



## Genome informatics for multi-omics and pangenome

## **Professor Kai Ye**

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**Host: LIU Jianjun** 





GIS Seminar Room (Level 2) 60 Biopolis Street, Genome, Singapore 138672

## **About The Speaker**

Prof. Kai Ye is a computational biologist whose work is focused on novel algorithm development for detecting indel and structural variation as well as their applications in evolution and disease. His invention Pindel, an indel/SV caller, was applied in 1000 Genomes Project and The Cancer Genome Atlas while another tool, MSIsensor, identifying microsatellite instability samples from NGS data, was integrated as part of MSI-IMPACT toolset. Recently he reported the genomes of Opium Poppy and related species, revealing the formation of morphine gene cluster as a consequence of a burst of structural variants.

## **About The Seminar**

This presentation covers the latest advancements of genome informatics, with a focus on telomere-to-telomere (T2T) genome assembly and the analysis of complex genomic regions. The first section covers advanced genome assembly, revealing the evolutionary trajectory of the morphine gene cluster in Papaver, the comprehensive T2T genome assembly of Arabidopsis thaliana Col-XJTU, and the refined haplotype-resolved variant benchmarks in the Chinese Quartet for Homo sapiens. The second section delves into genome variant analysis, highlighting advanced methodologies for detecting complex structural variants and analyzing centromere sequence variations. Finally, we will discuss a general seq2image framework that integrates multi-omics data.