



Hong Kong Branch Seminar Series

Cold seep biodiversity, functioning, and genomics



Prof. Runsheng Li City University of Hong Kong

Title: Transcriptome complexity in a model organism revealed by full-length RNA sequencing, and potential application of the technique in non-model organisms

Abstract:

Reads derived from the current RNA-seq technologies are usually short and deprived of information on modification, compromising their potential in defining transcriptome complexity. Here, we applied a direct RNA sequencing method with long reads using Oxford Nanopore Technologies to study the transcriptome in *Caenorhabditis elegans*. To utilize these full-length transcripts in defining transcriptome complexity, we devised a method (trackcluster) to classify and quantify the long reads sequencing results. This pipeline used the sequence mapping tracks rather than existing intron/exon structures, which allowed us to identify roughly 57,000 novel isoforms and recover at least 26,000 out of the 33,500 existing isoforms in this model organism. We have applied this pipeline to analyze the long-read based transcriptome in some non-model species. And the genome annotation can be significantly improved in both gene and isoform levels.

18 September (Friday)

14:00 – 15:00 pm (GMT +8)

<https://hkust.zoom.us/j/94224294100>

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