



The 22nd International Symposium on Bioinformatics Research and Applications

July 22-24, 2026 | Macao SAR

Program Book



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Welcome Message

Dear Conference Participants,

On behalf of the General Chairs and Program Chairs, we are delighted to welcome you to the 22nd International Symposium on Bioinformatics Research and Applications (ISBRA 2026), held in Macau, China, July 22-24, 2026. The symposium brings together researchers, scientists, and industry professionals from around the world to share cutting-edge advancements, foster collaboration, and explore the future of bioinformatics and computational biology.

We received 168 submissions presenting original research across all areas of bioinformatics and computational biology. Each submission was reviewed in a single-blind process by at least two independent reviewers, with an average of nearly four reviewers per paper. The Program Committee selected 61 papers for full publication in the symposium proceedings.

The conference addresses a wide spectrum of topics, including:

- Biomarker discovery
- Biomedical databases and data integration
- Biomedical text mining and ontologies
- Biomolecular imaging
- Comparative genomics
- Computational genetic epidemiology
- Computational proteomics
- Data mining and visualization
- Gene expression analysis
- Genome analysis

- Structural biology
- Systems biology

We are privileged to host four distinguished keynote speakers: Dr. FangXiang Wu (University of Saskatchewan), Dr. Yuedong Yang (Sun Yat-sen University), Prof. Le Zhang (Sichuan University), and Prof. Zheng Hu (Shenzhen University of Advanced Technology).

We would like to express our sincere gratitude to all the Program Committee members and reviewers for their contributions. We also extend our special thanks to the steering committee and general chairs for their leadership and guidance throughout the organization of ISBRA 2026. We are grateful to the Macao Association of Convention, Exhibition & Tourism Sectors for their generous support in providing student travel grants to 30 students.

We wish all participants a fruitful and inspiring conference!

ISBRA 2026 Conference Committee

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Chao Song, University of South China
Joe Song, New Mexico State University
Emily Chia-Yu Su, National Yang Ming Chiao Tung University
Lingtao Su, JiLin University
Shiwei Sun, ICT, CAS
Sing-Hoi Sze, Texas A&M University
Jing Tang, University of Helsinki
Weitian Tong, Georgia Southern University
Xiaohua Wan, Beijing Institute of Technology
Shaokai Wang, HKUST
Kaili Wang, Donghua University

Xinyue Wang, Renmin University of China

Han Wang, Northeast Normal University

Hongqiang Wang, HIPS, CAS

Jianxin Wang, Central South University

Jiayin Wang, Xi'an Jiaotong University

Yaojun Wang, China Agricultural University

Yanjie Wei, SIAT, CAS

Ka-Chun Wong, City University of Hong Kong

Fangxiang Wu, University of Saskatchewan

Jingli Wu, Guangxi Normal University

Ju Xiang, Changsha University of Science and Technology

Linxia Xiao, SIAT, CAS

Yuying Xie, Michigan State University

Yungang Xu, Xi'an Jiaotong University

Shankai Yan, Hainan University

Cheng Yan, Hunan University of Chinese Medicine

Lulu Yan, Northwest A&F University

Yang Yang, Shanghai Jiao Tong University

Yaning Yang, Xiangtan University

Yusen Ye, Xidian University

Min Zeng, Central South University

Dongxu Zhang, Xiamen University

Fa Zhang, Beijing Institute of Technology

Fuhao Zhang, Northwest A&F University

Jingjing Zhang, SIAT, CAS

Wen Zhang, Huazhong Agricultural University

Lu Zhang, Hong Kong Baptist University

Le Zhang, Sichuan University

Shihua Zhang, AMSS, CAS

Xiaoqing Zhang, SIAT, CAS

Yiming Zhang, University of Connecticut

Yongqing Zhang, Chengdu University of Information Technology

Yuchen Zhang, Northwest A&F University

Haochen Zhao, Central South University

Qichang Zhao, Central South University

Ruiqing Zheng, Central South University

Xubin Zheng, Great Bay University

Jiancheng Zhong, Central South University

Binhai Zhu, Montana State University

Shanfeng Zhu, Fudan University

Xiaoshu Zhu, University of Electronic Technology

Conference Information

Conference Session

Session 01: Track 1 - Protein Structure & Language Models

Session 02: Track 1 - Single-Cell & Multi-omics

Session 03: Track 1 - Clinical Prediction & Multimodal Fusion

Session 04: Track 1 - CRISPR, RNA & Molecular Computing

Session 05: Track 1 - Drug Discovery & Molecular Interactions

Session 06: Track 1 - Spatial & Biomedical Imaging

Session 07: Track 1 - Neurodegenerative Disorders & Brain Imaging

Session 08: Track 1 - Drug Discovery & Repositioning

Session 09: Track 1 - Genomics, Transcriptomics & Evolutionary Sequences

Session 10: Track 1 - ncRNA & Disease Associations

Session 11: Track 2 - Multi-Omics, Spatial Transcriptomics & Health Medicine

Session 12: Track 2 - Protein Structure, Drug Design & Molecular Computing

Session 13: Track 1 - Biomedical Imaging, Advanced Inference & Applications

Session 14: Track 1 - Molecular Sequence & Biophysics

Session 15: Track 2 - Microbiome & Intelligent Disease Diagnosis

Session 16: Track 2 - Drug Design & Molecular Property Prediction

Presentation Duration

Keynote Lecture: 40 minutes

Oral Presentation: 12 minutes | Q&A: 3 minutes

Presentation Language: English

Friendly Reminders

- In each session, the discussion order will be managed by the session chair.
- We recommend the PDF format to avoid any issues with PowerPoint compatibility.
- Presentation Preparation & Data Security: Speakers must copy their PDF/PPT files to the designated venue computer in advance. Staff will conduct a technical pre-check to ensure compatibility and coordinate with absent speakers regarding PPT submission status.
- Conference photography will take place during the sessions. In case of non-consent, please inform the organizers.
- Assurance: All PPT files will be deleted immediately after the session, with no risk of data leakage.

Punctuality & Seating

Speakers must arrive 15 minutes before the session and take their seats in the front row. If delayed, notify the session chair in advance.

Parallel Sessions Notice

This conference includes parallel sessions. Please double-check your presentation schedule and assigned venue location.

Dress Code

The room is cold due to air conditioning. Please bring a light jacket.

