Elucidation of protein function using computational docking and hotspot analysis by *ClusPro* and *FTMap*

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Starting with a crystal structure of a macromolecule, computational structural modeling can help to understand the associated biological processes, structure and function, as well as to reduce the number of further experiments required to characterize a given molecular entity. In the past decade, two classes of powerful automated tools for investigating the binding properties of proteins have been developed: the protein–protein docking program *ClusPro* and the *FTMap* and *FTSite* programs for protein hotspot identification. These methods have been widely used by the research community by means of publicly available online servers, and models built using these automated tools have been reported in a large number of publications. Importantly, additional experimental information can be leveraged to further improve the predictive power of these approaches. Here, an overview of the methods and their biological applications is provided together with a brief interpretation of the results.

1. Introduction

X-ray crystallography provides atomistic structural details of macromolecules and is crucial for the mechanistic understanding of their cellular function. However, some applications such as drug discovery or the determination of protein–protein complexes may require further experiments and additional structures to answer all questions. In these instances, computational structural modeling tools can serve as an important alternative method to gain structural insights, as well as to guide or minimize the amount of further experiments.

This paper aims to briefly outline several state-of-the-art computational approaches that are used to help understand biological processes, structure and function, including *ClusPro*, a protein–protein docking web server, and *FTMap*, a family of web servers for determining and characterizing ligand-binding hotspots of proteins. Advanced features may be enabled to leverage pertinent *a priori* or experimental data, thereby offering more accurate predictions. Recently, *ClusPro* has been used to explore additional applications with *AlphaFold2*, including high-accuracy prediction of protein–protein interactions.

1.1. Protein–protein docking using *ClusPro*

*ClusPro* is a web server based on a rigid-body docking method, *PIPER*, that firstly samples all translations and rotations of a ligand protein with respect to a receptor protein and secondly uses the fast Fourier transform (FFT) correlation...
approach using knowledge-based or statistical potentials as the scoring function to sort the samples in order to select the best model of the complex (Kozakov et al., 2006; Xia et al., 2016). The server performs three computational steps as follows: (i) rigid-body docking by sampling billions of conformations, (ii) root-mean-square deviation (r.m.s.d.)-based clustering of the 1000 lowest-energy structures generated to find the largest clusters that will represent the most likely models of the complex and (iii) refinement of selected structures using energy minimization. The numerical efficiency of the method stems from the fact that such energy functions can efficiently be calculated using FFTs, which provide the ability to exhaustively sample billions of conformations of the two interacting proteins, evaluating the energies at each grid point. Thus, the FFT-based algorithm enables the docking of proteins without any a priori information on the structure of the complex. While ClusPro assumes that the proteins are essentially rigid, the method allows for moderate conformational changes due to the smoothness of the energy function and its tolerance of atomic overlaps. In fact, allowing a certain amount of overlap is key to the success of any rigid-body docking method. The resulting steric conflicts are then removed by local energy minimization of the generated complex structures. To account for larger conformational changes one can dock structures based on NMR experiments, multiple X-ray structures or structures generated by molecular-dynamics (MD) simulations. In spite of these approaches, we admit that without access to multiple representative structures, evaluating the site. The hotspots can be further combined to identify binding hotspots that substantially contribute to the binding free energy. Analogous to experiments, the larger the probe population at a particular site the more important the hotspot is. The number of probe clusters forming a consensus site is strongly correlated with ‘druggability’ and the relative importance of the site. The hotspots can be further combined to identify protein binding sites. This approach is performed by FTMap (Ngan et al., 2012), which builds on top of FTMap. The mapping process used by FTMap and FTSite can take into account small conformational changes for the reasons described above for ClusPro. Additionally, hotspots tend to be conserved despite moderate conformational changes (Kozakov et al., 2011). Large conformational changes can be explored by applying FTMap to ensembles of structures generated either by NMR, MD or multiple crystal structures using an MD ensemble.

2. Results

2.1. Protein–protein docking using ClusPro

Two protein–protein docking applications are presented here. The first is ab initio docking and the second is docking guided by experimental restraints.

2.1.1. Ab initio protein–protein docking. Here, we demonstrate a case of protein–protein docking starting from separately crystallized subunits. As an example, we consider a complex of subtilisin Carlsberg protease (PDB entry 1scn) and its inhibitor turkey ovomucoid third domain (OMTKY3; PDB entry 2gkr). The unbound structures, PDB entries 1scn and 2gkr, are submitted to ClusPro without any additional information. The top ten results of this docking run are shown in Fig. 1(a) superimposed onto an X-ray structure of the complex.
In Fig. 1(b) the near-native ClusPro model ranked 2 is highlighted. The model provides a reasonable approximation of the binding found in the crystal structure (PDB entry 1r0r) and shows an r.m.s.d. of 2.09 Å to the native structure.

