



国家基因组科学数据中心
National Genomics Data Center



The 11th Big Data Forum for Life and Health Sciences

第11届生命与健康大数据国际研讨会

会议手册

Program Book



国家生物信息中心

2026/10/13-15



会议网址

The 11th Big Data Forum for Life and Health Sciences

October 13-15, 2026, Beijing, China

Biological research has entered the era of big data, including a wide variety of omics data and covering a broad range of health data. Such big data is generated at ever-growing rates and distributed throughout the world with heterogeneous standards and diverse limited access capabilities. However, the promise to translate these big data into big knowledge can be realized only if they are publicly shared. Thus, providing open access to omics & health big data is essential for expedited translation of big data into big knowledge and is becoming increasingly vital in advancing scientific research and promoting human healthcare and precise medical treatment.

It is our great pleasure to announce that the 11th Big Data Forum for Life and Health Sciences will be held on October 13-15, 2026. You are cordially invited to participate in this exciting event.

Organizers



Acknowledgements



国际生物多样性与健康大数据联盟
Global Biodiversity & Health Big Data Alliance

Contact

E-mail: conference@cncb.ac.cn

Web site: <https://ngdc.cncb.ac.cn/conference/bdf2026>

Location

Venue: China National Center for Bioinformation (CNCB), No.1 Beichen West Road, Chaoyang District, Beijing 100101, China



Agenda

October 13 (Tuesday)

09:00 - 09:10

Welcome and Opening Remarks

Session 1: Data integration and curation, chaired by Zheng Wang and Lina Ma

09:10 - 09:30

ANSO: Promoting Inclusive Collaboration in
STIC for a Shared Sustainable Future

Shizhuan Zhang (张世专), ANSO



09:30 - 09:50

ENA: Evolving a Global Archive for the Next
Era of Life Science Data

Mar Gonzalez-Porta
European Bioinformatics Institute, UK



09:50 - 10:10

Genomic Information Infrastructure for Healthy
Longevity in Dogs and Cats

Yasukazu Nakamura
National Institute of Genetics, Japan



10:10 - 10:30

CNCB Biodata Resources

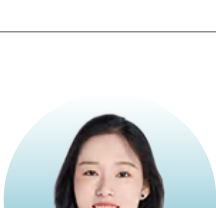
Shuhui Song (宋述慧), CNCB



10:30 - 10:50

Group Photo & Tea Break

10:50 - 11:10	Panning for Q: Target Enrichment of Coxiella Genomes from Complex Metagenomic Backgrounds Dmitrii Polev Saint-Petersburg Pasteur Institute, Russia	
11:10 - 11:30	Genetic target discovery for ageing-related diseases: a computational medicine approach Hai Fang (方海), Ruijin Hospital Shanghai Jiao Tong University of Medicine	
11:30 - 11:50	Decoding Disease Heterogeneity and Multimorbidity for Precision Nutrition Gengjie Jia (贾耿介), Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences	
Session 2: AI algorithms and models, chaired by Shengquan Chen and Yajing Hao		
13:30 - 14:10	Keynote talk: Designing Gene Regulatory Programs with AI Xiaowo Wang (汪小我), Tsinghua University	
14:10 - 14:30	AI cohort discovery for aging and healthcare Jinzhao Wang (王劲卓), Peking University	
14:30 - 14:50	Intelligent Literature Curation and Multi-Source Q&A Agents Bixia Tang (唐碧霞), CNCB	

14:50 - 15:10	Towards a Novel Diagnostic Tool: MicroRNA and Microbiota Profiling for Tuberculosis Staging in Cynomolgus Macaques and Animal Health Assessment Sunchai Payungporn Chulalongkorn University, Thailand	
15:10 - 15:30	Tea Break	
15:30 - 15:50	Deep-learning-enhanced Polyadenylation Analyses of 3'-tag scRNA-seq Data Li Yang (杨力), Fudan University	
15:50 - 16:00	From Codon Usage to Data-Centric Biological AI: Exploring Applications of Large-Scale Sequence Resources from DDBJ Ziyi He (何子易) National Institute of Genetics, Japan	
16:00 - 16:10	Decoding Transcription Start Sites from 5' Single Cell RNA-Seq Reveals a Diverse Initiation Landscape Across Human Cell Types Tan Wu (吴谈), CNCB	
16:10 - 16:30	AI-Driven Multi-Omics Data Integration: From Primate Cell Atlases to Precision Intervention Yidi Sun (孙怡迪) Institute of Neuroscience, CAS	

October 14 (Wednesday)

Session 3: Biodiversity and health genomics, chaired by Xuemei Lv and Tianyi Xu

09:00 - 09:40	Keynote talk: Genetic novelties in animal trait evolution and their implications in biomedical research Wen Wang (王文) Northwestern Polytechnical University	
09:40 - 10:00	Genomics, Evolution, and Conservation of Asian Wild Cats Shujin Luo (罗述金), Peking University	
10:00 - 10:10	Whole-genome and methylome characterization of the long-tailed macaque (<i>Macaca fascicularis</i>): a comprehensive biomedical resource toward a model for genetic and epigenetic research Vorthon Sawaswong, Mahidol University, Thailand	
10:10 - 10:30	Longer-lived mammals exhibit greater evolutionary conservatism and epigenetic modification at cancer-associated loci Xuming Zhou (周旭明), Institute of Zoology, CAS	
10:30 - 10:50	Tea Break	
10:50 - 11:10	Building conservation research capacity to protect biodiversity Pengfei Fan (范鹏飞), Sun Yat-sen University	

