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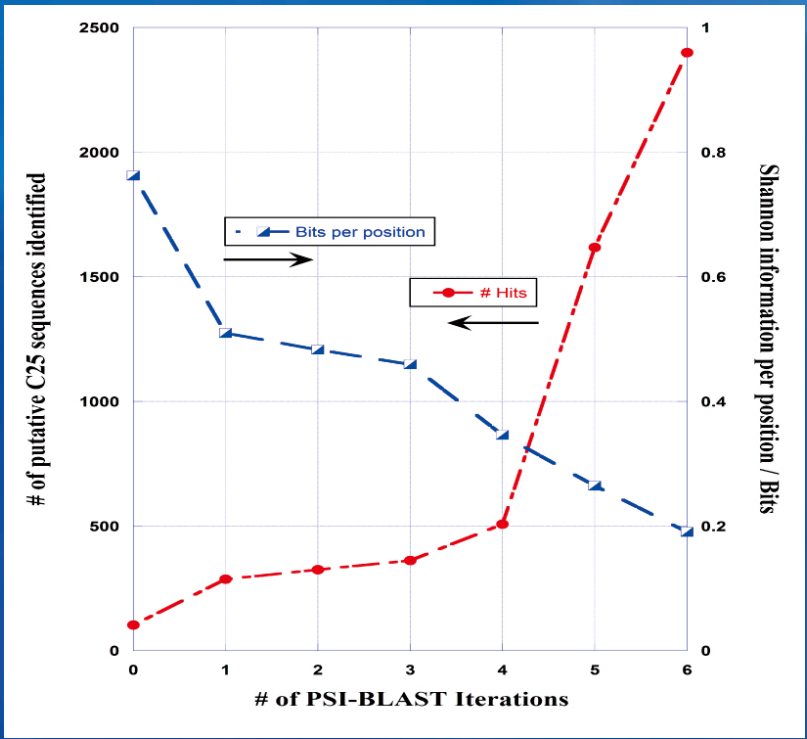

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Invited Speeches:

Title: Computational Analysis of Functional Divergence of Chemokine Receptors

Speaker: Prof. Hiroyuki Toh, National Institute of Advanced Industrial Science and Technology, Japan

Abstract

Chemokine receptors and their relatives constitute a diverse group in class A GPCR (G-Protein Coupled Receptor) family. The group is roughly classified into three subgroups from the functional viewpoint. One of them consists of chemokine receptors, which can bind to chmokines to yield signals. Decoy receptors constitute the second subgroup. Decoy receptors have the binding activity to chemokines, although they lack the signaling activity. The third subgroup is constituted by the receptors whose genes have been incorporated into the genomes of double-stranded DNA viruses such as herpes simplex virus and pox viruses. The viral receptors show constitutive signaling activity without ligand binding. Thus, the three subgroups are different in ligand binding activity and signaling activity. Such functional difference would cause the difference in functional constraint at the amino acid sites involved in the functions, and the difference in functional constraint would lead to the difference in amino acid composition at the corresponding alignment sites. Inversely, we tried to examine the difference in amino acid composition at each alignment site to detect the sites associated with the functional difference of the GPCRs. The site-specific amino acid composition was calculated with the method adopted in PSI-BLAST from a multiple alignment. The difference of the amino acid composition was calculated as the modified Kullback-Leibler information (KLI). The amino acid residues corresponding to the alignment sites with top 5% KLI were mapped on the coordinates of CXCR4, which are only available structural data of the chemokine receptors. Then, we found that such sites were relatively abundant in cytosolic side when chemokine receptors were compared with decoy receptors, whereas such distribution pattern was not observed in comparison with the viral receptors. That is, the amino acid residues corresponding to the sites with the large KLI were found in the extracellular side as well as cytosolic side. Based on the observation, the path of information from the ligand binding sites to the G-protein binding sites in chemokine receptors will be discussed.

Title: A Combinatorial Perspective of the Protein Inference Problem

Speaker: Prof. Weichuan Yu, Hong Kong University of Science and Technology, China

Abstract

In a shotgun proteomics experiment, proteins are the most biologically meaningful output. The success of proteomics studies depends on the ability to accurately and efficiently identify proteins. Many methods have been proposed to facilitate the identification of proteins from the results of peptide identification. However, the relationship between protein identification and peptide identification has not been thoroughly explained before.

In this talk, we provide a combinatorial perspective of the protein inference problem.
We employ combinatorial mathematics to calculate the conditional protein probabilities under three assumptions, which lead to a lower bound, an upper bound and an empirical estimation of protein probabilities, respectively. The combinatorial perspective enables us to obtain a closed-form formulation for protein inference.

Our method achieves competitive results with Protein Prophet in a more efficient manner in the experiment based on two datasets of standard protein mixtures and two datasets of real samples.

Title: Improving Statistical Powers in Large Scale Genetic Association Studies

Speaker: Prof. Taesung Park , Department of Statistics, Seoul National University, Korea (South)

Abstract

A large scale genetic association studies such as genome-wide association studies (GWAS) have successfully led to many discoveries of genetic variants affecting common complex traits. Although these genetic studies have made much progress in finding single nucleotide polymorphisms (SNPs) associated with many complex traits, such SNPs have been shown to explain only a very small proportion of the underlying genetic variance of complex traits. This is partly due to that fact that most current genetic studies have relied on single-marker approaches that identify single genetic factors individually and have limitations in considering the joint effects of multiple genetic factors on complex traits. In order to improve power in genetic studies, we first consider the joint identification of multiple genetic factors and then consider multivariate analysis considering multiple correlated phenotypes. Joint identification of multiple genetic factors would be more powerful and provide a better prediction of complex traits, since it utilizes combined information across variants. In this study, we applied this joint identification approach and multivariate approach to a large-scale GWA dataset (i.e., 8842 samples and 327,872 SNPs) for the Korean population.

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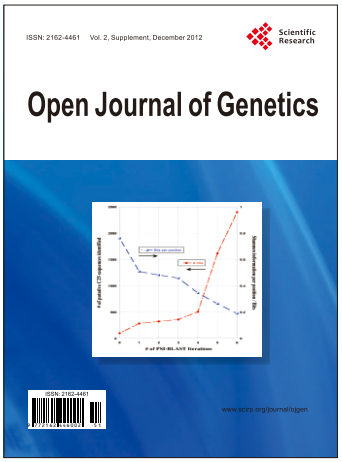

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