on an underlying coarse-grained model, to study interactions among hepatitis B capsid subunit dimers, treating each entire dimer as a rigid fragment. The tables reduce the computation time of the capsid simulations by 2-3 orders of magnitude, potentially enabling the study pathways for the assembly of capsids using more realistic models than previously possible.

2384-Pos Board B521
G-Losa: An Efficient Computational Tool for Local Structure-Centric Biological Studies
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Molecular recognition such as ligand binding and protein-protein interaction (PPI) is a fundamental way for biological molecules to play their functional roles. These specific interactions are involved in the local regions of the molecules, rather than global structures. Therefore, accurate characterization of local structures in protein is needed to better understand biological mechanisms and to rationally design effective drugs. G-LoSA, a recently developed local structure alignment tool, has the advantages of not only predicting the ligand binding sites with high accuracy, but also identifying a single template ligand that is highly similar to the target ligand. Here, we present an improved version of G-LoSA aiming at extending its applicability to broad local structure-centric biological studies. The method generates all possible alignments between two local structures by iterative maximum clique search and fragment superposition and then determines the final optimal alignment by a G-LoSA alignment scoring function, GA-score. GA-score is a length-independent and physicochemical property-based scoring function to measure structural similarity between two local structures. G-LoSA outperforms its previous version in identifying ligand templates and also shows robust performance in detecting similar ligand binding pockets and PPI interfaces from the benchmark sets. Finally, we introduce its application to in silico fragment-based drug design. As demonstrated by this work, G-LoSA is a promising computational tool that can be universally applied to diverse local structure-centric biological studies.

2385-Pos Board B522
Multi-Scale Deep Neural Network Microscopic Image Segmentation
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With digital technology and fast imaging speed, huge amount of microscopic images are produced in biomedical research every day. A key procedure in processing and analyzing the images involves recognition and segmentation of features, patterns, or regions that are of interest to the researchers. Such work is often manually done by humans, which is very time-consuming and thus impractical when image data are massive. Traditional image segmentation algorithms have difficulty in identifying high-level features (e.g. a particular morphology of a cell type or an organelle). Plus, many microscopic images, especially super-resolution STED images, are highly noisy. The analysis of noisy images poses an even higher challenge to traditional algorithms. Compared with computer algorithms, humans are incredibly good at identifying high-level features. Machine learning, which let computer learn human behaviors, is thus a suitable solution. Deep learning is a set of emerging machine learning methods that is being successfully applied in many applications, such as face recognition and speech recognition. It has also been used to process specific types of microscopic images.
We have designed a multi-scale convolution neural network for segmentizing noisy microscopic images. Images at original resolution and down-sampled images at multiple scales are feed to the network for information extraction. The purpose of adopting this multi-scale architecture is to obtain local fine resolution while maintain larger field of views, which gives network low classification error rate while maintain reasonable processing speed. The network has been tested on segmentation of mitochondria labeled with mitotracker. Network separate image pixels into two categories: ''background'' and ''mitochondria''. Training and testing of the network is done with standard back-propagation algorithm, with human labeled segmentation data. Preliminary result shows the trained network well outperformed multiple traditional image segmentation methods.

2386-Pos Board B523
Using Rules & Pathway Databases to Create Quantitative Mechanistic Models in Virtual Cell
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Recent technological advances have resulted in an accumulation of experimental data and a growing interest in using this data to build quantitative models of biological processes. The traditional approach to build such models involves manual formulation of model hypothesis and data search. This is becoming inadequate due to the degree of complexity in the models and the great variety of data available. In particular, for understanding and modeling the dynamics of protein-protein interactions, the mechanisms of interactions have to be described at the level of protein sites, the parts of proteins that are responsible for protein-protein interactions, such as protein phosphorylation sites and interaction domains. The rule-based approach provides modelers with an opportunity to efficiently use such information. However, despite the high relevance of the site-specific details of protein-protein interactions for understanding system behavior, rule-based models incorporating these details are not very common, because of difficulties in mining and using this information for modeling. To address this need, we developed 2 new capabilities within the Virtual Cell modeling and simulation framework. The first one is BioNetGen@VCell, which enables the user to create rule-based models and combine rules and reactions in a single interface. The other, PathwayCommons@VCell, enables the user to easily extract information from external pathway databases and create computational models of pathways. We describe the technology underlying these tools and present an example model that makes use of them.

2387-Pos Board B524
A Statistical Overview of Experimentally Defined Anisotropic Displacement Parameters (ADP) Currently Deposited in the RCSB PDB
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The potential of X-ray crystallography to provide information for protein dynamics has not yet been extensively investigated. In addition to atom XYZ coordinates, typical PDB files provide the temperature factor, also referred to as isotropic B-factor, which describes the magnitude of atomic fluctuations. Currently, approximately 5% (~5500 unique pdb files) of the structures deposited in the RCSB PDB are high resolution (< 1.4 Å). These high resolution structures generally provide an additional line for each atom entry, with the second containing a symmetric tensor with six integers that describes an ellipsoidal, instead of spherical, distribution of electron densities. Importantly, this asymmetric distribution of electron density reflects the anisotropic movement of the atomic nuclei. A diagonalization of this 3x3 tensor yields three eigenvalues (W1, W2, and W3), which define the distribution of electron density along those three prominent axes. The degree of anisotropy is defined as the ratio of W1 to W3 and varies between 0 (extremely anisotropic, like a rod or a pancake) and 1 (a sphere). Our preliminary analysis over the ADPs derived from ~1500 high resolution structures revealed that interestingly, the backbone carbon atoms are more anisotropic than the C-α and C-β atoms. The C-α atoms show the lowest degree of anisotropy, and proceeding out along the side chain from C-α to C-ε, the degree of anisotropy gradually increases. We also analyzed the trend of isotropic B-factors. Indeed, the value of isotropic B-factors increases outward from the backbone C to the C-ε atom. In summary, we performed a statistical analysis over the ADPs of structures in the RCSB PDB, with the aim to obtain useful information in order to gain a better understanding of the physical basis of ADP.

2388-Pos Board B525
Prediction of Functionally Linked Interface (FLIP) Regions in Residue Interaction Network (RIN) Models of Protein Structures
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Various cellular processes involve participation of proteins as monomers or oligomers. The function of the oligomers is often related to their structural stability and interaction capabilities. Here, we continue our work on the characterization of the physico-chemical patterns of amino acid residues involved in quaternary interactions that form Functionally Linked Interfaces of Proteins (FLIPs). Proteins are represented as a network with residues as nodes and proximity between residues (both bonded and non-bonded interactions) being the edges (a residue interaction network or RIN). Our previous studies of RINs have shown that FLIPS can be distinguished from Functionally uncorrelated Contacts (FunCs) with ~74% accuracy, indicating residues show organizational differences in the interfaces of FLIPS and FunCS. In the current work, we identify threshold values of network centrality features that predictively distinguish FLIP, FunC, and non-interface regions of RINs.