Yale SCHOOL OF PUBLIC HEALTH
Biostatistics

SEMINAR

Computational analysis of mRNA isoform expression using RNA-Seq data

Yi Xing, Ph.D.
Associate Professor
Department of Microbiology, Immunology and Molecular Genetics

University of California, Los Angeles

ABSTRACT

Alternative splicing is the process by which exons from precursor mRNA transcripts are differentially included during splicing, resulting in different mature mRNA isoforms from a single gene locus. Common genetic variation that affects splicing regulation can lead to differences in alternative splicing between human individuals and consequently impact expression level or protein function. Recently, ultra-deep RNA sequencing (RNA-Seq) has become a powerful technology for genome-wide analysis of alternative splicing. We have developed GLiMMPS, a robust method for detecting genetic variation of alternative splicing from RNA-Seq data. GLiMMPS takes into account the individual variation in sequencing depth and the noise prevalent in RNA-Seq data. Analyses of simulated and real RNA-Seq data demonstrate that GLiMMPS outperforms competing statistical models. Quantitative RT-PCR tests of randomly selected GLiMMPS predictions yielded a validation rate of 100%. As population-scale RNA-Seq studies become increasingly affordable and popular, GLiMMPS provides a useful tool for elucidating the genetic architecture of alternative splicing variation in humans and model organisms.

4:15 p.m. Tuesday, April 16, 2013

LEPH 115, 60 College Street