

CPH Seminar in Precision Medicine

“Identification of genome-wide non-canonical spliced regions, including IRE1a targeted regions with Read-Split-Fly algorithm”

Yongsheng Bai, PhD

Assistant Professor of Bioinformatics
Department of Biology, Center for Genomic Advocacy (TCGA)
Indiana State University

In recent years next-generation sequencing technologies have revolutionized the field. The “Read-Split-Walk” (RSW) and “Read-Split-Run” (RSR) methods were developed to identify genome-wide non-canonical spliced regions, including *IRE1α* targeted regions using RNA-Seq data. As the significant amounts of genome/transcriptome data have been sequenced, we have advanced a new memory-efficient version of algorithm “Read-Split-Fly” (RSF), which can load the whole genome into the memory and process multiple samples to detect non-canonical spliced regions including *IRE1α* targeted regions in a fast speed. The RSF combines the strengths of considering each unmapped read separately with the memory-efficiency of the new algorithm and higher sensitivity of rescuing false negative reads to achieve a combination of memory-efficiency, better sensitivity and specificity for identifying novel splice junction sites at a genome-wide level when compared to previous RSW and RSR algorithms. The RSF algorithm also outputs the spliced sequences for further downstream biological function analysis.

Friday, October 6, 2017 12p – 1p UCT1414

arlisa.k.ross@uth.tmc.edu

713 500-3912

 #SBMIseminar

