

# IsoRef Improves the Reference-Based Transcriptome Assembly Accuracy for RNA-Seq Data

**SPEAKER** Mr **AO Xiang**

PhD Student  
Department of Computer Science  
City University of Hong Kong  
Hong Kong

**DATE** 17 April 2018 (Tuesday)

**TIME** 3:00 pm - 3:30 pm

**VENUE** B5-416, 5th Floor, Blue Zone  
Yeung Kin Man Academic Building  
City University of Hong Kong  
83 Tat Chee Avenue  
Kowloon Tong

## ABSTRACT

Transcript reconstruction from mammal RNA-Seq data remains a challenging problem due to several biases, such as those from sequencing or mapping, the complexity of mammalian transcriptome generation from alternative splicing, fragmentary characteristics of reads, and from the unbalanced sequencing. Here, IsoRef, a reference-based transcriptome assembler for RNA-Seq data, is proposed. IsoRef investigates information from not only sequencing data, but from transcript annotation as well, in order to build accurate splice graphs. A flow balancing technique is proposed to reduce the impact of false positive transcripts and to narrow the search space of true positive transcripts. For each of two in silico datasets, IsoRef predicted 1,400 additional correct transcripts than StringTie; for each of the five actual datasets, IsoRef identified at least 1,500 additional correct transcripts than StringTie, which improves the transcript-level and gene-level accuracy compared to StringTie with a maximum improvement of 20%.

**All are welcome!**



In case of questions, please contact Dr LI Shuaicheng at Tel: 3442 9412, E-mail: [shuaicli@cityu.edu.hk](mailto:shuaicli@cityu.edu.hk), or visit the CS Departmental Seminar Web at <http://www.cs.cityu.edu.hk/news/seminars/seminars.html>.

