## **Tsinghua Information Forum**



Title:	Molecular Networks and the Internet:
	Are They Similar?
Speaker:	Prof. Fengzhu Sun
	University of Southern California
Time:	Mar.8, 19: 00-20: 30
Venue:	Lecture Hall, FIT Building, Tsinghua

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## Abstract:

Networks are ubiquitous ranging from the internet to biology. What are the relationships among the myriad of networks from the vastly different fields? Are analytical approaches developed for the study of the internet or social networks applicable to biological networks? We show through several examples that there are close relationships between the internet and molecular networks: 1) protein function prediction versus image analysis, 2) disease gene prioritization versus Google search, and 3) disease pathway inference versus information flow over networks. Future research directions involving molecular networks in the understanding of complex diseases, drug development and community genomics will also be discussed.

## Biography:

Fengzhu Sun is a Professor of Molecular and Computational Biology. His Bachelors in Mathematics is from Shandong University, Masters in Probability and Statistics is from Peking University, and PhD in Applied Mathematics is from University of Southern California. He came back to USC in 2000 as an associate professor after being an assistant professor of genetics and biostatistics at Emory University from 1995 to 2000. He has been a professor since 2006.

Professor Sun works in the area of Computational Biology and Bioinformatics, Statistical Genetics, and Mathematical Modeling. His recent research interests include protein interaction networks, gene expression, single nucleotide polymorphisms (SNP), linkage disequilibrium (LD) and their applications in predicting protein functions, gene regulation networks, and disease gene identification. He is also interested in metagenomics, in particular, marine genomics.

His previous research accomplishments include: 1) protein domain interaction and protein function prediction integrating multiple data sources, 2) dynamic programming algorithms for haplotype block partition and tag SNP selection, 3) 1-TDT: transmission disequilibrium test when one parent is available, and 3) theoretical studies of polymerase chain reaction (PCR) related biotechnologies.

Organizer: SIST

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