1P250 sociable な蛋白質の相互作用面の解析
○日暮 美穂¹、石田 貴士¹、木下 賢吾²
¹東大・医科研、²SORST, JST
Comparative analysis of the interface of sociable proteins and unsociable proteins
Miho Higurashi (1), Takashi Ishida (1) and Kengo Kinoshita (2). (1: Institute of Medical Science, University of Tokyo; 2: SORST, JST)

Many biological functions are based on the network of protein-protein interactions. There are so-called hub proteins that mediate interactions among numerous other proteins, and are said to be essential for the survival of the cell. Hub proteins were often defined as highly connected nodes in the map of protein-protein interactions based on high-throughput experiments such as yeast two-hybrid. Although proteins that interact with their partners transiently were chief objects of interest, previously defined hub proteins included proteins that interact with their partners permanently such as supramolecular complex. To focus on proteins that interact with their partners transiently, we removed subunit of supramolecular complex from hub proteins. We named the remaining proteins as 'sociable' proteins. We took interactions from complex structure in PDB rather than interactions from high-throughput experiments to identify the structural characteristics of their interface. We separated proteins into sociable proteins and unsociable proteins, based on number of binding state; proteins with only one binding state being classified as unsociable. We obtained 94 sociable proteins and 1013 unsociable proteins. We found that the surfaces of sociable proteins have more predicted disorder ed residues, however we didn't find a significant difference in percentage of predicted disordered residue between interfaces of sociable and unsociable proteins.

1P252 構造変化の大きなタンパク質におけるアミノ酸残基間の相互作用プロファイルを利用した複合体形成シミュレーション解析
1aD09 ○内古閑 伸之^{1,2}、広川 貴次²
¹(社)バイオ産業情報化コンソーシアム、²産総研・生命情報工学研究センター
Docking analysis of a large conformational changing protein by using an interaction profile of amino acid residues pairs
Nobuyuki Uchikoga (1, 2) and Takatsugu Hirokawa (2). (1: Japan Biological Information Consortium; 2: Computational Biology Research Center)

Proteins, with large structural changes, can work with various partner proteins, which might work as the hubs in terms of the networks between proteins in a cell. Structures of such proteins can change according to the partner molecules. Calmodulin (CaM), for example, can form a molecular complex with structural changes from extend to globular. In another case, an extended CaM forms a molecular complex, for example, with K⁺ or Ca²⁺. Therefore, computational analysis of such proteins involved in protein-protein interactions has been important.

We investigated protein-protein interactions between calmodulin (CaM) and a fragment of cyclic-nucleotide-gated olfactory channel (CNG) whose structural data are deposited in database as the NMR structural data. Single CaM and CaM-CNG binding states were used for a docking simulation. Then, after CNG were randomly arranged onto the surface of calmodulin with calculating scores, we could obtain top 2000 complex structures for each CaM structures.

This method could obtain various patterns of interactions between amino acid residues of CaM and CNG, resulted from various structures of CaM. Then, we classified the patterns of interaction into ten groups, which of each would be composed of the similar patterns. Each group would indicate a sample interaction for considering the process of the CaM-CNG complex. We would discuss about our methods for investigating a docking process.

1P251 タンパク質ファミリー内に見られる会合状態の変化
○西 羽美¹、太田 元規²
¹東工大・院生命理工、²東工大・学国情セ
1aD08 Alteration of oligomeric states within protein families.
Hafumi Nishi(1), Motonori Ota(2). (1: Graduate School of Biosci. & Biotech., Tokyo Inst. of Tech., 2: GSIC, Tokyo Inst. of Tech.)

Interactions among proteins play a key role in many biological processes. Most of proteins interact with others via the protein-protein interfaces, which are specific with respect to the rest of the surfaces. Here we focused on the variation of the oligomeric states in homologous proteins to reveal how proteins acquired its interfaces. We constructed a structural dataset that consists of 52 SCOP families each of which contains higher and lower oligomers (e.g., dimers and monomers). In the alignments, we regard the surface which was aligned with the interface of the higher order oligomer as "the shadow-interface". It is supposed that the differences between the interfaces and shadow-interfaces are major factors for the variations of oligomeric states. To investigate these differences, we first categorized them into three classes according to the gaps in the alignments. I. Almost no gaps in the alignments. Only residue substitutions occurred. II. Short insertions (less than 10 gaps). III. Long insertions (10 or more). For the type I regions, amino acid compositions were compared. The residues at the shadow interfaces are similar to those at the interfaces and at the surface. Their correlation coefficients are 0.79 (shadow interfaces and interfaces) and 0.80 (shadow interfaces and surfaces). However the residues at the interfaces and at the surfaces are different (0.55 correlation). The shadow-interfaces show the intermediate properties between the interfaces and the surfaces. The detail of the analyses will be reported at the conference.

1P253 混合正規分布モデルを用いた複合体低解像度3次元画像への短量体原子モデルの重ね合わせ計算 - 対称的な配置拘束の導入 -
○川端 猛^{1,2}、由良 敬^{2,3}
¹奈良先端大・情報、²CREST、³原子力機構・量子生命
Multiple protein docking guided by low-resolution image of complex using Gaussian mixture model under the symmetric constraint
Takeshi Kawabata(1,3) and Kei Yura(2,3). (1: Grad.Scl.Info.Sci., NAIST, 2: CREST, 3: Quantum Bioinf., Japan Atomic Energy Agency)

Electron microscopy of single-particles has recently provided low-resolution 3D images of large bio-molecular complex composed of many proteins. Superimposing several monomer structure models solved by X-ray crystallography into the 3D image provide a high-resolution model of large complex. The docking of multiple proteins, however, generally requires high computational costs. For reducing the cost, we employed the Gaussian mixture model to represent approximated shapes of the 3D image and the atomic models. A 3D image with ten thousands grids and an atomic model with thousands of atom spheres can be approximated by the sum of only 2-50 number of 3D Gaussian density functions. We introduced an attraction potential energy between an atomic model and a 3D image, and a repulsion potential energy between atomic models. To find the optimal configuration of protein chains, we implemented the steepest descent method using the analytically calculated force and torque of the potential energy. Test calculations for a simple dimer showed that our method efficiently found the reasonably good configurations within a short computational time. To apply our method to larger complexes, we introduced symmetric constraint energy of a given symmetric group, such as C4 and D2, because large protein complexes often contain identical subunits (homo-oligomers), and identical subunits tend to form symmetric configurations. We confirmed that our symmetric constraint energy is helpful to find the precise homo oligomer configurations.