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Translating multidimensional cancer omics data into biological insights

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Advancements in high-throughput omics technologies have provided an unprecedented opportunity for cancer studies. At the same time, advanced technologies have led to an increasing gap between data generation and investigators' ability to interpret the vast amount of interconnected data. In this talk, I will briefly review different bioinformatics approaches for omics data integration and demonstrate their applications using genomic and proteomic data generated from the TCGA (The Cancer Genome Atlas) and CPTAC (Clinical Proteome Tumor Analysis Consortium) projects. I will also introduce NetGestalt, a novel data integration framework that allows simultaneous presentation of large-scale experimental and annotation data from various sources in the context of a biological network to facilitate data visualization, analysis, interpretation, and hypothesis generation.

Biography

Bing Zhang is an Assistant Professor of Biomedical Informatics at the Vanderbilt University School of Medicine. He received his PhD degree in Molecular Genetics from the Chinese Academy of Sciences followed by a postdoctoral training in bioinformatics at the Oak Ridge National Laboratory. He has 10 years experience in the areas of bioinformatics and systems biology, with more than 40 publications in these areas. He currently serves as principal investigator, bioinformatics core director or co-investigator on several NIH grants. His research focuses on the development and application of integrative bioinformatics approaches to the study of complex diseases.

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