 2023). On the other hand, while pursuing this approach, we have learned about the similarities and dissimilarities of the ligands.

Then, since we could not find another free and open-source tool for pharmacophore construction, we decided to use the trial version of Schrödinger Maestro Phase software [3].

First, we tried developing ligand-based pharmacophore hypotheses using a subset of 15 ligands found natively in We have started with attempting to develop a ligand-based pharmacophore hypothesis, using multiple combinations of 15 preselected ligands. We found that the best combinations of ligands from PDB complexes were almost the same as the one presented in [1].

However, all of our ligand-based pharmacophores were not specific enough and we did not get any valid results from virtual screening of [4].

Moreover, after analyzing receptor-ligand interactions, we discovered that the common ligand features are located in different sites of the receptor's binding pocket and hence create different interactions. Consequently, we have realized that the ligand-based approach would not be specific enough for our purpose. We wanted to build the pharmacophore hypothesis based on the receptor-ligand interactions and not only on the common aspects of ligands' structure. Moreover, it is crucial to remember that the pharmacophore model in [1] was receptor-based, not ligand-based. Considering the mentioned arguments, we have decided to create a receptor-based pharmacophore.

2.2 DiffDock-based approach

3 Results

3.1 Pharmacophore-based approach

We have created a pharmacophore hypothesis for each of the 15 complexes separately and analyzed all of them visually. Based on ligand interaction diagrams (see example in Fig. 3) and the amount of information and specificity that a single hypothesis brings into the entire model, we have selected a subset of hypotheses to merge. For example, we have entirely excluded the 5RLW, 5RLJ, 5RLI,

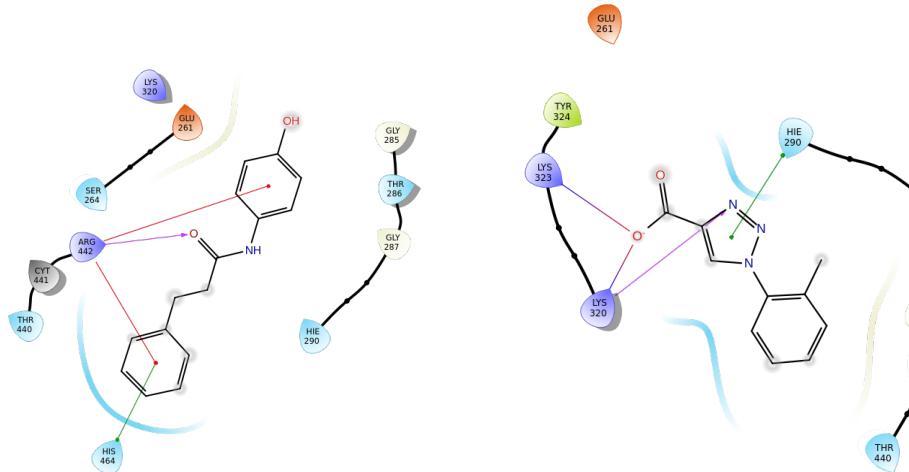


Figure 3: Ligand-receptor interaction diagrams (left: 5rm7, right: 7nng).

and 5RL7 since their hypotheses seemed ambiguous (a ligand's interaction diagram did not support its pharmacophore). From the remaining hypotheses, we were trying to identify the most common features. By merging such features, we have developed multiple hypotheses based on different subsets of the chosen 15 ligand-receptor complexes and screened against bioactives from ECB database. We validated the hypotheses by analyzing their results of screening a database composed of active molecules and decoys from DUDE database [?].

Finally, we have chosen a pharmacophore model (Fig. 4) consisting of:

- 2 donors,
- 3 aromatic rings,
- 2 negative charges.

