Gene annotation by the "interactome" analysis in KEGG

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Abstract

Post-genomics may be defined in different ways depending on how one views the challenges after the genome. A popular view is to follow the concept of the central dogma in molecular biology, namely from genome to transcriptome to proteome. Projects are going on to analyze gene expression profiles both at the mRNA and protein levels and to catalog protein 3D structure families, which will no doubt help the understanding of information in the genome. However complete, such catalogs of genes, RNAs, and proteins only tell us about the building blocks of life. They do not tell us much about the wiring (interaction) of building blocks, which is essential for uncovering systemic functional behaviors of the cell or the organism. Thus, an alternative view of post-genomics is to go up from the molecular level to the cellular level, and to understand, what I call, the "interactome" or a complete picture of molecular interactions in the cell.

KEGG (http://www.genome.ad.jp/kegg/) is our attempt to computerize current knowledge on various cellular processes as a collection of "generalized" protein-protein interaction networks, to develop new graph-based algorithms for predicting such networks from the genome information, and to actually reconstruct the interactomes for all the completely sequenced genomes and some partial genomes. During the reconstruction process, it becomes readily apparent that certain pathways and molecular complexes are present or absent in each organism, indicating modular structures of the interactome. In addition, the reconstruction uncovers missing components in an otherwise complete pathway or complex, which may result from misannotation of the genome or misrepresentation of the KEGG pathway. When combined with additional experimental data on protein-protein interactions, such as by yeast two-hybrid systems, the reconstruction possibly uncovers unknown partners for a particular pathway or complex. Thus, the reconstruction is tightly coupled with the annotation of individual genes, which is maintained in the GENES database in KEGG. We are also trying to expand our literature survey to include in the GENES database most up-to-date information about gene functions.

Curriculum Vitae

Name: Minoru Kanehisa

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Date of Birth: January 23, 1948

Professional Experience:

1987-	Professor, Institute for Chemical Research, Kyoto University
1999-	Professor (Concurrent), National Institute of Basic Biology
1991-1995	Professor (Concurrent), Human Genome Center, University of Tokyo
1985-1987	Associate Professor, Institute for Chemical Research, Kyoto University
1982-1985	Visiting Scientist, National Cancer Institute, U.S. National Institutes of Health
1981-1984	Staff Scientist, Los Alamos National Laboratory
1979-1981	Postdoctoral Fellow, Los Alamos National Laboratory
1976-1979	Postdoctoral Fellow, Johns Hopkins University School of Medicine
1975-1976	JSPS Research Fellow, Department of Physics, University of Tokyo
1970-1975	Graduate Student, Department of Physics, University of Tokyo
1970	Graduated from Department of Physics, University of Tokyo

Genome/Bioinformatics Projects:

2000-	Principal Investigator, Research for the Future Program "Biological Systems Database" (Japan Society for the Promotion of Science)
1998-	Principal Investigator, Genome Frontier Project "Gene Network"

(Science and Technology Agency)

1996- Principal Investigator, Genome Informatics Project 1996-2000 under the Japanese Human Genome Program (Ministry of Education)

1991-1995 Principal Investigator, Genome Informatics Project 1991-1995 under the Japanese Human Genome Program (Ministry of Education)

Degree:

1976 Doctor of Science, University of Tokyo

Research fields:

Theoretical molecular biology; especially, computational analysis of genes, molecules, and their interactions; prediction and reconstruction of biochemical pathways from genomic information; knowledge base for molecular and cellular biology.