Programme Overview

Day 0, July 22 (Wed), 2026

14:00-19:00	Registration
15:00-19:00	Technical Visit and Cultural Tour

Day 1, July 23 (Thu), 2026

Time	Meeting Room 17	Meeting Room 12+13	Meeting Room 14+15	Meeting Room 6+7
08:00-09:00	Registration & Coffee			
09:00-09:20	Opening Remarks @Meeting Room 17			
09:20-10:00	Keynote I : FangXiang Wu, University of Saskatchewan Session Chair: Yi Pan @Meeting Room 17			
10:00-10:40	Keynote II : Yuedong Yang, Sun Yat-sen University Session Chair: Fa Zhang @Meeting Room 17			
10:40-11:00	Coffee Break & Poster Session @Foyer			
11:00-12:30	<u>Session 1:</u> Track 1 - Protein Structure & Language Models <i>Session Chair:</i> <i>Fangxiang Wu</i>	<u>Session 2:</u> Track 1 - Single-Cell & Multi-omics <i>Session Chair:</i> <i>Wei Peng</i>	<u>Session 3:</u> Track 1 - Clinical Prediction & Multimodal Fusion <i>Session Chair:</i> <i>Yuedong Yang</i>	<u>Session 4:</u> Track 1 - CRISPR, RNA & Molecular Computing <i>Session Chair:</i> <i>Zhendong Liu</i>
12:30-14:00	Lunch @Meeting Room 16			
14:00-15:30	<u>Session 5:</u> Track 1 - Drug Discovery & Molecular Interactions <i>Session Chair:</i> <i>Qiaozhen Meng</i>	<u>Session 6:</u> Track 1 - Spatial & Biomedical Imaging <i>Session Chair:</i> <i>Juan Liu</i>	<u>Session 7:</u> Track 1 - Neurodegenerative Disorders & Brain Imaging <i>Session Chair:</i> <i>Qishi Zhang</i>	<u>Session 8:</u> Track 1 - Drug Discovery & Repositioning <i>Session Chair:</i> <i>Ruiqing Zheng</i>
15:30-16:00	Coffee Break & Poster Session @Foyer			

Time	Meeting Room 17	Meeting Room 12+13	Meeting Room 14+15	Meeting Room 6+7
16:00-17:30	<u>Session 9:</u> Track 1 - Genomics, Transcriptomics & Evolutionary Sequences <i>Session Chair: Fei Wang</i>	<u>Session 10:</u> Track 1 - ncRNA & Disease Associations <i>Session Chair: Yulian Ding</i>	<u>Session 11:</u> Track 2 - Multi-Omics, Spatial Transcriptomics & Health Medicine <i>Session Chair: Ming Xiao</i>	<u>Session 12:</u> Track 2 - Protein Structure, Drug Design & Molecular Computing <i>Session Chair: Fan Hu</i>
18:30-20:30	Conference Banquet @Multi-Function Room, 2F, Lisboaeta Macau Meeting Point: Registration Desk			

Day 2, July 24 (Fri), 2026

Time	Meeting Room 17	Meeting Room 12+13	Meeting Room 14+15	Meeting Room 6+7
08:00-09:00	Registration & Coffee			
09:10-09:50	Keynote III: Le Zhang, Sichuan University Session Chair: Xuefeng Cui @Meeting Room 17			
09:50-10:30	Keynote IV: Zheng Hu, Shenzhen University of Advanced Technology Session Chair: Yanjie Wei @Meeting Room 17			
10:30-11:00	Coffee Break & Poster Session @Foyer			
11:00-12:30	<u>Session 13:</u> Track 1 - Biomedical Imaging, Advanced Inference & Applications <i>Session Chair: Xuan Wang</i>	<u>Session 14:</u> Track 1 - Molecular Sequence & Biophysics <i>Session Chair: Bolin Chen</i>	<u>Session 15:</u> Track 2 - Microbiome & Intelligent Disease Diagnosis <i>Session Chair: Yajun Liu</i>	<u>Session 16:</u> Track 2 - Drug Design & Molecular Property Prediction <i>Session Chair: Shuang Wang</i>
12:30-12:50	Closing @Meeting Room 17			
12:50-14:00	Lunch @Meeting Room 16			

Biographies of Keynote Speakers



Dr. FangXiang Wu

Biography: Dr. FangXiang Wu is currently a full professor in the Departments of Computer Science, Division of Biomedical Engineering, and the Department of Mechanical Engineering at the University of Saskatchewan. He is a Fellow of the Engineering Institute of Canada (EIC) (for his exceptional contributions to artificial intelligence, computational biology, medical image analysis and complex bionetwork analytics), a Fellow of the Institute of Electrical and Electronics Engineers (IEEE) (for contributions to computational intelligence techniques for biomedical data analytics), a Fellow of the Institution of Engineering and Technology (IET), and a Fellow of the Asia-Pacific Artificial Intelligence Association (AAIA). He is a recipient of the University of Saskatchewan Distinguished Researcher Award (the institution's highest research honor).

Dr Wu's research interests include Artificial Intelligence, Machine/Deep Learning, Computational Biology, Health Informatics, Medical Image Analytics, and Complex Network Analytics. He has published over 500 journal/conference papers. His total Google scholar citations are over 20,200 and h-index is 77. Dr Wu is serving as the editorial board member of several international journals (including IEEE TCBB, Neurocomputing, etc.) and as the guest editor of numerous international journals, and as the program committee chair or member of many international conferences.

Title: Artificial Intelligence Empowered Fast PET Imaging: From physics-guided reconstruction to adaptive image-domain denoising

Abstract: Positron emission tomography (PET), as an advanced molecular imaging technique in

nuclear medicine, can provide information on human metabolism and physiological function, and plays an irreplaceable role in the diagnosis of cancer, neurological disorders, and cardiovascular diseases. However, conventional PET scans are often time-consuming, relatively inefficient, and associated with limited patient comfort. Therefore, the development of fast PET imaging is of great clinical significance. Nevertheless, shortened scan time also leads to several challenges, including reduced photon counts, increased Poisson noise, blurred structural boundaries, and unstable SUV quantification. This talk focuses on the key challenges in low-count PET imaging and systematically introduces our group's recent research progress in PET image reconstruction and post-processing algorithms. It will demonstrate how deep learning promotes the transition of fundamental nuclear medicine imaging algorithms from traditional mathematical modeling toward the integration of physical constraints and deep neural networks. The talk will also discuss how artificial intelligence can advance fast PET imaging toward higher image quality, improved efficiency, and greater intelligence while preserving PET physical interpretability and clinical quantitative reliability.



Dr. Yuandong Yang

Biography: Dr. Yuedong Yang is professor of the School of Computer Science at Sun Yat-sen University and the chief engineer of the National Supercomputing Center in Guangzhou.

Currently he focuses on integrating HPC and AI to advance drug design by fusing multi-scale biological information, where he has published more than 200 articles in top journals and conferences (including Nature Machine Intelligence/Nat Comp Sci/Chem/Nat Comm). He was selected as top 2% most influential scientists in the world by Stanford University, and has won the Best Paper Award of Cell Press for Chinese scientists. He also serves as an editorial board member for Communications Biology.

Title: Integrating HPC and AI for Accelerated Drug Design

Abstract: AI drug design is becoming an efficient way to speed up drug discovery. It remains challenging to represent molecules in the algorithm development. In this talk, he will introduce their recent works to represent protein and compound molecules, and to fuse the representations for accurately assessing protein-drug interaction. They further integrate the AI models with large-scale molecular simulations, enabling successful discovery of new PROTAC candidate compounds within 7 weeks.