This hypothesis was the best in terms of validation performance. After screening it against the database [4], we obtained 76 hits. We then docked it into 7NN0 receptor (the reference structure chosen before). While analyzing the docking results, we encountered a problem. We wanted -10kcal/mol to be the maximal binding affinity threshold, but we get only 2 hits that fulfilled this criterion (UTP and ATP - common in human cells). Due to that, we were forced to lower the threshold - we set it to -9kcal/mol. The best binding affinities are presented in Table 3. Apart from molecules common in the human body, we found 4 molecules (ECBD codes EOS101850, EOS101674, EOS102024, EOS101092). Two of them have their trade names defined in ChEMBL database [8]: Folotyn and Tomudex. The rest can be found in ZINC databases and is available for purchase.

We visualized docking results in PyMol. The visualizations for EOS100357 and EOS101674 are presented in Fig. 5. A visual summary of the pharmacophore-based approach is presented in Fig. 6.

Compound name	Compound CID
A-385358	11556440
ABT-737	11228183
Adapalene	60164
Adomeglivant	91933867
Avasimibe	166558
CARM1-IN-1	24827559
Cintirorgon	124126348
Diphenyl Blue	6296
Elaidic acid	37517
Evans Blue	9409
Fenretinide	5288209
Gossypol	3503
GW7647	3392731
Idasanutlin	53358942
Navitoclax	24978538
NF 023	6093160
Oleic acid	445639
PDK1/Akt/Flt Dual Pathway Inhibitor	5113385
PPNDS	5311367
RO8994	53238217
Suramin	5361
TCID	2729042
TW-37	11455910
Zafirlukast	5717

Table 2: Actives used for Pharmacophore hypothesis validation [11].

ECBD code	Ligand name (if defined)	Binding affinity (kcal/mol)
EOS100357	Uridine 5'-triphosphate	-10.5
EOS100983	Adenosine 5'-triphosphate (sodium salt)	-10.1
EOS102340	Guanosine-5'-triphosphate	-9.8
EOS101850	-	-9.7
EOS101674	Pralatrexate (trade name Folotyn)	-9.1
EOS102024	-	-9.1
EOS100865	Adenosine-5'-diphosphate	-9.0
EOS101092	Raltitrexed (trade name Tomudex)	-9.0

Table 3: Top AutoDock Vina affinity binding scores for docked ligands.

3.2 DiffDock-based approach

4 Discussion

Our work in the project can be summarized not only by the results presented but also by the biological knowledge and practical insights into real-life bioinformatics problems, such as identifying potential inhibitors of different proteins. Due to differences in our academic paths and experience (mathematics, bioinformatics, machine learning, and computer science), first, we had to create a pipeline that would allow using our skills and experiences. Next, we needed to divide the tasks among the members of the team so that we could use the knowledge we already have as well as cooperate and learn from each other. Of course, we also gained many entirely new skills and intuitions - only one of us had heard of a pharmacophore hypothesis before.

While preparing the project, we encountered several problems and we still have some doubts considering the choices we made throughout the project. One of the doubts concerns selecting the ligands building the pharmacophore. As in [1], we chose the ligands from the ones found in complexes with Sars-CoV-2 Nsp-13 helicase in PDB database. The problem is that almost all of them are really shallow in the ADP binding pocket, however, redocked ligands are located deep inside the pocket. We consider such redocking outcomes invalid. Moreover, as in [1], screening the database with the

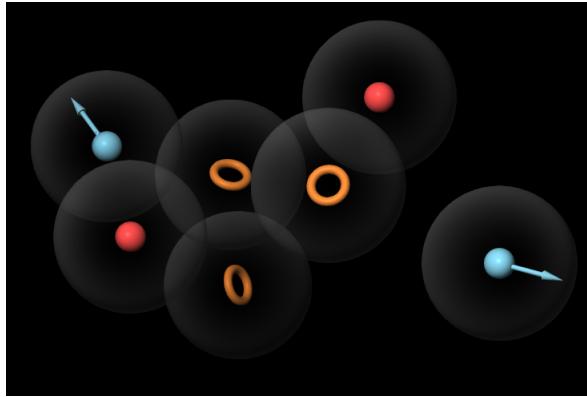


Figure 4: Pharmacophore hypothesis.

