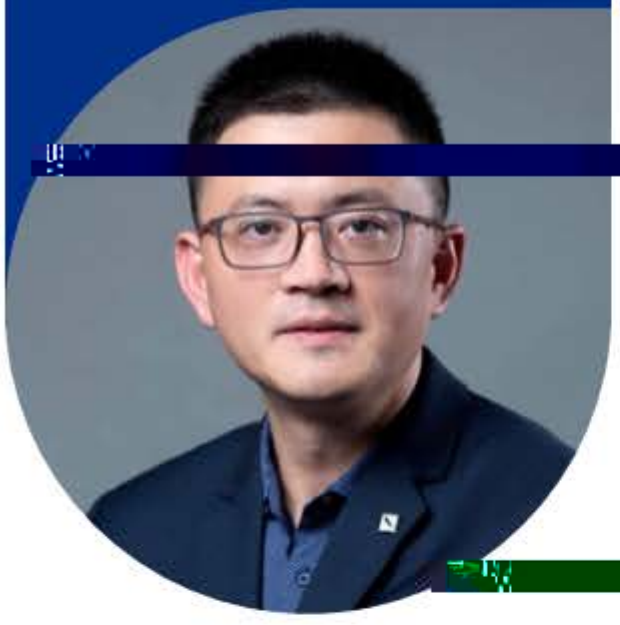
THE GIS

SPEAKER SERIES



From genetic associations to genes and cellular contexts for human complex traits and diseases

Professor Jian Yang

School of Life Sciences, Westlake University

Host: Wan Yue

10:00am - 11:00am | **60 Biopolis Street**

About The Speaker

Jian Yang is a Professor of Statistical Genetics at Westlake University, China. He received his PhD in 2008 from Zhejiang University, then conducted postdoctoral research at the QIMR Berghofer Medical Research Institute in Australia. In 2012 he joined the University of Queensland as a Research Fellow and was promoted to Professor in 2017. He moved to Westlake University in 2018. His research focuses on understanding genomic variations among individuals, populations and the links of these variations to phenotypes and diseases in humans.

He was the 2012 recipient of the Centenary Institute Lawrence Creative Prize, in recognition of his contribution to solving the "missing heritability" paradox. He was awarded the Australian Academy of Science Ruth Stephens Gani Medal for distinguished research in human genetics (2015) and the [illegible] Year (2017). He has published over 240 papers with more than 100,000 citations.

About The Seminar

Genome-wide association studies (GWAS) have identified numerous genetic variants associated with complex human traits including diseases. However, the molecular mechanisms and cellular contexts through which these variants affect phenotypes remain elusive. In this talk, I will present methods and tools leveraging molecular quantitative trait locus (xQTL) data from various omics layers to prioritize potential causal genes and uncover [illegible]. I will demonstrate how integrating data across tissues, cell types and [illegible] traits. I will then demonstrate the use of single-cell RNA-seq data as a reference to deconvolve [illegible] distributions and subsequently investigate cell state [illegible] complex traits. Finally, I will discuss the integration of GWAS and spatial transcriptomics data to profile the spatial distributions of [illegible], thereby enhancing our understanding of how spatial cellular contexts contribute to the manifestation of complex traits. This presentation will underscore the [illegible] multi-omics integration across various contexts in advancing our understanding of complex traits.