Prof. Le Zhang

Biography: Le Zhang is currently the vice dean of the School of Computer Science at Sichuan University, a professor. His research mainly focuses on artificial intelligence and computational biology. He has published more than 150 research papers with an H-index of 31 and over 3,000 citations.

He has led multiple research projects, including Major Special Projects of the Ministry of Science and Technology and projects funded by the National Natural Science Foundation of China. His achievements have been recognized with awards such as the Wu Wenjun Artificial Intelligence Science and Technology Award and Sichuan Science and Technology Progress Award.

Title: CryoPromptSeg: Prompt-guided Segmentation with Integrated Denoising for Cryo-EM Particle Picking

Abstract

Motivation: Cryo-electron microscopy (Cryo-EM) single particle analysis (SPA) is a key technique for revealing the structure of biomacromolecules by three-dimensional reconstruction. Achieving high-resolution reconstruction relies on the acquisition of a large number of authentic particles; however, manual particle picking is inefficient and inadequate for the demands of reconstruction, making automated particle picking a major research focus. Although the foundational segmentation model Segment Anything Model (SAM) has recently advanced automated particle picking, its segmentation advantages have not been fully realized in cryo-EM applications. Moreover, cryo-EM images often have significant noise. Conventional denoising decreases noise but frequently

overlooks high-level semantic information, leading to oversmoothed particle regions and reduced particle distinguishability.

Results: To address these challenges, we propose CryoPromptSeg, which employs prompt-guided SAM for particle picking while integrating a semantically enhanced image denoiser. Specifically, by performing domain adaptation fine-tuning of SAM and incorporating prompts generated by the proposed automatic prompt generator, it achieves precise segmentation of cryo-EM particles. In addition, it employs a parallel multi-task framework to jointly train the denoiser and the prompt generator, incorporating particle semantic information from the prompt generator into the denoiser to suppress noise while preserving highly distinguishable particle structures. To lower the barrier to practical application, we developed a user-friendly online prediction platform for particle picking. Experimental results demonstrate that CryoPromptSeg outperforms existing mainstream methods in both particle picking accuracy and image denoising quality, thus providing a novel solution for the automation of particle picking.

Availability: The code and platform are available at: <https://github.com/347251369/CryoPromptSeg>.



Dr. Zheng Hu

Biography: Dr. Zheng Hu is a Principal Investigator at Shenzhen Institute of Advanced Technology (SIAT), Chinese Academy of Sciences (CAS). He is also the Director of Center for Synthetic Biology and Evolution. Dr. Hu received his B.S. in Biomedical Engineering from Huazhong University of Science and Technology in

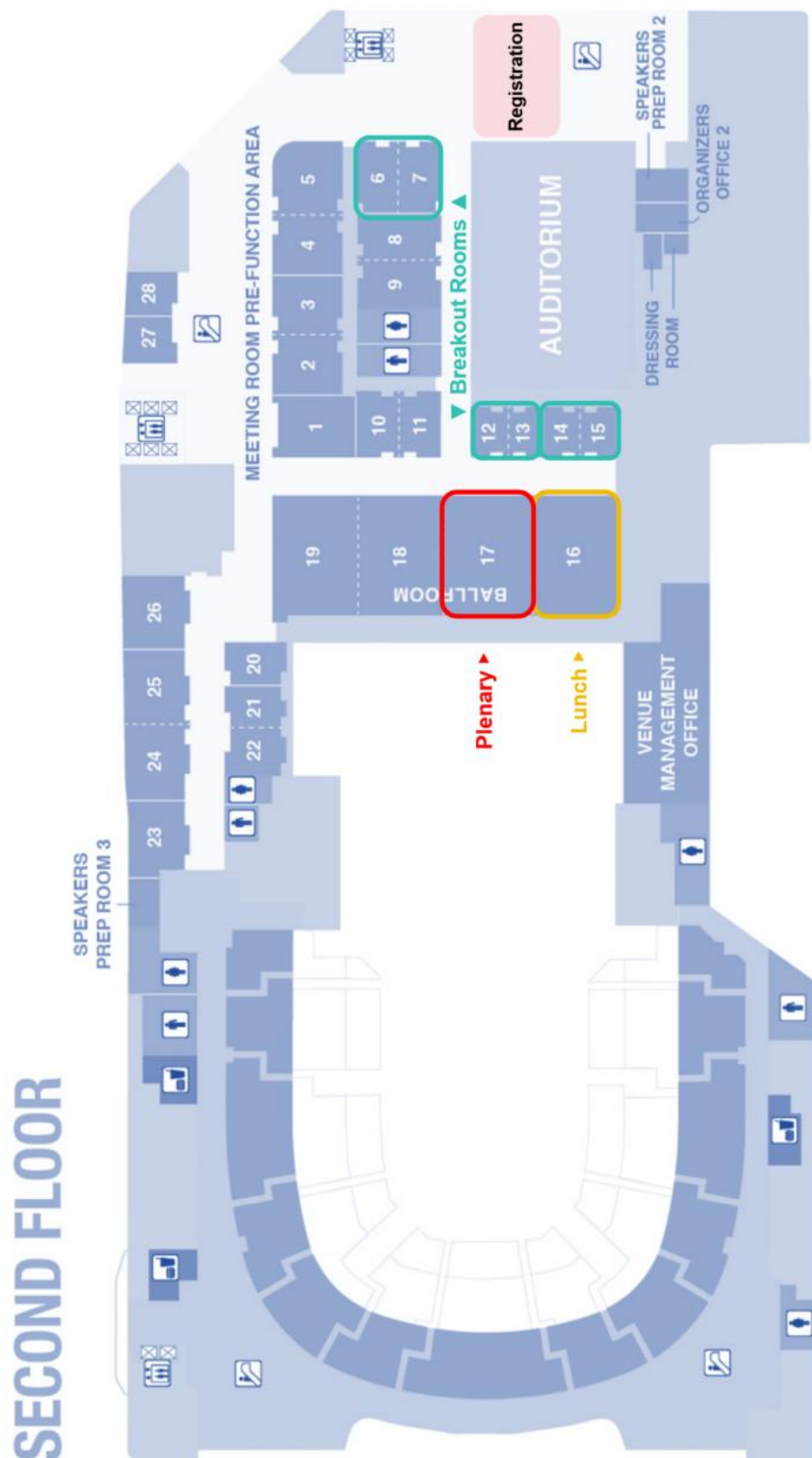
2010 and received his Ph.D in Evolutionary Genetics from Beijing Institute of Genomics, Chinese Academy of Sciences in 2015. From 2015 to 2020, he was a IGI Postdoctoral Fellow in Dr Christina Curtis's lab at Stanford University School of Medicine. Dr Hu's research interests span from cancer evolution, lineage tracing to computational biology. His research on measuring cancer evolutionary dynamics has yielded novel insights into cancer formation and metastasis, facilitating biomarker discovery for risk prediction and treatment decision making. Dr Hu's publications as corresponding author or first author include Nature (2024), Nature Reviews Genetics (2026), Nature Biotechnology (2023), Nature Genetics (2020, 2019, 2017), Genome Biology (2025), Cell Systems (2025), etc.

