



上海市生物信息学会
SHANGHAI SOCIETY FOR BIOINFORMATICS

The 22nd CJK Bioinformatics Conference Conference Handbook

Shanghai, China | November 6-9, 2025

Host organization

Shanghai Society for Bioinformatics

Collaborating organization

- China National Center for Bioinformation
- National Institute of Genetics
- Korea Bioinformation Center
- Shanghai Institute for Biomedical and Pharmaceutical Technologies
- Shanghai-MOST Key Laboratory of Health and Disease Genomics
- ISCB China
- IEEE SMC Shanghai Chapter
- IEEE SMC TC on Systems Biology

Supporting organization

- SAST Society Service Center
- Shanghai Science and Technology Development Foundation



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- Takashi Gojobori (National Institute of Genetics, Japan)
- Yasukazu Nakamura (National Institute of Genetics, Japan)

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- Lu Xie (Shanghai-MOST Key Laboratory of Health and Disease Genomics; Shanghai Institute for Biomedical and Pharmaceutical Technologies, China)
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Program

The 22nd CJK Bioinformatics Conference

6-9 November, 2025 | Fudan University, Shanghai, China

Day 1 Thursday, November 6th, 2025

Qingyun Hotel of Fudan University (Handan Campus)

Registration and Welcoming Ceremony

09:00-18:00 ○ Registration

18:00-21:00 ○ Welcome Ceremony/Discussion for future JKC organizing

Day 2 Friday, November 7th, 2025

Guanghua Building Fudan University (Handan Campus)

Opening and Keynote Talk

(Chairs: Xingming Zhao, Lu Xie, Zhiwei Cao)

08:45-10:30 ○ Opening Remarks/Parallel Conference Preliminary Talks

10:30-11:00 ○ **Kai Ye**, Xi'an Jiaotong University
Seq2Image: Concept and Applications

11:00-11:30 ○ **Masanori Arita**, National Institute of Genetics
Global Sequencing Projects and the International Collaboration of Databases

11:30-12:00 ○ **Daehee Hwang**, Seoul National University
Precision Medicine: Omics and Clinical Data

12:00-13:00 ○ Lunch

CJK Bioinformatics Symposium

(Chair: Lu Xie, Yong Zhang, Chaochun Wei, Yuan-Yuan Li)

13:00-13:10 ○ Opening Speech (Speaker: **Yixue Li**, Guangzhou Laboratory)

13:10-13:30 ○ **Xingming Zhao**, Fudan University
AI Driven Exploration of Human Gut Microbiome

13:30-13:50 ○ **Yosuke Kawai**, Japan Institute for Health Security
Sharing and Utilization of Controlled Access Data in Japan

Program

13:50-14:10 ○ **Sanghyuk Lee**, Ewha Womans University
AI-Driven Solutions for Digital Histopathology at the Single-cell Level

14:10-14:30 ○ **Zhang Zhang**, Beijing Institute of Genomics
Towards a Universe of Human Long Non-coding RNAs

14:30-14:50 ○ **Yasukazu Nakamura**, National Institute of Genetics
High Quality Analysis of Animal and Plant Genomes

14:50-15:10 ○ **Dongsup Kim**, KAIST
Building Prediction and Design Models for Immunoproteins

15:10-15:30 ○ Coffee Break

15:30-15:50 ○ **Luyi Tian**, Guangzhou Laboratory
Evaluation and Prospects of Single-cell Perturbation Prediction Models

15:50-16:10 ○ **Hiroshi Tsugawa**, Tokyo University of Agriculture and Technology
Metabolomics in Systems Biology

16:10-16:30 ○ **Jin-Wu Nam**, Hanyang University
AI-aided Design of Synthetic Regulatory RNAs

16:30-16:50 ○ **Youqiong Ye**, Shanghai Jiao Tong University
Decoding Spatial Tumor Microenvironment by Spatial-omics

16:50-17:10 ○ **Junil Kim**, Soongsil University
Single-cell Omics in Time and Space

