Abstracts of papers presented
at the 2024 Cold Spring Harbor Asia Conference

COMPUTATIONAL BIOLOGY OF THE GENOME

October 21–October 25, 2024

Arranged by

Jing-Dong Jackie Han, *Peking University*
Nicholas Luscombe, *Okinawa Institute of Science and Technology*
Jian Ma, *Carnegie Mellon University*
Chaolin Zhang, *Columbia University*

Cold Spring Harbor Conferences Asia
Cold Spring Harbor Laboratory

COMPUTATIONAL BIOLOGY OF THE GENOME
Monday, October 21 – Friday, October 25, 2024

Monday	7:00 pm	**1** Keynote Session
Tuesday	9:00 am	**2** Genotypes to Phenotypes and Diseases I
Tuesday	2:00 pm	**Poster Session**
Tuesday	3:00 pm	*Chinese Tea and Beer Tasting*
Tuesday	7:00 pm	**3** Genotypes to Phenotypes and Diseases II
Tuesday	7:45 pm	**4** Single Cell and Spatial Transcriptomic Analysis I
Wednesday	9:00 am	**5** Single Cell and Spatial Transcriptomic Analysis II
Wednesday	2:00 pm	*Visit to Old Suzhou**
Wednesday	7:00 pm	**6** Genome Organization and Evolution
Thursday	9:00 am	**7** Post-transcriptional Regulation
Thursday	2:00 pm	**8** Transcriptional and Epigenetic Gene Regulation
Thursday	5:00 pm	*Cocktails and Banquet*
Friday	9:00 am	**9** Frontiers of Algorithms and Technologies

Oral presentation sessions are located in the CSHA Auditorium
Poster session and Chinese Tea & Beer Tasting are in the Lake Front Hall.
Cocktail social hour is held outside in the Suz Garden.
Old Suzhou visits depart from the CSHA lobby
**optional tour requires additional fee.*

Meal locations and times are as follows:
Lunch: Main Cafeteria 12:00pm - 1:30pm
Dinner: Main Cafeteria 6:00pm - 7:30pm
Banquet: Suz Garden 6:00pm

More information will be available at CSHA office.
(Map at the end of this abstract book)

PROGRAM

MONDAY, October 21—7:00 PM

SESSION 1 KEYNOTE SESSION

Introduction by: **Chaolin Zhang**, Columbia University, New York, New York, USA

The assembly of a human pangenome
Heng Li [35'+10']
Presenter affiliation: Harvard Medical School, Boston, Massachusetts; Dana-Farber Cancer Institute, Boston, Massachusetts. 1

Introduction by: **Jian Ma,** Carnegie Mellon University, Pittsburgh, Pennsylvania, USA

Scalable analysis of large multi-ethnic biobanks and whole genome sequencing studies for genetic risk prediction and gene mapping of common diseases and traits
Xihong Lin [35'+10']
Presenter affiliation: Harvard University, Boston, Massachusetts. 2

TUESDAY, October 22—9:00 AM

SESSION 2 GENOTYPES TO PHENOTYPES AND DISEASES I

Chairperson: **Yi Xing,** University of Pennsylvania, Philadelphia, Pennsylvania, USA

Long-read RNA-seq strategies to study human diseases
Yi Xing [20'+10']
Presenter affiliation: The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; University of Pennsylvania, Philadelphia, Pennsylvania. 3

Using tandem repeats to understand the genetics of human health and disease
Wei Li [20'+10']
Presenter affiliation: University of California, Irvine, Irvine, California. 4

Expanded methylome and quantitative trait loci detection by long-read profiling and pangenome graphs
Guillaume Bourque, Cristian Groza, Bing Ge, Warren Cheung, Tomi Pastinen [10'+5']
Presenter affiliation: McGill University, Montreal, Canada. 5

Computation approaches to deciphering mutational processes from large-scale cancer genomics data
Mo Liu, Arnoud Boot, Qi Zheng, Steven G. Rozen [10'+5']
Presenter affiliation: Guangzhou Medical University, Guangzhou, China; Duke-NUS Medical School, Singapore. 6

