CCSU

DEPARTMENT OF MATHEMATICAL SCIENCES

COLLOQUIUM

Friday, April 1
2:00 – 3:00 PM
Maria Sanford, Room 101

MINING *NEXT GENERATION SEQUENCING* DATA IN SEARCH FOR GENE EXPRESSION PATTERNS COMMON FOR MULTIPLE TUMOR TYPES

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Abstract: Cancer is the second leading cause of mortality in the USA and accounts for over 500,000 deaths per year. Identification of gene expression patterns that are common for multiple tumor types may lead to significant improvement in early cancer diagnosis, which is the most important factor of successful treatment. High-throughput technologies (such as *Next Generation Sequencing*) are able to provide a large number of whole-genome-level data sets. *The Cancer Genome Atlas* (TCGA) is a new NIH's repository of cancer-related genomic and proteomic data. A data mining project utilizing TCGA data and state-of-the-art methods for multivariate biomarker discovery will be discussed.