Quantitative Methods Core
Methods Seminars

Tuesday, March 5, 2019
12:00-1:00pm
Albert Sherman Center, AS9.2072

“Statistical Methods for Reproducible Quantitative MS-Based Proteomics”

Presented by:

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Tsung-Heng Tsai is a postdoctoral associate in the lab of Olga Vitek at Northeastern University. He received his PhD in Electrical Engineering from Virginia Tech, and a postdoctoral training in translational research at MD Anderson Cancer Center. His research focuses on statistical mass spectrometry-based proteomics. He is a co-developer of MSstats, an open-source R package for statistical relative quantification of proteins and peptides. He has also developed several statistical and computational methods for large-scale high-throughput investigations in quantitative proteomics, metabolomics, and glycomics.

Statistical methodology is key for reproducible research. This is particularly true in quantitative mass spectrometry-based proteomic experiments, which must overcome many sources of bias and unwanted variation. This talk will illustrate challenges of reproducible research in quantitative mass spectrometry-based proteomics, and will discuss ways in which reproducibility is promoted by appropriate statistical methodology. I will introduce MSstats, an open-source R package for relative protein quantification, and will present new methods to handle the situations with inconsistent features (for technological reasons such as interferences, or for biological reasons such as post-translational modifications). These methods reduce the dependency of biological conclusions on tools used for initial data processing. Finally, I will present a Bayesian approach for reducing the retention time variation during data acquisition that can assist in conducting reproducible large-scale research.

Lunch will be provided, please RSVP to Sandra Manning (Sandra.manning@umsassmed.edu)