Statistics Seminar

Friday, April 30   12:00 pm - 1:00 pm

Statistical methods for analyzing alternative splicing from RNA sequencing data

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Abstract: Statistical genomics is an emerging field and has played a crucial role in discovering molecular mechanisms underlying complex biological phenomena. In this talk, I will discuss two statistical methods we have developed to study the post-transcriptional regulation mechanisms from RNA sequencing data. The first method, AIDE, is a statistical method that selectively incorporates prior knowledge into the modeling to improve the statistical inference of missing RNA structures. AIDE is the first method that directly controls false discoveries by implementing the statistical model selection principle. The second method, MSIQ, is a statistical model for robust RNA quantification by integrating multiple biological samples under a Bayesian framework.

Bio: Dr. Vivian (Wei) Li is an Assistant Professor in the Department of Biostatistics and Epidemiology at the Rutgers University, and an associate member of the Rutgers Cancer Institute of New Jersey. She obtained her Ph.D. degree in Statistics from the University of California, Los Angeles. Prior to joining UCLA, Vivian received her B.S. in Statistics from the School of Mathematics and Statistics at Huazhong University of Science and Technology. Vivian's lab is interested in statistical modeling and algorithm development, as well as their applications to high-throughput sequencing data in bioinformatics and clinical research.