11:10 - 11:30	Coral-symbiotic lifestyles drive the adaptive evolution of coral reef macrofauna Meng Qu (曲朦) South China Sea Institute of Oceanology, CAS	
11:30 - 11:50	Rumen protozoa modulate methane emissions in ruminants Jie Xiong (熊杰), Institute of Hydrobiology, CAS	
11:50 - 12:10	The Butterfly as a Model System: From Genomes to the Genetic Basis of Adaptive Evolution Xueyan Li (李学燕) Kunming Institute of Zoology, CAS	
Session 4: China-Hungary Symposium, chaired by Beata G. Vertessy and Shuhui Song		
13:30 - 13:50	Disease-related Mutations in the RNA Binding Region of the Histone Methyltransferase KMT2D Ágnes Tantos, Hungary HUN-REN Research Centre for Natural Sciences	
13:50 - 14:10	Ensuring Data Reproducibility for the AI-Omics Era with Reference Materials as a Common Ruler Leming Shi (石乐明), Fudan University International Human Phenome Institutes	
14:10 - 14:30	Transcription Reprogramming Maintains Persistent Antibiotic Tolerance in Mycobacterium smegmatis Without Detectable Resistance Mutations Judit Tóth, Hungary HUN-REN Research Centre for Natural Sciences	

14:30 - 14:50	Optimizing Tuberculosis Diagnosis in Cynomolgus Macaques for Breeding Colony Saradee Warit, National Center for Genetic Engineering Biotechnology (BIOTEC), NSTDA; Taratorn Kemthong, Chulalongkorn University, Thailand	 
14:50 - 15:10	Tea Break	
15:10 - 15:30	Web-Based Platforms for Translational Cancer Data Interpretation and Statistical Decision Support Otília Menyhárt, Hungary HUN-REN Research Centre for Natural Sciences	
15:30 - 15:50	Intelligent Decoding, Integration and Generation in Spatial Biology Shihua Zhang (张世华), Academy of Mathematics and Systems Science, CAS	
15:50 - 16:10	Multi-omics and systems biology analyses reveal molecular pathways of recurrent pregnancy loss András Szilágyi, Hungary HUN-REN Research Centre for Natural Sciences	
16:10 - 16:30	Tumor Etiology, Tumor Heterogeneity and Implications for Treatment Jing Li (李晶), Changhai Hospital	

October 15 (Thursday)

Session 5: Population and precision medicine, chaired by Hong Li and Chenxi Tian

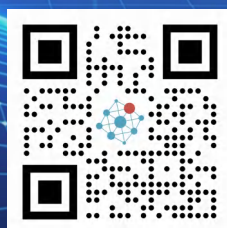
09:00 - 09:40	Keynote talk: Bioinformatics at National Scale: Integrating Sequencing, Supercomputing and AI at LNCC Ana Tereza Ribeiro de Vasconcelos, Brazil National Laboratory for Scientific Computing (LNCC)	
09:40 - 10:00	Research on Image-Text Fusion-Based Intelligent Assisted Diagnosis and Treatment of Tumors Di Dong (董迪), Institute of Automation, CAS	
10:00 - 10:20	The Impact of SARS-CoV-2 Genomic Evolution on the COVID-19 Epidemic Process in the North-Western Region of Russia Anna Gladkikh, Russia Saint-Petersburg Pasteur Institute	
10:20 - 10:30	From Frequencies to Priorities: Interethnic Distribution of Pharmacogenetic Phenotypes as a Basis for Prioritizing Preemptive Testing in Russia's Multi-Ethnic Population Sherzod Abdullaev, Russia Petrovsky National Research Center of Surgery	
10:30 - 10:50	Co-option of Tumor and Immune Microenvironment at Spatial and Single Cell Resolution Ruidong Xue (薛瑞栋), Peking University	

10:50 - 11:10	Tea Break	
11:10 - 11:30	Integrative Multi-omics Reveals Dynamic Regulation of Liver Regeneration and Fibrosis Jie Wang (王杰), Zhongshan Ophthalmic Center, Sun Yat-sen University	
11:30 - 11:40	From Single Cells to Population-scale Proteomics: Decoding Human Cellular Aging Jing Guo (郭婧), Xi'an Jiaotong University	
11:40 - 12:00	From Longitudinal Health Data to Risk Stratification: A LLM Empowered Multimodal Clinical Framework for Hepatic Steatosis Feng Xu (徐峰), Shandong Provincial Hospital	
Session 6: Single-cell and cancer omics, chaired by Shuai Jiang and Xudong Xing		
13:30 - 14:10	Keynote talk: Understanding the Protein Universe with AI Alex Bateman European Bioinformatics Institute, UK	
14:10 - 14:30	IMGT: Past Achievements, Present Work, and Future Perspectives in Immunogenetics Sofia Kossida, University of Montpellier, France	
14:30 - 14:50	Spatial Immunity - Decoding Immuno-Targets Zexian Zeng (曾泽贤), Peking University	

14:50 - 15:10	Decoding Human Polygenic Disease Using Statistical Genetics and Deep Learning Approaches Xushen Xiong (熊旭深), Zhejiang University	
15:10 - 15:30	Tea Break	
15:30 - 15:50	Multimodal Image-guided Surgery Navigation Danni Ai (艾丹妮), Beijing Institute of Technology	
15:50 - 16:00	TextBraTS: Bridging 3D MRI, Text, and Genotype for Data-Efficient Glioma Segmentation and Analysis Xiaoyu Shi (时晓宇), CNCB	
16:00 - 16:10	Extending incomplete spatial multi-omics maps across tissue sections with SPHERE Yukuan Liu (刘宇宽), CNCB	
16:10 - 16:30	Modeling Combinatorial Regulon Underpinning Cell Fate Landscape from Multi-omics Data Yong Wang (王勇), CAS Academy of Mathematics and Systems Science	
16:30 - 16:40	Concluding Remarks	



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