

CCSU
DEPARTMENT OF MATHEMATICAL SCIENCES

COLLOQUIUM

Friday, November 16
2:00 – 3:00 PM
Maria Sanford, Room 101

CURRENT TRENDS IN MULTIVARIATE BIOMARKER DISCOVERY

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Abstract

Biomarker discovery studies based on current high-throughput genomic and proteomic technologies analyze data sets with thousands of variables, p , and much fewer biological samples, n . To successfully deal with such $p \gg n$ data, bioinformaticians, biomedical researchers, or data miners have to be familiar with intricacies of multivariate analysis, and particularly with approaches capable of efficiently dealing with the *curse of dimensionality*.

In this presentation, we will discuss current trends in multivariate biomarker discovery based on high-dimensional ‘omic’ data. First, we will take a look at common misconceptions in biomarker discovery, and provide guidance on when to use (and when to avoid) which methods and why. Then we will focus on the methods and concepts maximizing the chances for discovering parsimonious multivariate biomarkers that are robust and biologically interpretable.

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