17:10-18:30 ○ Poster session

18:30-20:00 ○ Dinner



Program

Day 3 Saturday, November 8th, 2025

09:00-11:00

○ Visiting Fudan University (Handan Campus)

11:00-14:30

○ Cultural Activities

Young Scholar Presentation

(Chair: Haifeng Chen, Hong Li, Yi Shi, Jun Wu)

14:50-14:58

○ Shohei Nakamukai, RIKEN CSRS
Retention Order Prediction Using SVM

14:58-15:06

○ Seokju Park, Hanyang University
From Data to Discovery: AI-Guided Biological Insights

15:06-15:14

○ Siqiong Yao, Shanghai Jiao Tong University
Research on the Precise Diagnosis of Rare Tumor
Imaging Guided by Knowledge-Driven Collaborative Transfer
Learning

15:14-15:22

○ Saeideh Ashouri, National Institute of Global Health and
Medicine
Pangenome Graphs of Japan and Saudi Arabia

15:22-15:30

○ Minhak Choi, Hanyang University
Population-Scale Detection and Characterization of De
Novo SNVs, Indels, and Structural Variants in the Atomic
Bomb Survivor Cohorts

15:30-15:38

○ Ming Chen, China National Center for Bioinformation
Kingdom-wide Evolutionary Analysis of RNA Editing Factors
in Archaeplastida

15:38-15:46

○ Takaki Oka, Tokyo University of Agriculture and Technology
Multi-omics Integration for Alzheimer's Cohort

Program

15:46-15:54

○ Nahyeon Kwon, Korea University
Exome Sequencing Analysis of Amyotrophic Lateral
Sclerosis in the Korean Population

15:54-16:02

○ Siyu Jing, Shanghai Institute of Nutrition and Health,
Chinese Academy of Sciences
Multimodal AI Model for Early Detection of Hepatocellular
Carcinoma

16:02-16:10

○ Nami Sakamoto, Tokyo University of Agriculture and
Technology
Lipid Class Identification from Mass Spectra

16:10-16:18

○ Young Seok Choi, Korea University
Construction of AI Model for Human Brain Organoid

16:18-16:26

○ Zhengyu An, Fudan University
Characterizing Schizophrenia-relevant Structural Variants and
Tandem Repeats through Long-read Sequencing

16:26-16:34

○ Mohamed Elmanzalawi, National Institute of Genetics
Ultrafast Identification of Species from Their Genomes

16:34-16:42

○ Chaewon Min, Korea University
Investigation of De Novo Variants in Autism Using Whole
-Genome Sequencing

16:42-16:50

○ Axian Liu, Fudan University
Disease Association Study of Autoimmune and Auto
-inflammatory Diseases by Integrating Multi-modal Data
and Hierarchical Ontologies

16:50-17:30

○ Young Scholar Discussion

17:30-17:45

○ Close Remarks

Day 4 Sunday, November 9th, 2025

09:00-17:00

○ Departure



Keynote Speaker



Kai Ye, Professor
Xi'an Jiaotong University
Research Interests: Artificial intelligence, structural variant
Topic: Seq2Image: Concept and Applications

Biography: Kai Ye, Professor and Ph.D., has received funding from the National Science Fund for both key projects and Distinguished Young Scholars, the Ministry of Science and Technology's Key R&D Program. He earned his bachelor's and master's degrees from the School of Life Sciences and the School of Pharmacy at Wuhan University, respectively. He completed his Ph.D. (cum laude) at the Faculty of Computer Science at Leiden University in the Netherlands. During his postdoctoral research under Professor Rolf Apweiler at the European Bioinformatics Institute (EBI), he transitioned his bioinformatics research focus from protein sequences to genomics.

Subsequently, he served as an assistant professor at Leiden University Medical Center in the Netherlands and at The Genome Institute at Washington University in St. Louis, USA. He developed a series of genomic variant detection methods, including Pindel and MSIsensor, and was invited to participate in several major international genomics projects such as The 1000 Genomes Project and The Cancer Genome Atlas (TCGA).