Title: Deciphering Cell Fate and Tumor Evolution with Multimodal Lineage Tracing

Abstract: Understanding how cells commit to distinct fates over time is fundamental to elucidating the principles and mechanisms that govern organismal development, tissue regeneration and disease progression. Multimodal lineage tracing, which couples heritable lineage information with single-cell multi-omics, has revolutionized our ability to chart cellular dynamics and fate decisions at unprecedented resolution. In this talk, I will present our recent efforts in developing experimental lineage tracing technologies and computational methods for multimodal lineage tracing. I will

introduce a high-resolution base-editing lineage barcoding system (SMALT/eSMALT) that enable multimodal measurements of lineage and transcriptomic information, revealing previously unrecognized principles of tumor evolution, including the polyclonal-to-monoclonal transition during colorectal tumorigenesis. I will further describe computational frameworks, including PhyloVelo and PhyloFate, for reconstructing ancestral cell states and developmental trajectories by integrating lineage trees with single-cell transcriptomes. Finally, I will discuss our transition map-based foundation model, scTransition, which leverages cellular dynamics to improve trajectory inference, perturbation prediction, and virtual cell modeling, highlighting how dynamic information can empower next-generation AI for developmental biology and precision medicine.

Conference Venue Map



Paper List

Session 1: Track 1 - Protein Structure & Language Models

(11:00-12:30, Day1 @Meeting Room 17, Session Chair: Fangxiang Wu)

11:00 - 11:15 | #13

Dynamically Modeling Residue-level Contact Map for Predicting Protein-Protein Interactions

Weizhong Zhao, Jingyun Zhang

11:15 - 11:30 | #107

AttentionNABP: Attention-Based Deep Learning Framework for Nucleic Acid-Binding Proteins Classification and Identification

Jianxin Wang, Haochen Zhao, Md. Sifat Ali, Muhammad Habibulla Alamin, Qichang Zhao

11:30 - 11:45 | #125

BioFC-GAT: Biomarker-Oriented Graph Attention Learning for ASD from rs-fMRI data

Hongyu Guo, Fangxiang Wu

11:45 - 12:00 | #26

Reconstructing Qwen3 into Qwen3-Protein: A Versatile Biophysics-Grounded Protein Language Foundation Model for PTMs and Downstream Tasks

Huaiyang Sun, Yiyu Lin, Yan Wang, Lun Zhu, Sen Yang, Jiahui Wu, Hao Wu

12:00 - 12:15 | #168

HiFuseVEP: Hierarchical Fusion of Multi-Source Protein Language Model Embeddings for Missense Variant Effect Prediction

Yanjie Wei, Haowen Zhao, Shaozhen Cai, Guan Wang, Huiling Zhang, Ganzhang Zheng, Siya Huang, Nuoxian Xu, Zihan Zhou

12:15 - 12:30 | #50

Sin-PPI: Sub-linear Proteome-Wide PPI Screening via Orthogonal Manifold Learning

Xinqi Zeng, Sen Yang, Huajian Mao, Dongsheng Zhao, Zhiguang Chen, Nong Xiao

Session 2: Track 1 - Single-Cell & Multi-omics**(11:00-12:30, Day1 @Meeting Room 12+13, Session Chair: Wei Peng)****11:00 - 11:15 | #11*****scMMGC: A generative multi-omics integration method based on dual-mask contrastive fusion of co-expression graph***

Xiang Chen, Zihan Yang, Yongkang Ma, Xiaoyu Liu

11:15 - 11:30 | #102***Pretrained Biological Sequence Embedding-Guided MoE for Cancer Driver Gene Prediction***

Yang Hu, Wei Dai, Xinyue Xu, Wei Peng, Xiaodong Fu, Li Liu, Lijun Liu

11:30 - 11:45 | #118***AFLink Enables Multiview Analysis of Atrial Fibrillation Genes Through Integrating Heterogeneous Functional Genomic Data***

Cuixiang Lin, Menglong Wang, Yating Tang

11:45 - 12:00 | #44***scAQUA: A Quintuplet Constraint-Based Batch Effect Correction Method for Single-Cell Multi-Omics Data***

Tiezheng Qiao, Fei Teng, Huiyong Zhang, Xiaoshu Zhu

12:00 - 12:15 | #140***scRQMeta: Residual Quantization for Single-Cell Multi-Omics Metacell Inference***

Yunhe Wang, Peiru Zhang, Songyu Guo, Yanchi Su, Xiangtao Li

12:15 - 12:30 | #166***A single-cell perturbation analysis framework integrating metabolic constraints and chain-based interpretability***

Min Li, Ju Xiang, Ruiqing Zheng, Jiawen Huang, Fengkai Liu

Session 3: Track 1 - Clinical Prediction & Multimodal Fusion**(11:00-12:30, Day1 @Meeting Room 14+15, Session Chair: Yuedong Yang)****11:00 - 11:15 | #18*****MCAF: Improving Mortality Risk Prediction using Multimodal Learning with Balanced Pre-training and Correlation-aware Fusion***

Abdulrahman Al-Badwi, Hulin Kuang, Abdulrahman Al-Dailami, Chengchao Shen, Raed Al-Sabri, Jianxin Wang

11:15 - 11:30 | #31***DIMIR: Deep Incomplete Multi-View Information Recovery for Breast Cancer Subtype Classification***

Wei Lan, Yinghao Liu, Xuhua Yan, Cong Peng, Qingfeng Chen, Liangliang Liu, Min Li, Yi Pan

11:30 - 11:45 | #49***A Misaligned Multi-modal Clinical Time Series Representation Learning Framework for In-hospital Mortality Prediction***

Tianyu Wang, Guanglei Cai, Lin Guo, Xianlai Chen, Yi Tang, Ying An

11:45 - 12:00 | #72***Drug-Target-Disease Association Prediction Based on Multi-Modal Feature Fusion Transformer***

Ju Xiang, Wenjun Li, Han Xiao, Wanjun Ma, Hua Sun, Xiwei Tang, Weijun Liang

Session 4: Track 1 - CRISPR, RNA & Molecular Computing**(11:00-12:30, Day1 @Meeting Room 6+7, Session Chair:Zhendong Liu)****11:00 - 11:15 | #131*****Predicting CRISPR-Cas13d On-Target Efficacy via Deep Learning***

Zhendong Liu, Jiamin Jiang, Hao Zhang, Rui Jiang, Jingran Niu, Xiao Liu, Tengbo Zhao, Hebing Chen

11:15 - 11:30 | #157***miRNA Target Prediction Based on Similarity Network Fusion and Graph Attention Network***

Chenbing Zheng, Hui Jiang, Zhiming Liu, Shiyu Yan, Shunheng Zhou

11:30 - 11:45 | #174***Dual-Axis Message Passing on Molecular Graphs: Layerwise Multi-Hop Convolution Meets Depthwise Dense Mixing***