Break

Quantitative maps of gene expression dosage driving cellular and physiological phenotypes
Tuuli Lappalainen [20'+10']
Presenter affiliation: Science for Life Laboratory, KTH Royal Institute of Technology, Stockholm, Sweden, Sweden, New York Genome Center, New York, New York. 7

Prediction potential and pitfalls in pervasive population personal genomics—Interpreting newborn genomes
Steven E. Brenner [20'+10']
Presenter affiliation: University of California, Berkeley, Berkeley, California. 8

Data-driven drug discovery targeting genome instability based on tumor genomes
Lixing Yang [10'+5']
Presenter affiliation: University of Chicago, Chicago, Illinois. 9

An accurate Bayesian linkage analysis method for noninvasive PGT-M
Hao Ge, Ruiqi Zhang, Lei Huang, Jie Qiao, Xiaoliang Xie [10'+5']
Presenter affiliation: Peking University, Beijing, China. 10

POSTER SESSION

Overcoming selection bias in RNA-seq studies of alternative splicing
Jenea I. Adams, Qiang Hu, Qian Liu, Eric Kutschera, Song Liu, Yi Xing
Presenter affiliation: University of Pennsylvania, Philadelphia, Pennsylvania; Children's Hospital of Philadelphia, Philadelphia, Pennsylvania. 11

Peak analysis of cell-free RNA finds recurrently protected narrow regions with clinical potential
Pengfei Bao, Taiwei Wang, Xiaofan Liu, Zhi Lu
Presenter affiliation: Tsinghua University, Beijing, China. 12

Integrating rare pathogenic variant prioritization with gene-based association analysis to identify novel genes and relevant multi-modal traits for Alzheimer's disease
Jixin Cao, Cheng Zhang, Chun-Yi Zac Lo, Qihao Guo, Jing Ding, Xiaohui Luo, Zi-Chao Zhang, Tian-Lin Cheng, Jinggi Chen, Xing-Ming Zhao
Presenter affiliation: Fudan University, Shanghai, China. 13

Discovering cell types and states from reference with heterogeneous single-cell ATAC-seq features
Yuqi Cheng, Xiuwei Zhang
Presenter affiliation: Georgia Institute of Technology, Atlanta, Georgia. 14

DeepMM—Identify and correct metagenome misassemblies with deep learning
Yi Ding, Jin Xiao, Bohao Zou, Lu Zhang
Presenter affiliation: Hong Kong Baptist University, Hong Kong, China. 15

FemXpress—Systematic analysis of X chromosome inactivation heterogeneity in female single-cell RNA-seq samples
Xin Wang, Yingke Ma, Fan Li, Wentao Cui, Pengfei Wang, Qi Zhou, Guihai Feng
Presenter affiliation: Institute of Zoology, Beijing, China. 16

High-resolution, noninvasive single-cell lineage tracing in mice and humans based on DNA methylation epimutations
Ruijiang Fu, Mengyang Chen, Yiqian Chen, Li Li, Shouwen Wang
Presenter affiliation: Westlake University, Hangzhou, China. 17

Mosaic integration and knowledge transfer of single-cell multimodal data with MIDAS
Zhen He, Shuofeng Hu, Yaowen Chen, Sijing An, Jiahao Zhou, Runyan Liu, Junfeng Shi, Jing Wang, Guohua Dong, Jinhui Shi, Jiaxin Zhao, Le Ou-Yang, Yuan Zhu, Xiaochen Bo, Xiaomin Ying
Presenter affiliation: Beijing Institute of Basic Medical Sciences, Beijing, China. 18

SAFB restricts contact domain boundaries associated with L1 chimeric transcription
Yaqiang Hong, Luyao Bie, Tao Zhang, Nian Liu
Presenter affiliation: Tsinghua University, Beijing, China. 19

