



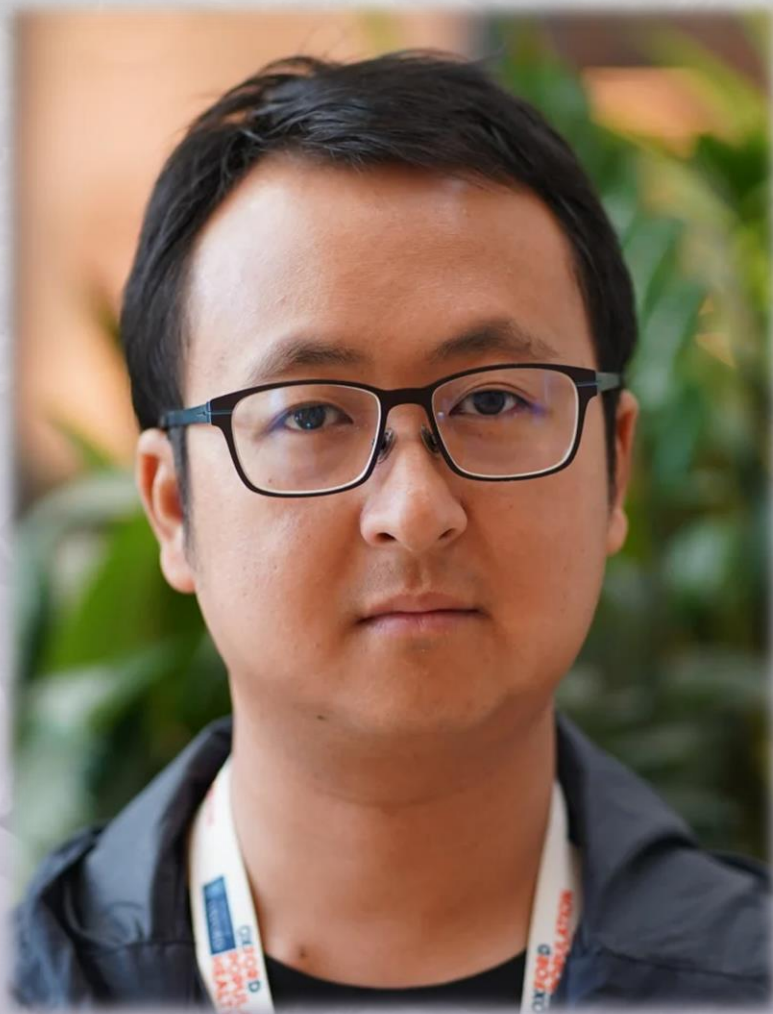
中央研究院生物多樣性研究中心

Biodiversity Research Center, Academia Sinica

biodiv@gate.sinica.edu.tw  
02-2789-9621

Microbial Diversity and Bioinformatics

## Scalable Recombination-Aware Approaches for Genome Analysis of Pathogens



**Dr. Shing Hei Zhan**

**Research Fellow**

**Big Data Institute and Oxford Population Health  
University of Oxford**

**Time: 2026. 02. 03 Tue. 15:00**

**Venue: Auditorium, 1st Floor,**

**Interdisciplinary Research Building**

**跨領域科技研究大樓1樓演講廳**

**Host: Dr. Isheng Jason Tsai 蔡怡陞研究員**





## Abstract

Recombination is a major evolutionary force in pathogens. In the presence of recombination, a single phylogenetic tree cannot adequately represent the evolutionary relationships among a set of sampled genomes. Ancestral recombination graphs (ARGs) offer a rich and comprehensive framework for capturing the genetic ancestry of recombining genomes; however, until recently, inferring ARGs from real genomic data was deemed intractable. Recent computational breakthroughs have enabled efficient storage, simulation, inference, and analysis of genome-wide ARGs for humans, yielding new insights about the evolutionary and population genetic forces that have shaped modern-day genetic variation in human populations. With the ongoing surge of genomic data for pathogens, ARGs hold the potential to propel our understanding of the evolutionary processes underlying the emergence, spread, and adaptation of major pathogens, but little work has been done on ARG methods for pathogens. In this talk, I will introduce sc2ts, a novel method for inferring ARGs from SARS-CoV-2 genomes in real time, and present insights into SARS-CoV-2 evolution and epidemiology learned from analysing a pandemic-scale ARG comprising ~2.48 million SARS-CoV-2 samples.