VirginiaTech
VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY

Computer Science Seminar Series, 2014

National Capital Region

Identification of Association Patterns in Public Literature using Network-based Computational Approaches: Case Studies in Vaccine Research

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Friday, April 17, 2015
1:00PM-2:00PM, NVC 325

Abstract

Huge amount of associations among biomedical entities (e.g., disease, drug, and gene) are scattered in public domains, such as biomedical literature, electronic health records, and public health surveillance systems. Systematic analysis of such heterogeneous data provides biomedical scientists with unprecedented opportunities to infer novel associations among different biological entities in the context of personalized medicine and translational research studies. However, it is computationally challenging to perform queries directly from these databases (e.g., Semantic MEDLINE) where associations among different biomedical entities are very complex yet sparse. It is also a challenging task to investigate these associations at large scale. In recent years, network-based computational approaches have been widely used in informatics domain (e.g., bioinformatics, medical informatics and clinical informatics) aiming to better understand the molecular basis of human disease as well as interrelationships among different biomedical entities. In this talk, I will present my recent development of network-based computational applications to fill gaps between knowledge needs of translational researchers and existing knowledge discovery services. Specifically, I will describe my primary contributions made to 1) identification of association patterns in literature-based disease-drug-gene network; 2) knowledge comparison of vaccine-related associations in PubMed abstracts and the Vaccine Ontology; and 3) identification of sex-associated network patterns in Vaccine Adverse Event Reporting System (VAERS).

Biography

Dr. Yuji Zhang is an assistant professor in the Department of Epidemiology and Public Health, University of Maryland School of Medicine, Baltimore, Maryland. She received her Ph.D. degree in Computer Engineering from Virginia Tech in 2010. Dr. Zhang's research focuses on developing translational bioinformatics and systems biology approaches to understand the physiological states of the cell and the organism, including disease states. Specifically, she has developed various network-based computational approaches to integrate multi-omics data sources for gene regulatory network inference, disease biomarker discovery, disease-drug-gene association analysis, and disease-specific network identification. Dr. Zhang was appointed as assistant professor at Mayo Clinic College of Medicine between 2010 and 2014, where she has extended her research interest to develop integrative analytical approaches for different types of next-generation sequencing data, including exome and targeted re-sequencing, and RNA-sequencing of various diseases in the context of precison medicine. Dr. Zhang has participated in numerous federal and government-funded cancer research projects, in which she serves as co-principle principal investigator/co-investigator leading the bioinformatics and statistical analyses. Her mission is to leverage the gap between the analytical needs of arising from multi-source big data in cancer research and advanced computational approaches.