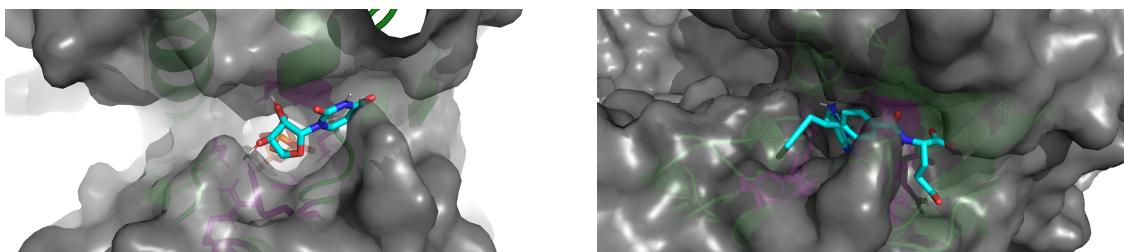


Figure 5: Docking results visualised in PyMol (left: EOS100357, right: EOS101674). The amino acids from ADP binding site are colored magenta and the surface of the receptor is colored gray.

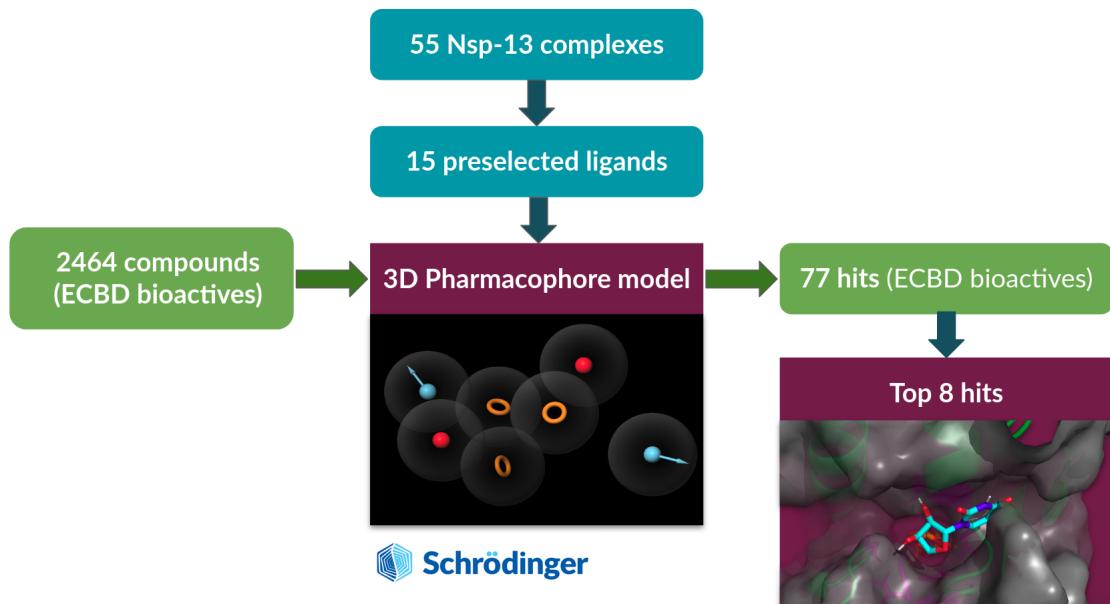


Figure 6: Result figure for pharmacophore-based approach.

receptor-based pharmacophore based on (not necessarily only) native ligands lying shallow in the pocket, returns ligands, that lie deep in the pocket. We were not sure whether this behavior of results is normal, however we accepted it, as was done in [?].

Considering our results from the pharmacophore-based approach, we hoped to get more ligands with scores higher than the threshold. However, after examining our results, we found out that the ligand (EOS101674) with the trade name Folotyn has been previously identified as a potential Sars-CoV-2 inhibitor [9]. The scientists at the Chinese Academy of Sciences Shenzhen Institutes of Advanced Technology (SIAT) showed that Folotyn (pralatrexate), a chemotherapy drug could be a potential remedy against SARS-CoV-2 - "They found that pralatrexate more strongly inhib-

ited SARS-CoV-2 replication than did Gilead Sciences' remdesivir under the same experimental conditions" [10]

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