In early 2016, Professor Kai Ye returned to China full-time and established an interdisciplinary team at the School of Automation, Xi'an Jiaotong University, integrating informatics and life sciences. His research focuses on artificial intelligence technologies and the in-depth study of structural variant detection, characterization, and function.

Professor Ye has published over 100 SCI-indexed papers in journals such as *Science*, *Nature*, *Nature Biotechnology*, *Nature Methods*, and *Nature Microbiology*, including 14 ESI Highly Cited Papers and 1 Hot Paper. His work has been cited more than 45,000 times in SCI literature.

Abstract: The talk introduces seq2image, a novel computational paradigm that transforms genomic sequences into images, enabling the use of deep learning models like CNNs, RNNs, and Transformers to capture both local features and long-range interactions. This holistic, model-free approach improves the detection of complex structural variations (SVs) with tools like SVision and Swave, which outperform traditional model-based methods in accuracy and scalability. Additionally, ANNEVO applies seq2image to gene annotation, integrating evolutionary information to deliver fast and highly accurate predictions across diverse species. Together, these applications demonstrate how seq2image enhances our ability to decode complex biological data.

Keynote Speaker



Masanori Arita, Professor
National Institute of Genetics
Research Interests: Bioinformatics, Metabolomics
Topic: Global Sequencing Projects and International Collaboration of Database

Biography:

2018.04 - Present Head, DNA Data Bank of Japan (DDBJ), National Institute of Genetics

2013.11 - Present Professor, National Institute of Genetics

2010.04 - 2013.10 Associate Professor, Department of Biophysics and Biochemistry, Graduate School of Science, The University of Tokyo

2007.04 - 2013.03 Deputy Group Director, Metabolome Research Group, RIKEN Plant Science Center

2001.04 - 2010.03 Project Research Staff, Institute for Advanced Biosciences, Keio University

2003.04 - 2010.03 Associate Professor, Department of Computational Biology, Graduate School of Frontier Sciences, The University of Tokyo

2001.04 - 2003.03 Researcher, Computational Biology Research Center, National Institute of AIST

1999.04 - 2001.03 Researcher, Electrotechnical Laboratory, Agency of Industrial Science and Technology

Abstract: Global sequencing initiatives are rapidly transforming biology and medicine, generating unprecedented volumes of genomic data from humans, pathogens, crops, and biodiversity. The reusability of these datasets critically depends on international collaboration among public repositories. The International Nucleotide Sequence Database Collaboration (INSDC) - comprising DDBJ, ENA, and Genbank - has long provided a foundation for open sequence data sharing to improve resilience and accessibility globally. Lessons from the COVID-19 pandemic further underscored the importance of FAIR open access. This open collaboration is now challenged, however, in terms of CARE data principles, where equitable, rather than equal, access and utilization are emphasized. Such recent trends highlight the growing need for more global coordination and open discussion to ensure the long-term benefit from digital sequence information including human genomes. I also introduce the GteX (Green Technologies of Excellence) project in Japan, where plant genomes are utilized for better biomanufacturing..



Keynote Speaker



Daehee Hwang, Professor

Seoul National University

Research Interests: Systems Biology, Multi-omics, Bioinformatics, Deep Learning

Topic: Precision Medicine: Omics and Clinical Data

Biography: During Ph.D. study at MIT, he developed bioinformatic tools for integrative analyses of gene expression and metabolomic data. In 2003, he started his postdoctoral career at ISB and developed a data integration tool, Pointillist; proteomic data analysis tools, MS-BID and Prequips; and a systems approach to prion disease. In 2006, he joined POSTECH in Korea and developed systems approaches for understanding complex human diseases. In 2010, he became the director of System Biodynamics-National Core Research Center. He developed tools for understanding spatiotemporal operations of biological networks. In 2013, he moved to DGIST in Korea and worked on proteogenomic analyses of diverse cancer types. In 2019, he moved to Seoul National University and have been developing diverse precision medicine approaches using multi-omics and clinical data (electric medical records, imaging data, etc.)