LOCATE—Long-read Characterization of All Transposable Elements
Zhongren Hu, Bo Xu, Tianxiong Yu
Presenter affiliation: Tongji University, Shanghai, China. 20

Simulation of allele-specific copy number variations in single cells
Xianjie Huang, Yuanhua Huang
Presenter affiliation: The University of Hong Kong, Hong Kong, China; Hong Kong Science and Technology Park, Hong Kong, China. 21

Spatiotemporal dynamics of mononuclear phagocytic cells reveals new cell clusters and key regulators responsible for plaque instability in atherosclerosis
Jinmeng Jia, Mingyuan Liu, Xi Xi, Chuhanwen Sun, Sijie Chen, Lei Wei, Tingting Lv, Aijuan Qu, Ping Zhang, Rui Jiang, Xuegong Zhang
Presenter affiliation: Tsinghua University, Beijing, China. 22

ReadCurrent—A VDCNN-based tool for fast and accurate nanopore selective sequencing
Mengfan Li, Dongsheng Zhao
Presenter affiliation: Academy of Military Medical Sciences, Beijing, China. 23

Single-cell data analysis via perturbation estimation
Yuzhe Li, Jinsong Zhang, Xiaolei Fu, Hui Gao, Kehkooi Kee, Qiangfeng C. Zhang
Presenter affiliation: Tsinghua University, Beijing, China. 24

Inexpensive and accurate genotyping methods are essential to modern genomics and health risk prediction
Zilong Li, Anders Albrechtsen, Robert W. Davies
Presenter affiliation: University of Copenhagen, Copenhagen, Denmark. 25

IRIS-long—A long-read RNA sequencing-based discovery platform for cancer immunotherapy targets
Yang Xu, Matthew Mouck, Feng Wang, Siwei Luo, Lingyu Guan, Ameya Chemphekar, Lan Lin, Antoni Ribas, Yi Xing
Presenter affiliation: The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; University of Pennsylvania, Philadelphia, Pennsylvania. 26

E2VD—A unified evolution-driven framework for virus variation drivers prediction
Zhiwei Nie, Xudong Liu, Yutian Liu, Jie Chen, Peng Zhou, Yonghong Tian
Presenter affiliation: Peking University, Shenzhen, China. 27

scDIAGRAM—Annotating single-cell 3D genome compartments with direct statistical modeling and graph community detection
Yongli Peng, Jinzhu Jia, Dong Xing, Hao Ge
Presenter affiliation: Beijing International Center for Mathematical Research (BICMR), Beijing, China. 28

Genome-wide identification and analysis of human-specific splice sites
Zhuo Qu, Chie Kikutake, Mikita Suyama
Presenter affiliation: Kyushu University, Fukuoka, Japan. 29

Motif cluster domains, signature sequences overepresented in the DNA damage response, cell cycle control, and cell signaling pathways
Maia Larios-Sanz, Carlos Monroy, Jarvin Chavez, Ramiro Galvan, Nafil Atiq, MAria Bello, Carolina Carbajal, Alix Rieser, Albert Ribes Zamora
Presenter affiliation: University of St Thomas, Houston, Texas. 30

Inferring multimodal single-cell feature signatures with topic modeling
Piotr Rutkowski, Marcin Tabaka
Presenter affiliation: Polish Academy of Sciences, Warsaw, Poland. 31

Uncertainty-aware phenotypic cell state identification via weakly supervised learning
Bihan Shen, Xufeng Chen, Huicheng Ye, Hong Li
Presenter affiliation: Shanghai Institute of Nutrition and Health, Shanghai, China. 32

Regression for single-cell RNA-seq experiments—Experimental design and statistical inference
Fangda Song, Kevin Y. Yip, Yingying Wei
Presenter affiliation: The Chinese University of Hong Kong, Shenzhen, Shenzhen, China. 33

Population genomic insights into diversification and allorecognition in natural strains of the social amoeba *Dictyostelium discoideum*
Lei Tao, Cai Li
Presenter affiliation: Sun Yat-Sen University, Guangzhou, China. 34

