CSDS 500 and ECSE 500
Fall 2020 Colloquium

11:30AM to 12:30PM
Thursday, November 5, 2020

Zoom Webinar ID: 862 815 806
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"Overcoming Bias in Computational Characterization of Cellular Signaling"

Protein phosphorylation is a key regulator of protein function in signal transduction pathways. Kinases are the enzymes that catalyze the phosphorylation of other proteins in a target-specific manner. The dysregulation of phosphorylation is associated with many diseases, including cancers, neuro-degenerative disorders, and auto-immune diseases. Consequently, characterization of kinase activity in the context of these diseases is essential for the development of effective treatments. Indeed, in the last decade, kinase inhibitors have become central to the treatment of a broad range of cancers. Although technological advances enable the identification of phosphorylated sites for thousands of proteins, most of the phosphoproteome is still in the dark: more than 95% of the reported phosphorylation sites in humans have no known kinases. The incompleteness of kinase annotations and the limitations of data acquisition techniques give rise to two important computational problems in the study of cellular signaling: 1) How can we identify the kinases that target a given phosphorylation site? 2) How can we identify the kinases with altered activity based on the changes in the phosphorylation levels of their targets? In this talk, we demonstrate that the computational tools that are developed to address these fundamental problems have a common flaw that poses limitations on the expansion of knowledge: Both benchmarking data and algorithms are biased toward well-studied kinases. We then describe the algorithms we develop to overcome these hurdles by integrating a broad range of functional data Finally, we present comprehensive results that aim to systematically assess the robustness of algorithms with respect to missing data. Our results show that network algorithms can significantly enhance the utility of phospho-proteomic data and the ability of computational tools in generating new knowledge that pertains to cellular signaling.

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Mehmet Koyutürk is the Andrew R. Jennings Professor of Computing Sciences in the Department of Computer and Data Sciences at Case Western Reserve University (CWRU). He received his Ph.D. degree in Computer Science from Purdue University, and his B.S. and M.S. degrees from Bilkent University, respectively in Electrical Engineering and Computer Engineering. His research is on the development of algorithms for large-scale data mining and analysis, with particular emphasis on networks and graph-structured data. His research mainly focuses on biology as the application area, where he develops algorithms for analyzing biological networks and gaining insights into the systems biology of complex diseases. He also serves in the steering committee of CWRU's graduate programs in Systems Biology and Bioinformatics (SYBB) and he is an associate editor for IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB).

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