Department of Mathematics and Statistics Colloquium

Integrating Functional Genomic Data with Machine Learning Approach for Phenotype Classification

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Abstract: In this work, a 2-step phenotype classification method based on functional genomic data is proposed. In the first step, pathways relevant to specific phenotype conditions are identified. Then a sufficient dimension reduction process selects the most relevant sufficient sets of predictors from each pathway. In the second step, boosting a machine learning approach is used to isolate most significantly differential sets of sufficient pathway based predictors. We demonstrate our method using an RNA-sequencing dataset from a study of pediatric acute myeloid leukemia (AML).

Monday, March 25 at 3:50 in Roop 103

Refreshments at 3:30