Abstract: As huge amounts of global data (genomic, epigenomic, transcriptomic, proteomic, and metabolomic) generated from a broad spectrum of specimens collected from human patients have been accumulated in public repositories, together with electronic health records and drug treatment information, biology is now becoming an informational science. Accordingly, there have been significant needs for bioinformatic methods that can effectively extract useful information from these data. In this talk, I will present two different precision medicine approaches using multi-omics data and clinical big data, respectively.

Speaker



Xingming Zhao, Professor

Fudan University

Research Interests: microbiome, imaging genetics, BioMed AI

Topic: AI driven Exploration of Human Gut Microbiome

Biography: Xing-Ming Zhao received his PhD degree from the University of Science and Technology of China. Currently, he is a distinguished professor and vice dean of the Institute of Science and Technology for Brain Inspired Intelligence, Fudan University, China. He is also the chair of Shanghai Society for Bioinformatics. He focuses on the interdisciplinary research between biomedicine and artificial intelligence. He has published more than 150 papers in peer-reviewed journals, e.g. Nature and Cell. He is the senior member of IEEE, Co-Chair of IEEE SMC Technical Committee on Systems Biology and Vice-Chair of ACM SIGBIO China. He is also the lead guest editor and the editorial member of several journals, e.g. IEEE/ACM TCBB, Neurocomputing, Journal of Theoretical Biology, IET Systems Biology, and so on.

Abstract: The human body is composed of various types of microorganisms. However, our knowledge about human microbiome is far from comprehensive. In this talk, I'll present our recent work on the exploration of human gut microbiome with long-read sequencing, and some algorithms and tools we have developed for analysis of human microbiome. I'll also show some new findings on the enterotypes of gut mycobiome and the association between gut microbiome and diseases.



Speaker



Zhang Zhang, Professor

China National Center for Bioinformation

Research Interests: Big data integration and curation, computational molecular evolution

Topic: Towards a Universe of Human Long Non-coding RNAs

Biography: Dr. Zhang Zhang is a Distinguished Professor of China National Center for Bioinformation (CNCB) & Beijing Institute of Genomics, Chinese Academy of Sciences. He serves as Head of Data Resource Department in CNCB and Associate Director of the National Genomics Data Center. His research focuses on biological data integration & curation and development of multi-omics data resources and new algorithms & tools. Dr. Zhang is devoted to building the national data center by developing more than forty database resources and computational tools and his research achievements have been selected in the "Top 10 Advances in Bioinformatics in China". He was an Executive Committee member of the International Society for Biocuration (2015~2018), Asian Regional Editor for Briefings in Bioinformatics (2017~2024), and acts as Associate Editor-in-Chief for Genomics Proteomics & Bioinformatics (2012~).

Abstract: Long non-coding RNAs (lncRNAs), defined as transcripts longer than 200 nucleotides without protein-coding potential, represent a vast and rapidly growing class of RNA molecules. However, they remain poorly annotated, with limited integration and insufficient functional characterization. To advance towards a comprehensive landscape of human lncRNAs, we developed computational methods for cross-species lncRNA identification and established three dedicated resources, namely, LncBook for systematic multi-omics characterization, LncExpDB for expression profiles and LncRNAWiki for functionally curated annotations, respectively. All these resources, publicly available through the China National Center for Bioinformation, provide the global research community with open access to high-quality data, serving as critical foundations for elucidating the functional roles of lncRNAs in human biology and diseases and thereby charting a complete universe of lncRNAs in human.

