

THE GIS SPEAKER SERIES



The Chinese Pangenome Reference 2.0: Challenges and Solutions

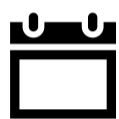
Prof. Dr. Shuhua Xu

Distinguished Professor & Principal Investigator

Human Population Omics Group

School of Life Sciences & Human Phenome Institute, Fudan University

Host: Liu Jianjun



Wednesday 18 December 2024
10.00am – 11.00am



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

About The Speaker

Dr. Shuhua Xu is a professor of human population genetics and a Distinguished Professor of Fudan University. He received his PhD at Fudan University, China. From 2012 to 2018, he held the position of Max-Planck Independent Research Group Leader at PICB. In 2013, he was appointed as Distinguished Adjunct Professor at ShanghaiTech University. Since 2015, he has been appointed a Distinguished Chinese Academy of Sciences Professor. He is the Award holder of The Royal Society Newton Advanced Fellowships (UK), Distinguished Young Scholars of the National Science Fund (China), and Prize of Natural Science Award (China). His scientific research has focused on population genomics research of human admixture history and biological adaptation to the local environment. His research aims to understand microevolution mechanisms in humans, while genetic admixture was taken as a cut-in point to pursue this ambition. The Population Genomics Group led by Dr. Xu is using computational approaches and developing new methods to dissect the genetic architecture of human populations, quantitatively characterize their admixture features, and reveal their migration history and adaptive divergence. Dr. Xu has authored many scientific papers published in *Science*, *Nature*, *Cell*, *PNAS*, etc.. Dr. Xu serves as an Editorial Board member of several international peer-reviewed journals such as *JGG*, *Hereditas*, *Molecular Genetics and Genomics* (co-Editor-in-Chief), and *BMC Genomic Data* (Senior Editor).

About The Seminar

In August, I was honored to deliver a brief presentation in GIS on the Chinese pangenome project titled "Genetic Diversity and a Pangenome Reference of Chinese Populations." For the coming seminar talk, I would focus on the ongoing projects of the Chinese Pangenome Consortium (CPC), in particular, I will share with the audience in GIS our experience in carrying on the Chinese Pangenome Reference 2.0. As expected and also to some degree similar to what is happening in Singapore or other countries, there are various challenges in managing human genetic diversity in China toward the building of high-quality pangenome references and their application to various basic research and clinical practices. Technically, we are making efforts to overcome limitations in the CPC Phase I, such as lack of data depth (10x-20x), limited sample size (n=58), insufficient sampling of diverse geographical groups (n=36), not well-covered culturally endogamous and admixed groups, and also many biomedical issues beyond genomics. Moreover, the idea of "pangenome" is to collect and integrate genomic data of as diverse populations as possible from all around the world to build high-quality graph genome references. On the one hand, China has strict laws, regulations, and review mechanisms in the management of human genetic resources to ensure that the collection, storage, use, and sharing of genetic data meet ethical and legal requirements, effectively protecting personal privacy and preventing data abuse. On the other hand, the Chinese government and the scientific community have a strong willingness to open up data and cooperate with international counterparts. We are also seeking more effective data sharing mechanisms and solutions within the framework of Chinese laws and regulations.