MARQUETTE UNIVERSITY

HELEN WAY KLINGLER
COLLEGE OF ARTS AND SCIENCES

Department of Mathematics, Statistics and Computer Science

COLLOQUIUM ANNOUNCEMENT

Identification of functional MiRNA-Transcription factor-Target gene modules in cancer

Duc Do
MSCS Department
Marquette University

3:30 PM, Thursday, December 7, 2017

Cudahy Hall, Room 401

Abstract

Transcription factors (TFs) and microRNAs (miRNAs) are two important classes of gene regulators that govern many critical biological processes. Several studies have aimed to identify pairwise interactions between TFs or miRNAs and their target genes in normal and disease conditions such as cancer. However, few studies attempted to apply a systems biology approach to infer groups of TFs and miRNAs targeting groups of genes that are involved in similar biological processes. Identification of such MiRNA-TF-Target-Modules (MTTMs) would provide a better understanding of gene regulation at different layers and may also suggest better approaches for targeted therapy for diseases such as cancer. In this study, we propose a computational pipeline to discover cancer-specific MTTMs by integrating various types of biological data types such as miRNA expression, gene expression, DNA methylation, and copy number alteration. Our method aims to infer MTTMs that consists of target genes sharing similar biological functions and regulators (i.e., miRNAs and TFs) that can directly bind to their target genes and collectively regulate the expression of the target genes. We applied our pipeline on breast, kidney, and lung cancer datasets obtained from the Cancer Genome Atlas Project. Our preliminary results indicate that transcription factors and their target genes in different modules are enriched with cancer-related biological processes. We observed that several TFs and miRNAs that appear in multiple MTTMs are known oncogenes/tumor suppressor genes and have high prognostic power to predict survival outcomes of cancer patients.

1313 W. Wisconsin Avenue, Cudahy Hall, Room 412, Milwaukee, WI 53201-1881

For further information: see http://www.marquette.edu/mscs/resources-colloquium.shtml

or contact Dr. Daniel Rowe #414-288-5228, daniel.rowe@marquette.edu

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