Speaker



Youqiong Ye, Professor

Shanghai Jiao Tong University School of Medicine

Research Interests: Spatial omics and tumor microenvironment

Topic: Decoding Spatial Tumor Microenvironment by Spatial-omics

Biography: Youqiong Ye, a PI in Shanghai Jiao Tong University School of Medicine since 2020, she received Ph.D. from Tongji University and completed postdoctoral training at UTHealth. Her research focuses on tumor microenvironment and immunotherapy, develops tools to decode tumor spatial microenvironment by integrating single-cell and spatial omics with innovative bioinformatics, uncovering how tumor boundary components and interaction networks contribute to immune evasion, with work published in *Nat Metab*, *Cancer Cell*, *Nat Immunol*, *Cancer Res*, *Immunity*, *Cell Metab*, etc.

Abstract: Spatial omics technologies have provided novel approaches for deciphering the tumor spatial microenvironment (TSME). Our group has developed spatial omics tools, such as *Cottrazm*, *HiST*, and *SpatialMTAI*. These tools have elucidated key molecular mechanisms, including cellular composition and intercellular interactions, that regulate immune escape within the TSME. Based on spatial features, we further established a tumor spatial molecular classification framework, offering new perspectives for clinical diagnosis and therapeutic decision-making.



Speaker



Luyi Tian, Professor
Guangzhou Laboratory
Research Interests: Single-Cell Sequencing, Spatial Omics, and Single-Cell Fundamental Models
Topic: Evaluation and Prospects of Single-Cell

Biography: LuYi Tian, PI at the Guangzhou National Laboratory, Distinguished Professor at Guangzhou Medical University, and recipient of the National Major Talent Program (Youth), holds a Ph.D. in Biomedical Sciences from the University of Melbourne. He later conducted research at the Broad Institute of MIT and Harvard. His research group combines both wet-lab and dry-lab approaches, focusing on the development of new equipment and technologies for single-cell omics, spatial omics, and nanopore sequencing, as well as corresponding data analysis pipelines and novel algorithm development. The group uses advanced omics technologies to study the regulation of the immune system in time and space and its role in respiratory diseases. Biological research achievements include hematopoietic stem cell differentiation lineage tracking, investigating immune system cancer resistance, and establishing multi-omics time series maps of immune responses in COVID-19 infections. In terms of technology, his group developed single-cell full-length transcriptome technology and corresponding data analysis pipelines, as well as a 3D stitching algorithm for spatial transcriptomics. As first or corresponding author, he has published high-impact papers in leading journals such as Nature Methods, Nature Immunology, Immunity (cover article), Nature Genetics, Nature Biotechnology, Blood, STTT, and Genome Biology. His work has been cited over 3,000 times, with an H-index of 21.

Abstract: The single-cell perturbation prediction model is a key tool for understanding cellular responses to genetic and chemical perturbations. However, the complexity and high-dimensionality of single-cell data present challenges for model development. Despite advances in deep learning and foundational models, there is still a lack of comprehensive performance evaluation benchmarks. This study systematically evaluates the performance of over 10 models on more than 20 datasets, covering various cell types and perturbation conditions. The results show that many models struggle to accurately capture the heterogeneous cellular responses following perturbation. Although foundational models outperform earlier methods, they still have limitations when predicting unknown perturbations, such as new cell types or experimental conditions. This study provides important insights into model effectiveness and guides future development.

Speaker



Yosuke Kawai, Professor
National Institute of Global Health and Medicine,
Japan Institute for Health Security
Research Interests: Human population genetics
Topic: Sharing and Utilization of Controlled Access Data in Japan

Biography: Dr. Yosuke Kawai earned his Ph.D. from the Graduate School of Science and Technology at Tokyo University of Science in 2006. His recent works are human population genomics, conducting genome medicine research using biobank resources and investigating human evolution through population genetic approaches.

Abstract: Practicing open science with human genome data involves unique challenges, including privacy protection and appropriate data management. In Japan, dedicated databases exist for sharing human subject research data. For example, the Japanese Genotype-phenotype Archive (JGA) stores and provides access to individual-level genetic and phenotypic data through a controlled-access system, available only to approved users via a Data Access Committee. In addition, several project-specific mechanisms for controlled access are in place. In this talk, I will introduce genomic research conducted within a biobank in which I have participated and discuss its relationship with these databases.