Shiwei Sun, Xuefeng Cui

Session5: Track 1 - Drug Discovery & Molecular Interactions**(14:00-15:30, Day1 @Meeting Room 17, Session Chair: Qiaozhen Meng)****14:00 - 14:15 | #111*****Hierarchical Contrastive Learning for Multi-Domain Protein-Ligand Binding***

Shuo Zhang, Rongqi Hong, Huifeng Zhang, Jian K. Liu

14:15 - 14:30 | #137***Paratope-GLoMe: Gated Low-rank Memory Model for Nanobody Paratope Prediction***

Xin Wang, Lixin Liang, Zikang You, Fengcheng Mei

14:30 - 14:45 | #144***MPATDTI: A Meta-Path-Aware Transformer with Contrastive Learning for Drug-Target Interaction Prediction***

Jianxin Wang, Haochen Zhao, Haoyuan Li

14:45 - 15:00 | #160***Motif-Aware Graph Attention Networks for Hemolytic Peptide Prediction***

Qiaozhen Meng, Bangguo Tan, Yuchen Ma, Fei Guo

15:00 - 15:15 | #33***UGCA-DTI: Uncertainty-Gated Cross-Attention for Robust Drug-Target Interaction Prediction***

Wei Lan, Tian Huang, Hangsak Huy, Jingyuan Zhou

15:15 - 15:30 | #51***A Triple-Modal Contrastive Learning Framework with Sequence, Graph, and 3D Features for Drug-Target Interaction Prediction***

Le Xu, Xi Zhang, Dan Luo, Ting Wang, Xuan Lin

Session6: Track 1 - Spatial & Biomedical Imaging**(14:00-15:30, Day1 @Meeting Room 12+13, Session Chair: Juan Liu)****14:00 - 14:15 | #1*****A Dependency-Aware Generative Model with Bi-Decoders for Super-Resolving Spatial Transcriptome Data from Histology Images***

Yuqi Chen, Peng Jiang, Tian Tian, Juan Liu

14:15 - 14:30 | #113***Identifying Spatial Domains via Hierarchical Fusion of Multi-scale Biological Priors***

Wei Lan, Wei Dai, Wei Peng, Xiaodong Fu, Li Liu, Lijun Liu, Zhihao Ping, Xingyu Zhou

14:30 - 14:45 | #2***Precision Disease Stratification in Parkinson's Disease: Fairness-Aware Imputation and Longitudinal Subtype Discovery***

Moad Hani, Fatima Zahra Ouadirhi, Mohamed Amine Hamzaoui, Zainab Ouadirhi, Said Mahmoudi, Mohammed Benjelloun

14:45 - 15:00 | #65***SpaAGMF: Adaptive Gated Multi-Scale Fusion of Histology and Spatial Transcriptomics for Cancer Region Classification***

Fangfang Zhu, Wenwen Min, Yunfeng Mao

15:00 - 15:15 | #95***FusionODE: Biochemical Function Prediction from Microscopy Images via Multimodal Continuous-Time Learning***

Rui Zhou, Qiucheng Miao, Shengqi Zhou, Yanjie Wei, Jovial Niyogisubizo

Session7: Track 1 - Neurodegenerative Disorders & Brain Imaging**(14:00-15:30, Day1 @Meeting Room 14+15, Session Chair: Qishi Zhang)****14:00 - 14:15 | #94*****Dynamic Cross-modal Fusion and Feature Alignment for Multi-stage Diagnosis of Alzheimer's Disease***

Han Wang, Jing Qu, Kangwei Geng, Xiao Ma, Huairon Zhang, Guixia Liu

14:15 - 14:30 | #143***SecPredNet: Joint Modeling of PLM Embeddings and Physicochemical Features for Signal Peptide Secretion Efficiency Prediction***

Chengchao Shen, Jianxin Wang, Haochen Zhao, Xiao Liang

14:30 - 14:45 | #136***Dynamic Spatiotemporal Graph Learning of EEG for Multi-Type Epileptiform Event Detection***

Yanjie Wei, Sheng Liu, Mingyu Wang, Linxia Xiao, Shizhong Lian

14:45 - 15:00 | #161***Swin Transformer-Based Interpretable Facial Recognition for Autism Spectrum Disorder with Dual Supervision Strategy***

Yi Pan, Keying Ren, Ruitao Xie, Xiaoqing Zhang

Session8: Track 1 - Drug Discovery & Repositioning**(14:00-15:30, Day1 @Meeting Room 6+7, Session Chair: Ruiqing Zheng)****14:00 - 14:15 | #23*****Memory-Aware and Coarse-to-Fine Representation Learning for Medication Recommendation***

Ziwei Ma, Xianghan Wang, Jinzhong Ning, Yijia Zhang

14:15 - 14:30 | #32***FusionMa-DTA: Cross-Modal Fusion and Global-Local Sequence Modeling for Drug-Target Affinity Prediction***

Wei Lan, Xinyi Zhang, Tian Huang, Hangsak Huy

14:30 - 14:45 | #85***An Interactive Web Server for Multi-Model Drug Repositioning and Evidence Tracing***

Xiangyu Zeng, Xinqiang Wen, Ju Xiang, Xiangmao Meng

14:45 - 15:00 | #90***DuoDR: Dual-Stream Collaborative Contrastive Learning with Dual-Axis Neighborhood-Aware Refinement for Drug Repositioning***

Ju Xiang, Wenjun Li, Xiangmao Meng, Shengyi Xu, Zihao Guo, Tianyang Peng, Ruiqing Zheng

15:00 - 15:15 | #173***TargetNPBind: A Pharmacophore-Guided Dual-Stream Fusion Framework for Natural Product-Target Binding Affinity Prediction***

You Wu, Yongkang Wang, Wen Zhang, Shichao Liu

Session9: Track 1 - Genomics, Transcriptomics & Evolutionary Sequences**(16:00-17:30, Day1 @Meeting Room 17, Session Chair: Fei Wang)****16:00 - 16:15 | #100*****AlloMut: Dual-View Self-Supervised Representation Learning for Predicting the Pathogenicity of Allosteric-Site Variants***

Yanjie Wei, Ziqi Xu, Haowen Zhao, Shaozhen Cai, Yuxiang Huang, Siya Huang, Nuoxian Xu, Guan Wang, Huiling Zhang

16:15 - 16:30 | #156***IPRLLM: Iterative Prompt Refinement with Large Language Models for Enhancing Phage-Host Association Prediction***

Ying Wang, Yiyang Zhang, Feng Zhou, Lan Cao, Jiaying Bai

16:30 - 16:45 | #164***A Unified Benchmark and Conditional Sequence Modeling Framework for Future Influenza Evolution Prediction***

Fa Zhang, Zhuolun Li, Xulinyi Huang, Jiayu Yang, Qian Yao Lin, Dongxu Zhang

16:45 - 17:00 | #41***circ-EGAT: Enhanced Graph Attention Network with Multi-Information Integration for circRNA-RBP Binding Sites Prediction***