Gene regulation inference from single-cell multi-omics data by deep learning
Kang Tian, Qiangfeng C. Zhang
Presenter affiliation: Tsinghua University, Beijing, China. 35

OmniReg-GPT—A large window foundation model for comprehensive genomic sequence understanding
Aowen Wang
Presenter affiliation: Zhejiang University, Hangzhou, China. 36

Ethnic-divergent enhancer sequence induces aging rate variations between Asian and African cohorts by altering blood transcriptome
Yiyang Wang, Jing-Dong J. Han
Presenter affiliation: Peking University, Beijing, China; Peking University, Chengdu, China. 37

HarmoDecon—Harmonious cell-type deconvolution for spatially resolved transcriptomics
Zirui Wang, Ke Xu, Lu Zhang
Presenter affiliation: Hong Kong Baptist University, Hong Kong, China. 38

Effective binning of metagenomic contigs using contrastive multi-view representation learning
Ziye Wang, Ronghui You, Haitao Han, Wei Liu, Fengzhu Sun, Shanfeng Zhu
Presenter affiliation: Fudan University, Shanghai, China. 39

Gastric cancer genomics study using reference human pangenomes
Du Jiao, Xiaorui Dong, Shiyu Fan, Xinyi Liu, Yingyan Yu, Chaochun Wei
Presenter affiliation: Shanghai Jiao Tong University, Shanghai, China. 40

m6AConquer—Unified quantification and integration of m^6A detection techniques
Xichen Zhao, Haokai Ye, Tenglong Li, Daniel J. Rigden, Zhen Wei
Presenter affiliation: Xi'an Jiaotong-Liverpool University, Suzhou, China; University of Liverpool, Liverpool, United Kingdom. 41

scDiffusion—Conditional generation of high-quality single-cell data using diffusion model
Erpai Luo, Minsheng Hao, Lei Wei, Xuegong Zhang
Presenter affiliation: Tsinghua University, Beijing, China. 42

TEDDY—An effective and comprehensive tool for large-scale identification and quantification of TE-chimeric transcripts and its application in mouse preimplantation development
Yihan Xiao, Lu Shen
Presenter affiliation: Tongji University, Shanghai, China. 43

TRAFICA—An open chromatin language model to improve transcription factor binding affinity prediction
Yu Xu, Chonghao Wang, Ke Xu, Yi Ding, Aiping Lyu, Lu Zhang
Presenter affiliation: Hong Kong Baptist University, Hong Kong, China. 44

InPACT—A computational method for accurate characterization of intronic polyadenylation from RNA sequencing data
Xiaochuan Liu, Hao Chen, Chenghao Xuan, Jiapei Yuan, Yang Yang.
Presenter affiliation: Tianjin Medical University, Tianjin, China. 45

DeepTFBS—A hybrid network based on omni-dimensional dynamic convolution network and CubeMLP for predicting the plant transcription factor binding site
Zhou Yao, Xinru Ding, Ke Li, Shangpo Yang, Jianxiao Liu
Presenter affiliation: Huazhong Agricultural University, Wuhan, China. 46

Size-based expectation maximization for characterizing nucleosome positions and subtypes
Jianyu Yang, Kuangyu Yen, Shaun Mahony
Presenter affiliation: Chinese Academy of Medical Sciences & Peking Union Medical College, Tianjin, China; Southern Medical University, Guangzhou, China. 47

Transposon regulation of immune cell senescence and receptor diversity during aging
Haotian Zhai, Jing-Dong J. Han
Presenter affiliation: Peking University, Beijing, China. 48

Single-cell multimodal analysis of chromatin accessibility and gene expression unveils regulatory landscape of pediatric brain tumor
Jinsong Zhang, Yuzhe Li, Yifan Wei, Kaiyu Fan, Zihan Yan, Jian Gong, Qiangfeng C. Zhang
Presenter affiliation: Tsinghua University, Beijing, China. 49