2.1.2. Protein–protein docking with distance restraints

To demonstrate docking with experimental restraints we consider the case of the Bmi1/Ring1b–UbcH5c complex (PDB entry 3rpg) binding to a nucleosome core particle (PDB entry 3lz0). When the docking run is submitted without the use of restraints the Bmi1/Ring1b–UbcH5c complex is modeled as binding to the DNA strand, which contradicts experimental evidence. The ubiquitination process indicates that the Cys85 residue on UbcH5c needs to be proximal to the Lys119 residue on H2A of the nucleosome (Bentley et al., 2011). There are also mutational studies which indicate that Lys97 on Ring1b is involved in binding to the surface of the core histones (Bentley et al., 2011). These experimental details can be used to specify geometric restraints which will limit the search space to the relevant areas. The generation of restraints can be performed using the restraint generator provided at https://cluspro.bu.edu/generate_restraints.html. The generator outputs a restraint file formatted as shown in Fig. 2. The results of the restrained docking can be viewed in Fig. 3(b) compared with the crystal structure of the complex found in PDB entry 4r8p. This can be compared with the unrestrained docking results shown in Fig. 3(a). The restrained results provide a binding pose close to the reported structure among the top predictions: this is the pose ranked 2 and it has an iRMSD of 4.9 Å (see Fig. 3b).

2.2. Identification of ligand-binding hotspots using FTMap

In this section, we demonstrate hotspot identification using FTMap in various drug discovery-related applications starting from the crystal structure of the protein.

2.2.1. Fragment screening for SARS-CoV-2 main protease with FTMap. As a first example of computational binding-site prediction with FTMap, we applied FTMap to SARS-CoV-2 main protease (Mpro; Douangamath et al., 2020), a recognized COVID-19 drug target. Fig. 4(a) demonstrates the global mapping of Mpro shown in a gray surface representation. FTMap produced nine consensus sites or hotspots ranked by
cluster population and shown as different carbon-color line representations. There are four mostly minor consensus sites outside the active site of Mpro, including two near the dimerization interface. The majority (4/5) of highly populated consensus sites with over ten probe clusters can be found in the active site of Mpro, including the consensus site with the highest population (26 probe clusters), which implies that the site is druggable. Indeed, to date, several compounds with submicromolar binding to Mpro have been reported in the literature. Enlarging the active site shown in Fig. 4(b), one can see that the compounds depicted in stick representation overlap with FTMap hotspots in different combinations.

2.2.2. Druggability analysis of protein–protein interfaces using FTMap. The low druggability of protein–protein inter-

Figure 3
Protein–protein docking with restraints. Docking results using ClusPro, both restrained and unrestrained. (a) The unrestrained docking results for the Bmi1/Ring1b–UbcH5c complex and nucleosome. The Bmi1/ Ring1b–UbcH5c complex is bound to the DNA in this instance. (b) This is the number 2 ranked pose using restraints; it binds to the appropriate location and has a near-native pose.

Figure 4
Fragment screening for Mpro using FTMap: the top-ranking consensus clusters of probes are depicted in green, cyan, magenta and yellow. The SARS-CoV-2 Mpro protein structure is depicted as a gray surface in a global view (a) and the active site (b). The inhibitors are peptide-like (pale green sticks; Jin et al., 2020), Diamond Fragalysis (wheat sticks; XChem@Diamond; https://fragalysis.diamond.ac.uk/viewer/react/landing) and PostEra COVID Moonshot (light blue sticks; https://postera.ai/moonshot).
with those found in traditional protein–ligand interactions, and the requirement of the ligand to compete with protein interactions. FTMap can be used to identify ‘hotspots’ on the protein surface, the presence, strength and relative distance of which on the interface can indicate druggable sites. Fig. 5(a) highlights the FTMap results of mapping interleukin-2 at its interface with the interleukin-2 receptor. There are strong hotspots present (≥16 probes) along with other hotspots that indicate a druggable site. Indeed, low-nanomolar inhibitors were found for this interface. Fig. 5(b) highlights the contrasting results for ZipA at its interface with FtsZ, where although some hotspots are present they are weak and do not indicate a druggable site. In fact, only weak ligands were found for this interface, which supports the prediction.

