

Title: Robust methods for biomarker discovery in studies with many candidate biomarkers but limited sample size

Speaker: David Kepplinger, Ph.D, Assistant Professor of Statistics, Volgenau School of Engineering, George Mason University

Date: Wednesday, June 16th, 12:30pm – 2:00pm ET

Location: Zoom

WSS Section: Public Health/Biostatistics and Methodology

Abstract:

Biomarker discovery studies have seen a proliferation with increasingly affordable high-throughput proteomics and genome sequencing. Given the abundance of such studies, the number of generalizable and clinically relevant discoveries is lacking. In particular, many discovery studies are based on samples of limited size and from potentially heterogeneous populations, while at the same time hundreds or even thousands of genes are sequenced. In addition to the heterogeneity of the population, this increasingly large pool of candidate biomarkers also comes with a greater risk of outliers and other forms of contamination. In this talk I will elucidate some of the detrimental effects of such “data-artefacts”, specifically on biomarker discovery and related feature selection tasks, and how they can lead to spurious discoveries. I will then discuss a novel method for reliably identifying relevant biomarkers in the presence of these artefacts. The new method harnesses as much information in the data as possible, while not requiring prior specification of the form or source of data-artefacts. It is shown to outperform other methods commonly employed for biomarker discovery studies and I will demonstrate the usefulness of the method in a proteomic biomarker discovery study.

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