TUESDAY, October 22—3:00 PM

Chinese Tea and Beer Tasting

TUESDAY, October 22—7:00 PM

SESSION 3 GENOTYPES TO PHENOTYPES II

Chairperson: **Tuuli Lappalainen,** Science for Life Laboratory, Sweden, Sweden / New York Genome Center, New York, New York, USA

An artificial intelligence model for embryo selection in preimplantation DNA methylation screening in assisted reproductive technology
Jianhong Zhan, Jiang Liu [20'+10']
Presenter affiliation: Institute of Biophysics, Beijing, China. 50

Diagnosing rare diseases by long-read RNA sequencing
Robert Wang, Feng Wang, Xinjun Ji, Rebecca D. Ganetzky, Andrew C. Edmondson, Lan Lin, Yi Xing [10'+5']
Presenter affiliation: Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; University of Pennsylvania, Philadelphia, Pennsylvania. 51

TUESDAY, October 22—7:45 PM

SESSION 4 SINGLE CELL AND SPATIAL TRANSCRIPTOMIC ANALYSIS I

Chairperson: **Xuegong Zhang,** Tsinghua University, Beijing, China

How and why foundation models work on single-cell transcriptomics?
Xuegong Zhang, Lei Wei [20'+10']
Presenter affiliation: Tsinghua University, Beijing, China. 52

Modeling multisample variation of the spatial transcriptome with POPARI
Shahul Alam, Tianming Zhou, Ellie Haber, Sophia Liu, Fei Chen, Jian Ma [10'+5']
Presenter affiliation: Carnegie Mellon University, Pittsburgh, Pennsylvania. 53

Tokenizing single-cell transcriptomics with codebooks for cellular foundation model
Chuxi Xiao, Haiyang Bian, Lei Wei, Xuegong Zhang [10'+5']
Presenter affiliation: Tsinghua University, Beijing, China. 54

WEDNESDAY, October 23—9:00 AM

SESSION 5 SINGLE CELL AND SPATIAL TRANSCRIPTOMIC ANALYSIS II

Chairperson: **Jingyi Jessica Li,** University of California, Los Angeles, Los Angeles, California, USA

Permutation enhances the rigor of single-cell data analysis
Jingyi Jessica Li [20'+10']
Presenter affiliation: University of California, Los Angeles, Los Angeles, California. 55

Spatial and single cell diversity of cells and humans
Shyam Prabhakar [20'+10']
Presenter affiliation: ASTAR Genome Institute of Singapore, Singapore; Lee Kong Chian School of Medicine, Singapore; Cancer Science Institute of Singapore, Singapore. 56

Multiomics analysis of the tumor microenvironment
Yin Xu, Zurui Huang, Yawei Zhang, Zhenghang Wang, Meng M. Xu, Dali Han [10'+5']
Presenter affiliation: China National Center for Bioinformation, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing, China; University of Chinese Academy of Sciences, Beijing, China. 57

Cell-type specific inference from bulk RNA-sequencing data by integrating single cell reference profiles via EPIC-unmix
Chenwei Tang, Quan Sun, Xinyue Zeng, Xiaoyu Yang, Fei Liu, Jinyin Zhao, Yin Shen, Boxiang Liu, Jia Wen, Yun Li [10'+5']
Presenter affiliation: University of North Carolina at Chapel Hill, Chapel Hill, North Carolina. 58

Break

Machine learning for modeling gene regulatory networks from single-cell sequencing data
Jianyang Zeng [20'+10']
Presenter affiliation: Westlake University, Hangzhou, China. 59

Single-cell multi-omics analysis of aging human brain
Sheng Zhong [20'+10']
Presenter affiliation: University of California San Diego, La Jolla, California. 60

High-resolution, noninvasive single-cell lineage tracing in mice and humans based on DNA methylation epimutations
Shou-Wen Wang [10'+5']
Presenter affiliation: Westlake University, Hang Zhou, China. 61

