



Stony Brook University

Department of Biomedical Informatics

Special Seminar

Monday, September 9, 2019

1:00 pm to 2:00 pm

Basic Science Tower Level 9 Classroom 145



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Molecular subtyping and drug target discovery at Transcript/Splice Variant (Isoform) Level

Seminar Abstract

With each successive discovery in genetics the dynamic complexity of the gene structure and gene regulation have become increasingly apparent. It's now understood that the majority of human genes produce multiple functional products, or isoforms, primarily through alternative transcription and splicing. Different isoforms within the same gene have been shown to participate in different functional pathways, and the altered expression of specific isoforms have been associated with numerous cancers. Consequently, transcriptome analyses based on gene-centric informatics methods; (a) may result in wasted resources in following up "leads" that cannot be replicated because they are false, (b) may result in missing important findings that should have been discovered, and most importantly (c) misinterpretation of the underlying biology. In this talk, I will describe application of recent machine learning methodologies, some of which are based on "old ideas", to account for the underlying splice- and transcript-variants. These informatics methods are illustrated using our recent published studies on platform-independent Informatics pipeline for molecular sub-typing of glioblastoma and ovarian cancers. I will also discuss our ongoing work on discovery of drug-target genes at isoform/splice-variant level.

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