Gene expression and gene isoforms in cancer transcriptome are informative for phenotype prediction. Network-based learning models are playing increasing role in cancer transcriptome analysis. These methods integrate large scale patient transcriptome data with structural information in biological networks to improve phenotype prediction accuracy, model robustness and biological interpretation of results. In this talk, I will present two such reliable network-based methods. First, I will introduce a Network-based method for RNA-Seq-based Transcript Quantification (Net-RSTQ), which integrates protein domain-domain interaction information with RNA-Seq short read alignments for isoform abundance estimation under the assumption that the abundances of the neighboring transcripts by domain-domain interactions in transcript interaction network are positively correlated. Second, I will present a Network-based Cox regression model (Net-Cox), which integrates gene network information into the Cox’s proportional hazard model to explore the co-expression or functional relation among high-dimensional gene expression features in a gene network. In the experiments of studying the cancer transcriptome data in The Cancer Genome Atlas (TCGA), it was observed that both models can improve cancer treatment outcome prediction. Throughout the talk, I will also talk about my future research direction.

Dr. Wei Zhang
Research Associate, University of Minnesota Twin Cities

Dr. Wei Zhang is a Research Associate in Computer Science and Engineering at the University of Minnesota Twin Cities. His research interests include computational biology and machine learning. His research has centered around developing network-based algorithms to better understand three specific topics in cancer transcriptome: alternative splicing, alternative polyadenylation and interactions. He received his PhD and MS from University of Minnesota Twin Cities in 2015 and 2011, BS from Hebei University of Technology in 2009, all in computer science.

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