Geometric quantification of cell phenotype transition manifolds with information geometry
Weikang Wang [10'+5']
Presenter affiliation: Chinese Academy of Sciences, Beijing, China. 62

WEDNESDAY, October 23—2:00 PM

Visit to Old Suzhou

WEDNESDAY, October 23—7:00 PM

SESSION 6 GENOME ORGANIZATION AND EVOLUTION

Chairperson: **Inkyung Jung,** Korea Advanced Institute of Science and Technology, Daejeon, South Korea

MAZ mediates the interplay between the 3D genome and nuclear bodies
Inkyung Jung [20'+10']
Presenter affiliation: Korea Advanced Institute of Science and Technology, Daejeon, South Korea. 63

Genomic upheaval—Evolution through rapid chromosomal rearrangement
Nicholas M. Luscombe, Charles Plessy, Michael Mansfield [20'+10']
Presenter affiliation: Okinawa Institute of Science & Technology (OIST), Okinawa, Japan. 64

Learning multiscale genome and cellular organization
Jian Ma [20'+10']
Presenter affiliation: Carnegie Mellon University, Pittsburgh, Pennsylvania. 65

Lightening the genome structure to understand its biological function
Peng Dong, Zhe Liu [10'+5']
Presenter affiliation: Shenzhen Institute of Advanced Technology, CAS, Shenzhen, China. 66

A generalizable deep learning framework for inferring fine-scale germline mutation rate maps
Yiyuan Fang, Shuyi Deng, Cai Li [10'+5']
Presenter affiliation: Sun Yat-sen University, Guangzhou, China. 67

The structure, evolution, and function of structural variation in primate genomes
Yafei Mao [10'+5']
Presenter affiliation: Shanghai Jiao Tong University, Shanghai, China. 68

SESSION 7 POST-TRANSCRIPTIONAL REGULATION

Chairperson: **Xinshu Grace Xiao,** University of California, Los Angeles, Los Angeles, California, USA

Systematic analysis of RNA splicing—Bridging genetic variation and disease
Xinshu Grace Xiao [20'+10']
Presenter affiliation: University of California, Los Angeles, Los Angeles, California. 69

A deep learning model embedded framework to distinguish RNA editing from DNA mutations in RNA sequencing data
Li Yang [20'+10']
Presenter affiliation: International Laboratory of Medical Epigenetics and Metabolism, Ministry of Science and Technology, Shanghai, China; Fudan University, Shanghai, China. 70

Impact of rare non-coding variants on human diseases through alternative polyadenylation outliers
Xudong Zou, Zhaozhao Zhao, Yu Chen, Kewei Xiong, Zeyang Wang, Wei Li, Ting Ni, Lei Li [10'+5']
Presenter affiliation: Shenzhen Bay Laboratory, Shenzhen, China. 71

SpliceTransformer predicts tissue-specific splicing linked to human diseases
Ningyuan You, Chang Liu, Shanshan Pei, Zhihong Liu, Ning Shen [10'+5']
Presenter affiliation: Zhejiang University, Hangzhou, China. 72

Break

Towards quantitative prediction of alternative splicing from prirmary sequences
Chencheng Xu, Suying Bao, Ye Wang, Wenxing Li, Hao Chen, Yufeng Shen, Tao Jiang, Chaolin Zhang [20'+10']
Presenter affiliation: Columbia University, New York, New York. 73

m6ACali—Machine learning-powered calibration for accurate m6A detection in MeRIP-Seq
Haokai Ye, Tenglong Li, Daniel J. Rigden, Zhen Wei [10'+5']
Presenter affiliation: Xi'an Jiaotong-Liverpool University, Suzhou, China; University of Liverpool, Liverpool, United Kingdom. 74

Deep learning modeling of translation and RBP binding reveals regulatory underpinnings of human genetic diseases
Jialin He, Jianche Liu, Xinlu Zhu, Yang Yin, Lei Xiong, Xushen Xiong [10'+5']
Presenter affiliation: Zhejiang University, Hangzhou, China. 75