Speaker



Yasukazu Nakamura, Professor
National Institute of Genetics
Research Interests: Plant and Animal
Genome Analyses
Topic: High Quality Analysis of Animal
and Plant Genomes

Biography: Professor Yasukazu Nakamura is a faculty member at the National Institute of Genetics, where he leads the Genome Informatics Laboratory. His work centers on genome analysis, annotation, and database development, with contributions to microbial, plant, and animal genomics. He also helps manage the DNA Data Bank of Japan (DDBJ) and promotes open data sharing and global standards in genome informatics.

Abstract: Our research focuses on producing high-quality analyses of animal and plant genomes by integrating advanced sequencing technologies, genome informatics, and annotation pipelines. In particular, we are advancing the genomic analysis of important companion animals such as the domestic cat and emerging model plants such as *Marchantia polymorpha*. These efforts not only enhance the reliability of sequence databases such as DDBJ but also provide valuable resources for the global community, supporting fundamental biology.

Speaker



Hiroshi Tsugawa, Professor
Tokyo University of Agriculture and Technology
Research Interests: Computational science,
Mathematics Metabolomics, Lipidomics, Multiomics
Mass Spectrometry
Topic: Metabolomics in Systems Biology

Biography: Hiroshi Tsugawa specializes in computational mass spectrometry and metabolomics. He obtained his Ph.D. in Biotechnology from Osaka University in September 2012, and continued his career at RIKEN from 2012 to 2021. In 2021, he joined the Tokyo University of Agriculture and Technology (TUAT) as an Associate Professor in the Department of Biotechnology and Life Science, and was promoted to full Professor in October 2024. Dr. Tsugawa is internationally recognized for developing MS-DIAL, a universal software program for untargeted metabolomics and lipidomics, facilitating comprehensive metabolome analyses.

Abstract: Metabolomics has emerged as a central discipline in systems biology, enabling the comprehensive profiling of both known and unknown metabolites. The immense chemical diversity—spanning endogenous metabolites, plant natural products, microbiome-derived compounds, and the human exposome—presents a major challenge for accurate annotation and biological interpretation. Our research group has developed integrative computational platforms, including the MS-DIAL and MS-FINDER software suites, to advance untargeted metabolomics and lipidomics. Our efforts have revealed sex- and microbiota-dependent lipid regulations, age-associated sulfonolipids, and very long-chain polyunsaturated fatty acid (VLC-PUFA)-containing phospholipids, providing new biochemical insights into aging and disease. Furthermore, the latest MS-DIAL 5 environment supports multimodal mass spectrometry, including emerging fragmentation techniques and imaging, thereby facilitating in-depth structural and spatial metabolomics.



Speaker



Sanghyuk Lee, Professor
Ewha Woman's University
Research Interests: Spatial single-cell omics
Topic: AI-Driven Solutions for Digital Histopathology at the Single-Cell Level

Biography:

1995 - present: Prof. Ewha Woman's University
2009 - 2012: Director of Korea Bioinformation Center
2011 - 2022: President of KSBi, KOGO

Abstract: Histopathology has traditionally relied on subjective visual interpretation of H&E-stained slides, making precise cell type identification challenging. Deep learning methods, particularly vision transformer (ViT)-based foundation models, have advanced prediction of clinical features, but direct cell type prediction remains an unmet need. We developed Hist2Cell, a ViT-based model trained with spatial single-cell data to classify cell types directly from histology images. By integrating pretrained pathology foundation encoders, Hist2Cell achieved an AUROC of 0.72 in distinguishing 17 cell types, including nine immune and four stromal subsets. Beyond classification, we inferred clinically relevant tumor microenvironment features such as tumor-infiltrating lymphocyte (TIL) subtypes, tertiary lymphoid structure (TLS), and spatial tumor patterns. This approach enables prediction of microenvironment characteristics directly from H&E slides, offering a path toward AI-driven precision pathology.