Yajing Guo, Xiujuan Lei

17:00 - 17:15 | #5***Gated Bottleneck Convolution with High-Similarity-Pass Attention Enables Accurate Drosha and Dicer Cleavage Site Prediction***

Yang Zhou, Wen Chen, Fang Ge, Dong-Jun Yu

17:15 - 17:30 | #21***scCT: Mapping Single-Cell Data to Human Reference Atlases to Identify Deviated Cell States***

Yuman Li, Zikang Yin, Yanhong Wu, Jin Gu

Session10: Track 1 - ncRNA & Disease Associations**(16:00-17:30, Day1 @Meeting Room 12+13, Session Chair: Yulian Ding)****16:00 - 16:15 | #135*****MORM: Multi-Omics-guided Region Mining and Cross-Modal Interaction for Multimodal Survival Prediction***

Yan Li, Jiadi Luo, Qingchun Liang, Shaoliang Peng

16:15 - 16:30 | #34***Pathogenicity Prediction of Missense Mutations Through Attention-based Multi-omics Feature Integration***

Chenlu Wang, Zongxuan Li, Shuqi Chen, Hongdong Li

16:30 - 16:45 | #145***HCPDA: Identification of piRNA-disease association based on heterogeneous graph attention and contrastive learning***

Yajun Liu, Yongliang Wang, Fan Zhang, Yulian Ding, Xuefeng Cui

16:45 - 17:00 | #53***EG-TransAttention: Edge-Aware Multiscale Attention Network for Computational Prediction of CircRNA-Disease Associations***

Dengju Yao, Ting Wang, Xiaojuan Zhan, Qianqian Zhao, Junyuan Wang, Xiangkui Li

17:00 - 17:15 | #99***Predicting Drug Synergy via Cross-Modal Contrastive Learning and Masked Multi-Omics Hypergraphs***

Xuan Lin, Xinqiang Wen, Xiangmao Meng, Xixi Yang, Zhiyong Li, Chengqian Lu

Session11: Track 2 - Multi-Omics, Spatial Transcriptomics & Health Medicine**(16:00-17:30, Day1 @Meeting Room 14+15, Session Chair: Ming Xiao)****16:00 - 16:15 | #48*****SpaDDA: Image-Guided Generative Diffusion Imputation for Spatial Transcriptomic Data***

Jingcheng Zhao, Fangfang Zhu, Wenwen Min

16:15 - 16:30 | #61***T-MAP: A Transformer-based Framework for Multi-mapping Hi-C Read Pair Assignment***

Gao Binyu, Chen Jiayu, Xie Peng

16:30 - 16:45 | #89***scGLA: integrating Large Language Model Embeddings with Graph-Based Autoencoders for Batch Correction of Single-Cell RNA-Seq Data***

Xiaohua Wan, Fa Zhang, Haichuan Liu, Jinrui Hou, Zhengke Pan, Le Li

16:45 - 17:00 | #93***TASER: A Two-Stage Pseudotime-Aware Framework for Directed Gene Regulatory Network Inference from Dynamic scRNA-seq Data***

Bin Hu, Xiaohua Wan, Fa Zhang, Jinrui Hou, Haichuan Liu, Shuang Feng, Letian Wang

17:00 - 17:15 | #141***Improving Pan-genome Graph Index Construction for Reads Mapping***

Lilu Guo, Shugui Bu, Wei Liu, Yufeng Wang, Xiaoshu Zhu

17:15 - 17:30 | #169***Task-Aware Benchmarking of Batch Correction Methods for scRNA Triple-Negative Breast Cancer Atlas Construction***

Peter Scheible, Jing He, Amy Tang, Jiangwen Sun

Session12: Track 2 - Protein Structure, Drug Design & Molecular Computing**(16:00-17:30, Day1 @Meeting Room 6+7, Session Chair: Fan Hu)****16:00 - 16:15 | #22*****IDeepCLD: Top CHO Clones through Integrated Deep Data Analysis in Cell Line Development***

Zhiheng Yi, Zuping Zhang, Fan Wu, Jiasen Liu, Qiuya Xiong, Guohao Xie, Shuo Liu, Min Li

16:15 - 16:30 | #105***A Semidefinite Programming Approach to Balanced Minimum Evolution Phylogeny Inference***

Pavel Skums

16:30 - 16:45 | #158***An ESM3-Driven Motif-Guided Algorithm for Nanobody CDR3 Optimization with Enhanced Humanization Profiles***

Xin Wang, Lixin Liang, Bingding Huang, Chenxiang Hong, Zhendong Yang

16:45 - 17:00 | #171***HaploFold: Enhancing Protein Inverse Folding with 3D Physicochemical Representation Modeling***

Yi Pan, Jiancheng Zhong, Shaokai Wang, Jie Qiu, Ruorong Jia

17:00 - 17:15 | #70***Mut-ADM: Latent Diffusion Model for Protein Mutation Effect Prediction***

Huazhen Huang, Zhenpeng Li, Juncai Zhang, Limai Jiang, Ying Lin, Fan Hu, Yunpeng Cai

17:15 - 17:30 | #167***Improving Rice lncRNA Functional Annotation through Pre-trained DNA Large Language Model and Relational Graphs***

Wei Dai, Xinyue Xu, Wei Peng, Zhangqian Li

Session13: Track 1 - Biomedical Imaging, Advanced Inference & Applications**(11:00-12:30, Day2 @Meeting Room 17, Session Chair: Xuan Wang)****11:00 - 11:15 | #17*****BioRxnReasoner: Multi-Agent Reasoning for Biochemical Reaction Diagram Question Answering***

Rui Zhou, Qiucheng Miao, Jingjing Zhang, Boya Zhang, Shengqi Zhou, Yanjie Wei

11:15 - 11:30 | #24***CryoDETR: a Deformable DETR-based method for particle picking in cryo-EM micrographs***

Xuan Wang, Chunyi Li, Xiaohua Wan, Fa Zhang

11:30 - 11:45 | #77***Construction and Practice of a 5C3S Collaborative Innovation Model for Graduate Education Reform: A case study based on a Biomedical Imaging Analysis Project***

Min Li, Yang Gao, Hongdong Li, Senzhang Wang

11:45 - 12:00 | #68***MTCNet:A Multi-Task Collaborative Network for Accurate Identification of Different Types of Colorectal Lesions***

Xiaohua Wan, Fa Zhang, Yufeng Sun, Yue Du, Dehui Qiu, Li Zhang, Han Wang

12:00 - 12:15 | #38***LongTrack: Long-range Motion-Constrained Cell Tracking***

Xiaohua Wan, Fa Zhang, Buqing Cai, Xinsheng Wang, Zhuo Jia, Shiwei Sun

12:15 - 12:30 | #56***IPKDUN:An Interpretable Deep Unfolding Network with Implicit Neural Representation and Multi-Scale Interaction***