2.2.3. Identifying allosteric sites using FTMap. Targeting allosteric sites on kinases is an emerging area in drug discovery. Since FTMap searches for sites on the entire protein surface, it can be useful for finding such sites. Here, we demonstrate the application of the approach to the identification of allosteric sites on PDK1 kinase. The kinase example
is also interesting since kinases are multi-domain proteins and *FTMap* was optimized to work on single domains. To address this, in addition to mapping the entire protein (PDB entry 1h1w) we separately map the domains (N and C lobes in this case). These two lobes are then submitted to *FTMap*. PDK1 binds ATP in its main pocket; in addition, an allosteric regulation site has also been identified, the PDK1-interacting fragment (PIF) pocket. The mapping results for the N lobe are located in Fig. 6(a), and the two most populated identified pockets, corresponding to the ATP-binding site and the PIF site, are shown in Fig. 6(b) along with a bound ligand (PDB entry 4xx9). Application of *FTMap* in the analysis to identify cryptic and allosteric sites is discussed in more detail in Beglov *et al.* (2018). Analysis of structures in the kinome are provided in Yueh *et al.* (2019).

2.2.4. Detection of ligand-binding sites using *FTSite*. Nearby hotspots predicted by *FTMap* can be further combined to predict entire binding sites. This is performed by the *FTSite* algorithm available as part of the *FTMap* family of servers. We demonstrate binding-site identification of the ribosome-inactivating protein (RIP) momordin. The protein is known to bind adenosine. We predict the binding site of the protein starting with unliganded momordin (PDB entry 1ahc). The top two pockets predicted by *FTSite* are shown in Fig. 7 along with the ligand overlapped from the bound structure (PDB entry 1mrg). The adenosine pose lies within the first-ranked pocket.

2.3. Docking and mapping using high-accuracy protein models

*AlphaFold2* has made landmark advances in protein structure prediction (Jumper *et al.*, 2021). Here, we present several applications of high-accuracy protein models to predict both protein–protein interactions (PPI) using *ClusPro* and ligand-binding sites using *FTMap*.

2.3.1. Predicting protein–protein interactions with *AlphaFold2* and *ClusPro*. Firstly, we demonstrate the docking of models of individual protein monomers using *ClusPro*. We consider the complex between the β-lactamase inhibitory protein and β-lactamase as an example, and construct the monomer models using *AlphaFold2*. The sequences of the component proteins are those of the unbound structures in the PDB. We then used the *MMseqs2* API to generate multiple sequence alignments (MSA) for each sequence, which were then combined (Mirdita *et al.*, 2019). In order to allow generation of the complex, we introduced a 200-residue gap in the residue-index numbering between each protein. We used the pTM model parameter set to generate models using *AlphaFold2*. *AlphaFold2* provided a predicted aligned error (PAE) for each residue of the model, which we used to calculate an average PAE score for those residues at the interface of the interacting proteins. The interface was defined to be those residues that were within 10 Å of the other protein. The *AlphaFold2* model of the complex with the lowest average interface PAE score was selected and split into...
two separate structures representing the receptor and the ligand. As can be seen from Fig. 8, AlphaFold2 was not able to generate an accurate protein complex in this case. However, when we provided the monomer model to ClusPro for docking, it was able to generate a high-accuracy model of the complex.

2.3.2. Predicting binding sites with AlphaFold2 and FTMap. Similar to the case of protein docking, accurate models of proteins can be used with FTMap to perform the mapping of predicted binding sites on protein surfaces. The binding properties of high-quality protein models produced by AlphaFold2 (generally GDT_TS > 90) have been shown to correlate with the binding properties of experimental structures in the functional analysis of CASP14 targets (Egbert et al., 2021). For example, the protein 2-hydroxyacyl-CoA lyase (HACL) was co-crystallized with ADP bound and was utilized as a CASP14 target. The model predicted by AlphaFold2 is almost an exact match (GDT_TS = 99.07) to the X-ray structure, and the ADP-binding pockets are nearly identical (see Fig. 9). FTMap of both the X-ray structure and the AlphaFold2 prediction identified the ADP-binding site as the strongest site, with 33 and 26 probe clusters, respectively. Visually, the predicted binding sites in HACL appear to be almost identical between the X-ray structure and the AlphaFold2 model.

3. Conclusions

In this work, we show various applications of computational docking using ClusPro and hotspot identification using FTMap. Both servers use protein crystal structures as inputs. We demonstrate that ClusPro can be used to predict high-accuracy models of protein complex structures with and without the use of experimental information. FTMap enables the identification of orthosteric and allosteric binding sites in proteins, determining the druggability (i.e. the ability to develop high-affinity small molecules) of sites of biological interest and also provides information for the design of small-molecule inhibitors and modulators. We demonstrate that the tools can also be used with high-accuracy protein models provided by novel deep-learning algorithms such as AlphaFold2. The methods are available for free to academic users by means of public web servers. All of the input models for the server are available at https://cluspro.bu.edu/examples/inputs.zip.

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