Abstract of Presentation

Note: This paper should be typed in "Times New Roman" of 12pt.

Presentation Title(Should be no more than 20 words):

Human Genome Network

Abstract :

In Japan, the "genome network" project has been completed this March after spending 5 years. The main purpose of this project was to construct the infrastructure of research on the genome-wide overview of transcriptional regulation and to conduct its relevant researches. In practice, our collaborators, such as RIKEN and Keio University, have produced a tremendous amount of transcript-oriented data such as hundred millions of CAGE data (cDNA sequence segments of about 20 nucleotides from the transcription start sites (TSSs)), gene expression profile data based on the gene chips, protein-to-protein interaction (PPI) data, CHIP-SEQ data for DNA-protein interactions. All the data produced in this project has been sent to us at the National Institute of Genetics to construct the information platform of the genome network project. Thus, we constructed the information platform for this project, integrating these original data into the publicly available data. Utilizing all the currently available data, we conducted the data analysis of CAGE. As a result, we obtained a distribution of all the possible TSSs over the human genome, which gave us an aspect of the genome-wide transcriptional landscape. Moreover, the combinatorial analysis of PPIs and gene expression profiles led us to new discoveries of transcriptional regulation control particularly in the process involving transcription factors. In this talk, I am going to present some of examples of those results. I would, then, conclude that it is essential to combine different kinds of data into the integrated information platform in order to elucidate the genome-wide overview of transcriptional regulation system.