Modeling Networks to Accelerate Biomedical Discoveries in Translational Medicine

Jake Y Chen
The University of Alabama, USA

Here we describe the challenges of using high-throughput sequencing data directly to solve translational medicine problems for complex polygenic diseases such as cancer and autoimmune diseases. It introduces the basic concept of building biomolecular networks, from protein-protein interaction building blocks to gene set and gene signature modules, also describing the common computational approaches to analyzing network components, from gene ranking to edge ranking. And how the advanced informatics development could help put together these network building blocks and unravel the complexity of disease biomarker discovery or drug discovery. Opportunities for future research and development efforts to accelerate translational medicine discoveries will also be described in the network medicine context.

Biography:

Dr. Jake Y Chen is a Professor of Genetics, Computer Science, Biomedical Engineering at the University of Alabama at Birmingham (UAB). He is also the Chief Bioinformatics Officer of UAB's Informatics Institute and Head of the Informatics Section of the Genetics Department. He holds a BS degree in Biochemistry and Molecular Biology and MS and PhD degrees in Computer Science and Engineering. He has more than 20 years of research experience in biological data mining, systems biology and translational bioinformatics, with more than 150 peer-reviewed publications. Prior to join UAB, he holds tenured faculty positions at Indiana University and Purdue University.

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Page 8