













## Westlake Symposium for

## Al Virtual Cell

**AIVC Series 3** 

Host: School of Medicine, Westlake University

Location: Westlake University in Hangzhou, China

Date: 7-8 June, 2025

Supported by:











14:50-15:20 Discussion













## **AGENDA** (DAY 1)

	ACEINDA (DAY I)
9:30-9:35	Opening Kai Lei (Westlake University)
	Session 1 Biology
	Jession i biology
9:35-10:05	The genetic landscape of a human cell reveals conserved topology and principles of genetic networks Charles Boone (University of Toronto)
10:05-10:35	Elucidating, tracking, and targeting the evolution of genome instability through the lens of the budding yeast Jia-Xing Yue (Sun Yat-sen University Cancer Center)
10:35-11:05	Metabolic control of DNA replication in budding yeast Huiqiang Lou (Shenzhen University Medical School)
•	Lunch
11:05-11:35	Building Al Virtual Cells (AIVC) with active learning Tiannan Guo (Westlake University)
11:35-12:05	Distinct Genetic Control of Transcriptome and Proteome Variation in Natural Populations Joseph Schacherer (University of Strasbourg)
12:05-12:35	Case studies on roles of lipids and proteins in yeast organelle dynamics Zhiping Xie (Shanghai Jiao Tong University)
12:35-13:05	Single cell imaging and quantitative image analysis for deep phenotyping in budding yeast Brenda Andrews (University of Toronto)
13:05-13:15	De novo Design of Proteases Based on AI: Helping Break Through the Functional Limitations of Natural Enzymes Xuan Liu (YINJIA Bioscience)
13:15-13:30	Refreshment Break
Session 2 Data	
13:30-14:00	The combination of super-resolution imaging with omics: our trial Liangyi Chen (Peking University)
14:00-14:30	Towards Understanding the Principles of Cellular Organization: A Cell-Type-Resolved Proteomic Atlas Xiaowen Wang (National Center for Protein Sciences (Beijing))
14:30-14:50	Unravel the Mechanism of Whole-Body Regeneration Kai Lei (Westlake University)















## **AGENDA** (DAY 2)

9:30-9:50	Opening Session 3 Al
9:50-10:20	From the mechanism-driven model towards the digital cell and digital human
	Feiran Li (Tsinghua Shenzhen International Graduate School)
10:20-10:50	Efficient Biomedical multi-modal multi-omics Data Analysis Hui Lv (Shanghai Jiao Tong University)
10:50-11:20	Knowledge exploitation and exploration with Al models Linhai Xie (National Center for Protein Sciences (Beijing))
	Lunch
11:20-11:50	Whole-Worm Simulation of C. elegans: A Data-Driven Step Towards Simulating Life
	Lei Ma (Future Technology Institute & National Biomedical Imaging Center, Peking University)
11:50-12:20	AIVC enabled by multimodal and dynamical foundation model Han Wen (Beijing AI for Science Institute and RNA center, Peking University)
12:20-12:50	Towards Al Virtual Cell Through Dynamical Generative Modeling of Single-cell Omics Data Peijie Zhou (Center for Machine Learning Research, Peking University)
12:50-13:10	Decoding Biological Complexity: Al Strategies in Vector Space and Scalable Design Siqi Sun (Fudan University)
13:10-13:35	Refreshment Break
Session 4 Data 2	
13:35-14:05	Creating AIVC via next-generation structural biology
	Huaizong Shen (Westlake University)
14:05-14:35	Fluorescent protein-based ticker tapes for multiplexed recordings of transcriptional histories in single cells in culture and in vivo
	Kiryl D. Piatkevich (Westlake University)
14:35-15:00	Discussion
15:00-15:10	Closing & Group Photo