

When: Friday 10:20-11:20

Where: ETB 1020

Speaker: Xiaoqian Jiang

Director, Christopher Sarofim Associate Professor
Center for Health Security and Phenotyping
School of Biomedical Informatics (SBMI)
University of Texas Health Science Center at Houston



Title: Discriminative and Distinct Phenotyping by Constrained Tensor Factorization

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Abstract: Adoption of Electronic Health Record (EHR) systems has led to collection of massive healthcare data, which creates opportunities and challenges to study them. Computational phenotyping offers a promising way to convert the sparse and complex data into meaningful concepts that are interpretable to healthcare givers to make use of them. We propose a novel supervised nonnegative tensor factorization methodology that derives discriminative and distinct phenotypes. We represented co-occurrence of diagnoses and prescriptions in EHRs as a third-order tensor, and decomposed it using the CP algorithm. We evaluated discriminative power of our models with an Intensive Care Unit database (MIMIC-III) and demonstrated superior performance than state-of-the-art ICU mortality calculators (e.g., APACHE II, SAPS II). Example of the resulted phenotypes are sepsis with acute kidney injury, cardiac surgery, anemia, respiratory failure, heart failure, cardiac arrest, metastatic cancer (requiring ICU), end-stage dementia (requiring ICU and transitioned to comfort-care), intra-abdominal conditions, and alcohol abuse/withdrawal.

Bio: Dr. Jiang is a Christopher Sarofim associate professor and center director for health security and phenotyping in the School of Biomedical Informatics (SBMI) at The University of Texas Health Science Center at Houston (UTHealth). Before joining UTHealth, he was an associate professor with tenure in the Department of Biomedical Informatics (DBMI) at UCSD. He is an associate editor of BMC Medical Informatics and Decision Making and serves as the editorial board member of Journal of American Medical Informatics Association. He works primarily in health data privacy and predictive models in biomedicine. In the last five years, he received R00, R13, R21, R01, U01, OT3, CPRIT Rising Stars, UT Stars awards as PI as well as best and distinguished paper awards from American Medical Informatics Association (AMIA) Joint Summits on Translational Science (2012, 2013, 2016). He is one of the organizers of the iDASH Genome Privacy Workshops, which was reported by Nature News and GenomeWeb.