Abstract:

Although high-throughput RNA sequencing (RNA-seq) technology has shown many advantages in gene studies in the past few years, alignment of RNA-seq reads to a reference genome, which is the primary step for subsequent RNA-seq analyses, has not been perfectly solved. The main challenge is exon-exon splicing events in RNA. This requires an aligner to map a spliced read to a non-continuous region, increasing the computational complexity.

In this talk I will present a new software tool for RNA-seq alignment. It first performs gapped alignment to detect potential splicing junctions with the help of GPU-based short read aligner SOAP3. These potential junctions are used to build a junction-flank index. Reads are realigned to the junction-flank index using SOAP3-dp, a more sensitive unspliced aligner with index-assisted dynamic programming in GPU, to improve the overall sensitivity and accuracy. Experimental result shows that our method is much faster than most existing RNA-seq aligners, and achieves high sensitivity and accuracy at the same time.

About the Speaker:

Li Dinghua is a full-time PhD Student at the Department of Computer Science, The University of Hong Kong. His supervisor is Prof. T.W. Lam and his research interest is computational biology.