Jinjie Wang, Yuli Chen, Ziheng Cai, Zixuan Pei, Xin He

Session14: Track 1 - Molecular Sequence & Biophysics**(11:00-12:30, Day2 @Meeting Room 12+13, Session Chair: Bolin Chen)****11:00 - 11:15 | #121*****Prime-DiffNovo: Accurate Peptide De Novo Sequencing via Non-Autoregressive Generation and Diffusion Refinement***

Xuan Yu, Kunyi Li, Lusheng Wang

11:15 - 11:30 | #122***Gene-M1: Cross-Species Genomic Discovery Enhanced by a Taxon-Specific Mixture-of-Experts Model***

Yuhang Li, Jiaqi Tang, Jianmin Chen, Yourui Han, Xuequn Shang, Bolin Chen

11:30 - 11:45 | #79***Identifying Nuclear Export Signals from Large-Scale Candidate Pools with a Deep Reranking Method***

Zhixuan Piao, Xiaoyong Pan, Hong-Bin Shen

11:45 - 12:00 | #170***MACE: A Multi-scale Attention Convolutional Evaluation Model for Top-down Mass Spectrometry Isotopic Envelopes***

Jiancheng Zhong, Maoqi Yuan, Yaoyao Li, Shaokai Wang

12:00 - 12:15 | #57***GradGE: Gradient-Augmented Genetic Evolution for Prediction of SARS-CoV-2 Variants with Enhanced Immune Escape Potentials***

Ziming Liu, Jialu Zuo, Yikai Li, Jian Zu

12:15 - 12:30 | #66***IMM-GNN: An Integrative Multi-hop and Multi-scale Graph Neural Network for Molecular Property Prediction***

Xianlai Chen, Ying An, Xing Zhao, Qiong Zhang, Yunbo Wang, Haochen Zhao

Session15: Track 2 - Microbiome & Intelligent Disease Diagnosis**(11:00-12:30, Day2 @Meeting Room 14+15, Session Chair: Yajun Liu)****11:00 - 11:15 | #110*****Network-based metabolomics reveals pathway-level metabolic rewiring in Chronic Obstructive Pulmonary Disease***

Xincheng Zou

11:15 - 11:30 | #112***MicroSPECTRA decodes the hidden rhythms of the gut microbiome through a phase-frequency-amplitude framework***

Kang Ning, Yuli Zhang, Haohong Zhang, Kouyi Zhou

11:30 - 11:45 | #114***Understanding the microbiota-gut-brain axis behind the methamphetamine psychological addiction and the possible intervention treatment***

Kang Ning, Kouyi Zhou, Mingyue Cheng, Liang Zhang, Xiaoke Li, Yingxuan Xiong, Yizehui Yang, Yixuan Zhang, Changzhu Qi, Wei Deng

11:45 - 12:00 | #15***Spatially-Aware Lesion Feature Aggregation for Chest X-ray Disease Diagnosis***

Yang Pan, Yi Hong, Peng Qiu, Chao Zhang, Jiwen Kang, Yang Yang

12:00 - 12:15 | #35***MLARGAT: Multi-level Information Aware Residual Graph Attention Network for Alzheimer's Disease Pathogenic Gene Prediction***

Hongdong Li, Hui Pan

Session16: Track 2 - Drug Design & Molecular Property Prediction**(11:00-12:30, Day2 @Meeting Room 6+7, Session Chair: Shuang Wang)****11:00 - 11:15 | #29*****ICTNODE: Disentangling Intrinsic, Coupling, and Contextual Dynamics for Causal Inference and Dynamics Prediction***

Jinling Yan, Shao-Wu Zhang, Luonan Chen

11:15 - 11:30 | #88***Invariant learning with substructure alignment and dual augmentation for out-of-distribution molecular property prediction***

Jiaying Yang, Xinlong Wen, Rongbo Zhu

11:30 - 11:45 | #120***Advancing Structure-Based Drug Design with Stochastic Differential Equations***

Tao Song, Shuang Wang, Junteng Ma, Yaoxiang Zhang, Mao Li, Tianle Ma

11:45 - 12:00 | #149***DMMRL: Disentangled Multi-Modal Representation Learning via Variational Autoencoders for Molecular Property Prediction***

Wei Lan, Long Xu, Yanmei Lin, Junping Guo, Zhuhong You, Jianbo Lu, Yuzhong Peng

12:00 - 12:15 | #96***SMF-Net: A Multi-modal Fusion Network for Predicting Concentration of FGFR1 Inhibitor***

Zhijie Chen, Ziyang Dong, Le Zhang, Ming Xiao

Poster List

#P-1| *TGCA: A Text-Guided Cross-Attention Multimodal Fusion Framework for Prognosis Prediction*

Jiawei Wang, Qieshi Zhang, Jun Cheng, Yinzhong Ma, Yabin Ji

#P-2| *DiNovo enables high-coverage and high-confidence de novo peptide sequencing via mirror proteases and deep learning*

Zixuan Cao, Xueli Peng, Di Zhang, Piyu Zhou, Li Kang, Hao Chi, Ruitao Wu, Zhiyuan Cheng, Yao Zhang, Jiaying Dai, Yanchang Li, Lijin Yao, Xinming Li, Yaoyu He, Jinghan Yang, Haipeng Wang, Ping Xu, Yan Fu

#P-3| *KSSD-Arrayhash: Segmented Random-Array Mapping for Efficient k-mer Minimizer Construction*

Xiaoxin Lu, Huiguang Yi

General Information

Conference Venue

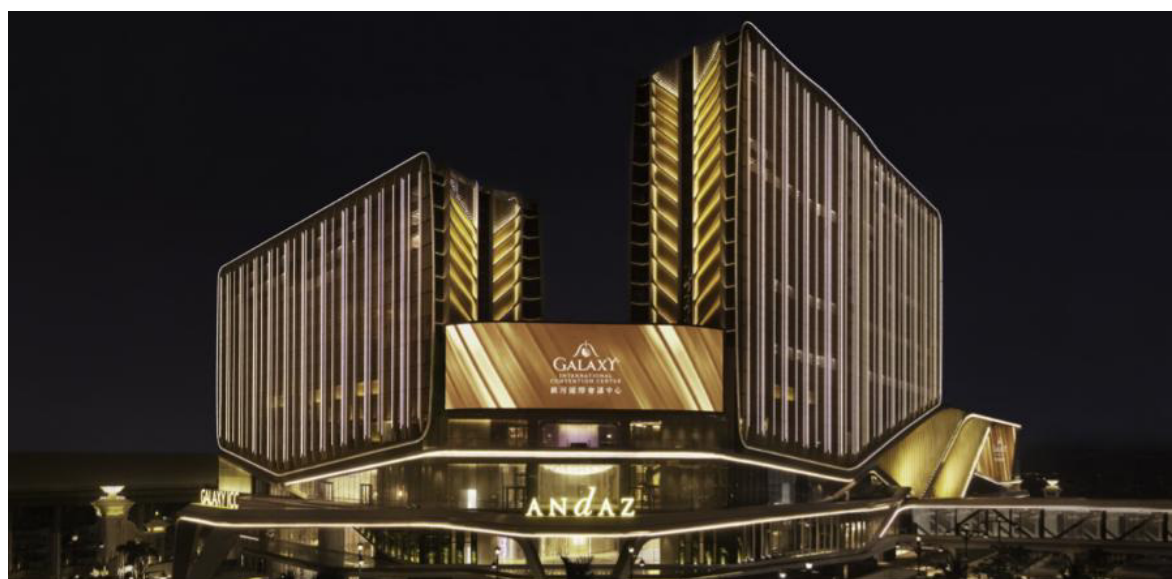
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Google Map: [Address: Galaxy Macau, Cotai, Macau](#)

