

Department of Mathematics, Statistics and Computer Science

COLLOQUIUM ANNOUNCEMENT

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11:00 AM, Wednesday December 12, 2018

Cudahy Hall, Room 401

Abstract

Cancer is one of the deadliest diseases in the world with its complex genetic biology. With increasing technology, various biological datasets from cancer tissues have been generated to better characterize the cancer biology. Using these datasets, subtypes of various cancers have been discovered and cancer subtype prediction tools have been developed. Several of the cancer subtype prediction studies rely only on one type of biological dataset such as gene expression, microRNA expression, and DNA Methylation. However, each of these data types explain a unique aspect of the underlying biology and thus developing integrative computational methods have been an important problem in bioinformatics. In this study, we develop a cancer subtype prediction methodology called SUPREME that will integrate multiple types of biological datasets with the aid of gene coexpression networks to predict subtypes of cancer patients.

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For further information: see <http://www.marquette.edu/mcs/resources-colloquium.shtml>

or contact Dr. Debbie Perouli #414-288-3889,