



DATA SCIENCE SPEAKER SERIES

Title: Searching Post-translational Modifications in Cross-linking Mass Spectrometry Data



with **Dr. Weichuan Yu, Professor**

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Abstract: Cross-linking mass spectrometry (XL-MS) is a high-throughput technique widely used in the studies of protein-protein interactions (PPIs) and protein structures. In the realm of biology, post-translational modifications (PTMs) play a critical role in regulating PPIs and reshaping protein structures. However, the identification of PTMs in XL-MS data poses a great computational challenge and thus remains unexplored. Here we propose a new XL-MS data analysis tool named SeaPIC that enables biologists to investigate PTMs in PPIs and protein structures. Real data experiments show that SeaPIC identifies many PTMs from XL-MS data, which were previously undiscovered. [This is a joint work with C. Zhou, S. Lai, S. Dai, P. Zhao, and N. Li.]

Bio: Weichuan Yu received his Ph.D. degree in Computer Vision and Image Analysis from University Kiel, Germany in 2001 and did his postdoc training at Yale University. He is now Professor in the Department of Electronic and Computer Engineering at the Hong Kong University of Science and Technology. He is interested in computational analysis problems with biological and medical applications. He has published over 100 journal articles and referred conference papers on a variety of topics including bioinformatics, computational biology, biomedical imaging, signal processing, pattern recognition and computer vision.



THURSDAY, July 18, 2024

Time: 1-2 PM

Location: Summerlee Science Complex, Room: SSC 1303



DEPARTMENT OF
MATHEMATICS AND STATISTICS

MASTER OF DATA SCIENCE