Baidu Map: [Address: Galaxy Macau, Cotai, Macau](#)



Registration Desk

Venue: Meeting & Convention Foyer, 2/F, GICC

Date and Time:

14:00-19:00, July 22

08:00-18:00, July 23

08:00-12:30, July 24

Lunch

Venue: Meeting Room 16, 2/F, GICC

Date & Time:

12:30-14:00, July 23

12:50-14:00, July 24

Banquet

Venue: Multi-Function Room, 2F, Lisboeta Macau

Date & Time: 18:30-20:30, July 23

Meeting Point: Registration Desk

Shuttle Bus

Date	Time	Route
July 23	08:30	Broadway Hotel → GICC
	18:00	GICC → Lisboeta Macau (Meeting Point: Registration Desk)
	20:30	Lisboeta Macau → GICC → Broadway Hotel
July 24	08:30	Broadway Hotel → GICC

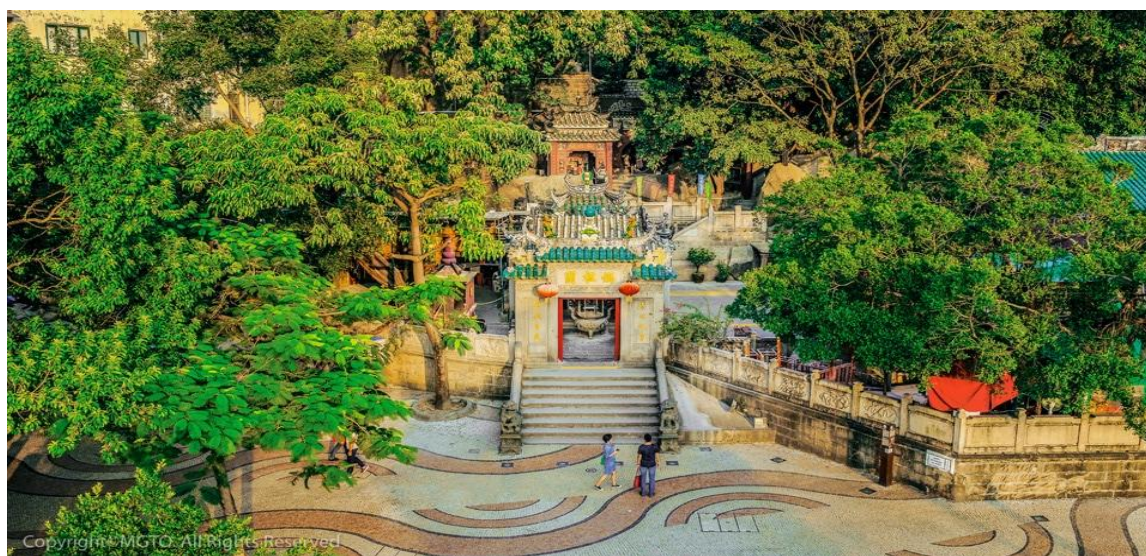
Technical Visit and Cultural Tour

Explore Macao's iconic sites and heritage following professional tour guide

Date & Time: 15:00-19:00, July 22 (Gather at 14:50 at Registration Foyer)

Route: GICC -> Lotus Square -> Return Gifts Exhibition Hall + Art Museum -> Ruins of St. Paul's + Mount Fortress -> Fountain -> Civic and Municipal Affairs Bureau -> A-Ma Temple -> GICC.

This is a tentative plan, and the specific itinerary will be adjusted according to the schedule the on day.



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For more information, please visit the Galaxy Shuttle Bus website: [Galaxy Shuttle Bus](#)

Border Gate	To Galaxy Macau	09:00 – 23:30
	From Galaxy Macau	09:00 – 23:30
	Average 5-15 minutes (Around 25 minutes drive)	
	Border Gate → Diamond Lobby# → Border Gate	
Macao International Airport	To Galaxy Macau	10:00 – 21:00
	From Galaxy Macau	10:15 – 20:45
	Average 35 minutes (Around 20 minutes drive)	
	Macao International Airport → Crystal Lobby# → Macau International Airport	
Andaz Macau	To Galaxy Macau	09:00 – 02:00
	From Galaxy Macau	09:00 – 02:00
	Average 5-10 minutes (Around 10 minutes drive)	
	Andaz Macau → Crystal Lobby → Andaz Macau	
StarWorld Hotel / Macao Ferry Terminal	To Galaxy Macau	09:30-22:00
	From Galaxy Macau	09:30-22:00
	Average 10-20 minutes (Around 35 minutes drive)	
	Crystal Lobby → StarWorld Hotel → Macau Ferry Terminal → StarWorld Hotel → Crystal Lobby	

Taipa Ferry Terminal	To Galaxy Macau	09:00 – 23:00
	From Galaxy Macau	09:15 – 23:15
	Average 15-40 minutes (Around 20 minutes drive)	
	Taipa Ferry Terminal* → Crystal Lobby# → Taipa Ferry Terminal*	
Hengqin Port	To Galaxy Macau	09:00 – 22:00
	From Galaxy Macau	09:15 – 21:45
	Average 5 – 10 minutes, Non-Peak Hours (17:00-22:00) 30 minutes (Around 10 minutes drive)	
	Hengqin Port → Crystal Lobby# → Hengqin Port	
Hong Kong Zhuhai Macao Bridge	To Galaxy Macau	10:00 – 23:00
	From Galaxy Macau	10:00 – 23:00
	Average 10-25 minutes (Around 25 minutes drive)	
	Hong Kong Zhuhai Macau Bridge → Diamond Lobby → Hong Kong Zhuhai Macau Bridge	

Local Public Bus

You can download the following local APP to check Macau bus schedule. Here is the link and QR code: <https://www.dsat.gov.mo/dsat/index.aspx>



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If you need to call taxi, please download MaasPlus APP for local on-call taxi. Macau is a popular tourist destination, you are strongly recommended to reserve a taxi ahead of schedule. Here is the link for downloading the Taxi APP:

<https://www.maasplus.com/file-api/maasplus/comm/app/version/download.html>

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Please ensure that you have a valid Exit-Entry Permit for Travelling to and from Hong Kong and Macao (港澳通行证) if you are a Chinese Citizen, or Passport if you are a foreign citizen, and the appropriate endorsements to attend the conference smoothly. Upon entry into Macau, travelers will be issued an entry declaration/permission to stay (as shown in the white slip below). Please keep it properly during your hotel check-in and stay in Macau.

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