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Network analysis and applications in studying human diseases

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Abstract

Network representation using nodes and edges provides a unified language to describe various molecular systems, such as protein-protein interactions (PPIs). Applications based on network analysis have been proven useful in areas such as predicting protein functions, prioritizing targets for structural genomics, facilitating drug discovery and design, and expediting novel biomarker identification. In this presentation, I will introduce classic and the state-of-the-art network analysis methodologies and approaches. I will then provide two examples of our recent approach where network analysis is being applied to study human diseases. These include identification of targets for development of new drugs to treat Pseudomonas infections, and protein interactome in high-density lipoprotein particles that underlie development of cardiovascular disease.

Biography

Prof. Lu received his Ph.D. from Washington University School of Medicine and postdoctoral training from Yale University. Since 2007, he has been an Assistant Professor in Biomedical Informatics at Cincinnati Children's Hospital Medical Center. Prof. Lu has published more than 30 papers in reputed journals, such as *Science*, and *The American Journal of Human Genetics*. His laboratory is continuously supported by federal funding from NIH, NSF and private foundations, such as Gates Foundation. He served as a reviewer for NSF grant applications and more than a dozen scientific journals.