S07H6 物体イメージの脳内表現と視覚認識
○谷藤 学¹
¹理化学研究所
Representation of object images in visual association cortex and object recognition
Manabu Tanifuji

Area TE is located at the end of the ventral visual pathway and plays an essential role in visual object recognition. Neurons in this area respond to visual features that are less complex than object images. Thus, an object image is supposed to be represented by a combination of neurons each representing a visual feature. Tsunoda, Yamane, and myself have investigated how objects are represented by combinations of neurons using intrinsic signal imaging. Intrinsic signal imaging is the technique to detect hemodynamic response of neurons through absorption changes of cortex and enables us to visualize spatial patterns of activation at the columnar level. These studies showed that object images are indeed represented by combination of visual features, and that these features include local features and features related to spatial relationship among local features such as, on top of. Though these studies revealed representation of object images in area TE, anesthetized animals were used in these studies and thus it is difficult to relate the representation of objects to recognition of objects. Recently, Miyakawa and myself have developed a densely arranged multiple electrode array to visualize not only spatial but also temporal dynamics of activation patterns. This technique allows us to investigate modulation of activation patterns during the time when a monkey reaches recognition. In this talk, I will summarize object representation of object images in area TE and present recent results we obtained with the electrode array.

S08I2 Functional Annotation Sequence-weighted Structure Alignments
CStandley Daron M.^{1,2}, 藤 博幸³, 中村 春木^{1,2}
¹阪大・蛋白研, ²JST-BIRD, ³九大・生体防御医学研
Functional Annotation Sequence-weighted Structure Alignments
Daron M. Standley(1), Hiroyuki Toh (2) and Haruki Nakamura(2)(1:Protein Res
Inst. Osaka Univ and JST-BIRD, 2: Med Inst Bioreg, Kyushu Univ)

A method to functionally annotate structural genomics targets, based on a novel structural alignment scoring function, is proposed. In the proposed score, position specific scoring matrices are used to weight structurally aligned residue pairs, highlighting evolutionarily conserved motifs. The functional form of the score is first optimized for discriminating domains belonging to the same Pfam family from domains belonging different families but the same CATH or SCOP superfamily. In the optimization stage, we consider four standard weighting functions as well as our own, the maximum substitution probability, and combinations of these functions. The optimized score achieves an area of .87 under the receiver-operating characteristic curve with respect to identifying Pfam families within a sequence-unique benchmark set of 2,483,106 domain pairs. Confidence measures are then derived from the benchmark distribution of true-positive scores. The alignment method is next applied to the task of functionally annotating 230 query proteins released to the public as part of the Protein 3000 structural genomics project. Of these queries, 76 were found to align to templates with known function at a high confidence level (over 80%), 66 of which were further confirmed by the coincidence of the Pfam position specific scoring matrices for query and template. Another 51 queries were found to match more distantly related templates. Several such cases are discussed in detail.

S08I1 多様な参加者で構成されるターゲットタンパク研究プログラムにおける情報の流通・共有・拡散
○菅原 秀明¹
¹遺伝研・生命情報 DBJ・データベース運用開発
Information gathering, sharing and diffusion in the Targeted Proteins Research Program composed of diverse research groups
Hideaki Sugawara (Center for Information Biology and DNA Data Bank of Japan, National Institute of Genetics)

We have started creating a platform for the information gathering, sharing and diffusion in the Targeted Proteins Research Program (TPRP) last July, which is the second phase of the structural genomics project of Japan. The purpose of the information platform is to monitor the progress of research and development of 42 groups of the TPRP, to share accomplishments and related research information among the participants of the project, and to make relevant information publicly available.

To this end, we form three groups: the information management system group, the unified protein database group, and the liaison office. The database group is located at NIG, and aims to gather not only fruits of research in the project, but also related information, classify, systematize, and integrate them into a unified database, and, in coordination with DDBJ, PDBj and other institutions, contribute to the public. The unified database has four modules from the viewpoints of the protein sequence, the protein structure, the protein network, and the chemical library.

Our group has started the development from the protein sequence database. We have compiled and updated non-redundant amino acid sequences from relevant major databases in the world. We then annotate them with their physical properties, structures, functions, interactions, diseases, and add annotation. We will present details of the protein sequence database and other modules at the meeting.

S08I3 多ドメインタンパク質における構造ドメインの予測
○黒田 裕¹
¹農工大・工・生命工
Domain Prediction in high throughput analysis of large multi-domain proteins
Yutaka Kuroda (Dept of Biotech and Life Sci, Tokyo Univ of A & T (TUAT))

Computer aided/assisted approaches, where domains boundaries are predicted from sequence analysis, and the predictions are then experimentally assessed, are actively investigated as they may provide low-cost protocols for high throughput protein dissection. Here we report a neural network and a support vector machine for predicting domain linkers, which are loop sequences separating two structurally independent domains. Both methods significantly increased the probability of identifying a stable domain compared to both a random guess and a secondary structure prediction based guess. In addition, we used our method for identifying novel structural domains in large sequence databases. In the meeting, we will report the details of our prediction methods, as well as the experimental assessments of novel domains predicted using our methods.