Speaker



Dongsup Kim, Professor
KAIST
Research Interests: Structural bioinformatics, Computational drug design, Computational protein design
Topic: Building Prediction and Design Models for immunoproteins

Biography:

Education

1993. 09 - 1998. 05 : Ph.D. Dept. of Chemistry, Brown University, USA
1989. 03 - 1991. 02 : M.S. Dept. of Chemistry, Seoul National University
1985. 03 - 1989. 02 : B.S. Dept. of Chemistry, Seoul National University

Research Experience

2003.02 - Present : Professor, Dept. Bio and Brain Engineering, KAIST
2001.01 - 2003.01 : Postdoctoral Researcher, Oak Ridge National Laboratory
1998.05 - 2000.12 : Postdoctoral Researcher, University of Pennsylvania

Abstract: Immunoproteins, such as antibodies, antigens, TCRs, and MHCs, can be defined as proteins whose activities play a role in the functioning of the immune system. They are important for many biomedical applications such as vaccine design, diagnostics, and therapeutics. Many in silico tools have been developed to computationally predict and design their structures and interaction properties. As an example, we highlight a recently prediction model developed in our lab, pMHC-TCR interaction prediction model named TSPred, a deep learning model that significantly outperforms existing methods. We also discuss our recent work on antibody design model named AbFlex that exhibits state-of-the-art performance in terms of structure prediction accuracy and amino acid recovery rate.



Speaker



Jin-Wu Nam, Professor

Hanyang University

Research Interests: AI-enabled Design of RNAs, Computational RNA Biology, Scale Genomics

Topic: AI-aided Design of Synthetic Regulatory RNAs

Biography: Dr. Jin-Wu Nam is a professor in the Department of Life Science at Hanyang University in Seoul, South Korea. He received his M.E. and Ph.D. in an interdisciplinary bioinformatics program at Seoul National University (SNU), where Prof. Byoung-Tak Zhang advised him and Prof. V. Narry Kim co-advised him. During his postdoctoral research in Prof. David Bartel's laboratory at the Whitehead Institute/MIT, Dr. Nam studied novel forms of gene regulation by microRNAs (miRNAs) and discovered new long non-coding RNAs in different species. Since 2012, Dr. Nam has been a faculty member in the Department of Life Science at Hanyang University, where he established the Bioinformatics and Genomics (BIG) Lab. The BIG Lab explores the hidden wonders of the genome "outback," or the non-coding genome, through computational and experimental approaches. Recently, his lab developed an advanced bioinformatics framework to create highly reliable and efficient genomic tools. They are also pioneering AI-based computational methods to analyze the functions of non-coding elements and design synthetic molecules for applications in engineering biology and high-throughput screening. From 2021 to 2023, Dr. Nam served as deputy director of the Hanyang Institute of Bioscience and Biotechnology (HY-IBB). In December 2023, Dr. Nam was elected Division Director of Next-Generation Biotechnology at the National Research Foundation of Korea. In January 2025, he was elected to the Presidential Bio-Committee.

Abstract: The AI-assisted design of regulatory RNA elements provides innovative strategies for developing new vaccine platforms and RNA drug modalities. In this talk, we will discuss our recent progress in the AI-assisted design of synthetic RNA vaccines and drugs developed in our laboratory. Specifically, I will introduce our new deep neural network model for designing next-generation RNA interference (RNAi) for RNA drugs and for designing optimal 5' untranslated regions (5'UTRs) that maximize translation efficiency and mRNA stability. I will also discuss landmark studies and future prospects for intelligent RNA drug design for disease prevention.