THURSDAY, October 24—2:00 PM

SESSION 8 TRANSCRIPTIONAL AND EPIGENETIC GENE REGULATION

Chairperson: **Qiangfeng Cliff Zhang,** Tsinghua University, Beijing, China

Predicting cell fate transitions by estimating transcriptomic velocity field
Yuzhe Li, Jinsong Zhang, Qiangfeng Cliff Zhang [20'+10']
Presenter affiliation: Tsinghua University, Beijing, China. 76

Ethnic-related aging rate modification
Jing-Dong Jackie Han [20'+10']
Presenter affiliation: Peking University, Beijing, China. 77

DNA methylation of polymorphic human transposable elements
Ting Wang [20'+10']
Presenter affiliation: Washington University, St. Louis, Missouri. 78

Reconstructing gene regulatory networks underlying neural crest cell fate decisions using single-cell multi-omics and systematic perturbation
Zhiyuan Hu, Sarah Mayes, Weixu Wang, José M. Santos-Pereira, Fabian Theis, Tatjana Sauka-Spengler [10'+5']
Presenter affiliation: University of Oxford, Oxford, United Kingdom; Wuhan University, Wuhan, China. 79

Spatial enhancer code in control of gene expression
Jialiang Huang [10'+5']
Presenter affiliation: Xiamen University, Xiamen, China. 80

Comparative characterization of human accelerated regions in excitatory neurons
Yin Shen [10'+5']
Presenter affiliation: University of California, San Francisco, San Francisco, California. 81

Integrated computational analysis identifies therapeutic targets with dual action in cancer cells and T cells
Ce Luo, Rui Zhang, Rui Guo, Zexian Zeng [10'+5']
Presenter affiliation: Peking University Chengdu Academy for Advanced Interdisciplinary Biotechnologies, Chengdu, China. 82

THURSDAY, October 24—5:00 PM

COCKTAILS and BANQUET

FRIDAY, October 25—9:00 AM

SESSION 9 FRONTIERS OF ALGORITHMS AND TECHNOLOGIES

Chairperson: **Carlo Cannistraci,** Tsinghua University, Beijing, China

Network shape automata outperforms AlphaFold3 in protein interaction prediction
Carlo V. Cannistraci, Ilyes Abdelhamid [20'+10']
Presenter affiliation: Tsinghua University, Beijing, China. 83

Intelligent analysis of biomolecular phase separation and its applications
Tingting Li [20'+10']
Presenter affiliation: Peking University, Beijing, China. 84

A multi-modal deep language model for contaminant removal from metagenome-assembled genomes
Bohao Zou, Jingjing Wang, Yi Ding, Zhenmiao Zhang, Yufen Huang, Xiaodong Fang, Ka Chun Cheung, Simon See, Lu Zhang [10'+5']
Presenter affiliation: Hong Kong Baptist University, Hong Kong, China. 85

Quantitative detection of DNA methylation from Nanopore sequencing data without raw signals
Zhixing Feng [10'+5']
Presenter affiliation: Xinhua Hospital affiliated to Shanghai Jiao Tong University School of Medicine, Shanghai, China. 86

Break

Generative AI empowered design of synthetic gene regulatory elements
Xiaowo Wang [20'+10']
Presenter affiliation: Tsinghua University, Beijing, China. 87

Accurate multiple sequence alignment of massive genome sets
Xiao Lai, Haixin Luan, Pu Tian [10'+5']
Presenter affiliation: Jilin University, Changchun, China. 88

Endogenous labeling empowers accurate detection of m^6A from single long reads of direct RNA sequencing
Wenbing Guo, Zhijun Ren, Xiang Huang, Jialiang He, Jie Zhang, Zehong Wu, Yang Guo, Zijun Zhang, Yixian Cun, Jinkai Wang [10'+5']
Presenter affiliation: Sun Yat-sen University, Guangzhou, China. 89