CCSU

DEPARTMENT OF MATHEMATICAL SCIENCES

COLLOQUIUM

Friday, May 9
3:00 – 4:00 PM
Maria Sanford, Room 101

BIOMARKER DISCOVERY IN MAJOR DEPRESSIVE DISORDER

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Abstract: Depressive Disorder is the leading cause of disability worldwide affecting 5% of adults with a lifetime suicide rate of 20% among untreated individuals. The current method for diagnosing major depressive disorder (MDD) relies heavily on costly mental evaluations with room for errors in diagnosis. The goal of this study is to develop a blood-based test for an alternative cost-effective and more accurate method for diagnosing MDD. This study will seek to determine an optimal multivariate biomarker from DNA methylation data for the accurate classification of major depressive disorder (MDD) patients vs healthy controls. Since MDD is caused by a combination of many genetic and environmental factors, modeling epigenetic data could potentially provide more accuracy compared to modeling only genetic factors. DNA methylation is a gene regulation process in organisms where genes can be turned off or down regulated if promoter regions of a specific gene are methylated. There are many environmental differences like stress, age, diet and exercise that will result in different DNA methylation patterns between patients and thus different gene expression. Recursive feature elimination with random forests and recursive feature elimination with elastic net will be utilized for the feature selection process of biomarker discovery. The result of this study will be two models containing a multivariate biomarker of methylation sites that could be employed on future patients' methylation profiles from whole blood samples to determine if they have MDD or not.

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