Speaker



Junil Kim, Assistant Professor

Soongsil University

Research Interests: Single cell genomics

Topic: Global sequencing projects and the International collaboration of databases

Biography:

2021 - Present Assistant Professor, School of Systems Biomedical Science, Soongsil University

2018 - 2021 Postdoctoral Researcher, University of Copenhagen

2016 - 2018 Postdoctoral Researcher, Department of Genetics, University of Pennsylvania

2008 - 2014 Received Ph.D., Department of Bio and Brain Engineering, KAIST,

2005 - 2008 Received M.S., Interdisciplinary Graduate Program in Bioinformatics, Seoul National University

Abstract: Gene expression is regulated by multiple epigenetic factors including chromatin structure. Integrating single cell chromatin accessibility data with transcription factor (TF) binding motif information enhances our understanding of gene regulation. However, current motif-driven approaches have limited capacity to capture complex regulatory structure. Here, we introduce TENET+, a tool for reconstructing enhancer-driven causal gene regulatory networks by integrating single cell transcriptome and chromatin accessibility data. TENET+ leverages causal inference based on pseudotime-ordered gene expression and chromatin accessibility to predict interaction among TF expression, target gene expression, and open chromatin regions including long-range enhancer. When applied to a paired scRNAseq and scATACseq dataset from human peripheral blood mononuclear cells, we identified critical regulators and their epigenetic regulations. Interestingly, TENET+ successfully identified key regulators and their epigenetic control mechanisms. Notably, TENET+ outperformed existing GRN reconstruction tools in predicting promoter-enhancer interactions validated by cell type-specific Hi-C datasets. It also demonstrates superior performance in ChIP-seq validation even without relying on motif information. Finally, we experimentally validated the role of TF A in CD4T cell development-a regulator uniquely predicted by TENET+. These findings highlight that causality-based GRN reconstruction enable to uncover critical gene regulatory relationships that are missed by conventional motif-based methods.



Local Transportations

From Hongqiao Airport

Two convenient transportation options to reach Fudan University's Handan Campus

Metro Route Most economical option

- Take Metro Line 10**
From Hongqiao Terminal 1 or 2, board Line 10 toward Xinjiangwan City (新江湾城)
Cost: ~5 RMB | Duration: ~45 minutes
- Transfer at Jiangwan Stadium**
Get off at Jiangwan Stadium Station (江湾体育场) and take Exit 5 for Guanghua Building
Alternative: Exit 9 for hotels in Wujiaochang area
- Walk to Campus**
From Exit 5, walk northwest to Fudan University's East Gate (东门)
Distance: ~500 meters | Time: ~7 minutes

Operating Hours: 6:00 AM - 10:05 PM

Taxi Route Most convenient option

- Find Taxi Stand**
Follow signs to the official taxi stand on the ground floor of the airport
⚠️ Avoid unofficial drivers approaching you
- Show Destination**
Show driver: 复旦大学邯郸校区东门
East Gate of Fudan University Handan Campus
- Arrive at Campus**
Get dropped at the East Gate and enter with your passport information
Have your passport ready for campus security

Cost: 100-120 RMB

Before 10 PM: ~100 RMB
After 10 PM: ~120 RMB

From Pudong Airport

Multiple transportation options including the world's fastest commercial train

Metro Route Budget-friendly option

- Line 2 to Nanjing East Road**
Take Line 2 toward Xujing East
- Transfer to Line 10**
At Nanjing East Road, transfer to Line 10 toward Xinjiangwan City
- Exit at Jiangwan Stadium**
Take Exit 5 and walk to campus

Cost: ~20 RMB
Duration: ~120 minutes

Maglev + Metro Fastest experience

- Maglev to Longyang Road**
World's fastest commercial train (430 km/h)
- Transfer to Line 18**
At Longyang Road, take Line 18 to Fudan University Station
- Exit and Walk**
Take Exit 2 (NOT Exit 1) and walk to campus

Cost: 50 + 6 RMB
Duration: ~60 minutes

Taxi Route Direct & comfortable

- Official Taxi Stand**
Follow signs to ground floor taxi area
- Show Destination**
复旦大学邯郸校区东门
- Direct to Campus**
Get dropped at East Gate

Cost: 130-200 RMB
Duration: ~55 minutes

Venue, Dining, and Hotel Guide Map

