

PROGRAM

MONDAY, November 5—7:00 PM

SESSION 1 KEYNOTE SESSION

Chairperson: **Fuchou Tang**, Peking University, Beijing, China

KEYNOTE SPEAKER

Single cell genomics—When stochasticity meets precision

Xiaoliang Sunney Xie [35'+10']

Peking University, Beijing, China.

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Orit Rozenblatt-Rosen [20'+10']

Presenter affiliation: Broad Institute, Cambridge, Massachusetts.

Single-cell transcriptomic analyses reveal distinct dorsal/ventral pancreatic programs

Lin-Chen Li, Wei-Lin Qiu, Yu-Wei Zhang, Zi-Ran Xu, Yi-Ni Xiao, Caiying Hou, Linao Qiezhong, Peng Yu, Xin Cheng, Cheng-Ran Xu [10'+5']

Presenter affiliation: Peking University, Beijing, China.

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TUESDAY, November 6—9:00 AM

SESSION 2 APPLICATIONS FOR DEVELOPMENTAL BIOLOGY

Chairperson: **Gavin Kelsey**, The Babraham Institute, Cambridge, United Kingdom

Cellular heterogeneity in adult human skin

Fiona M. Watt [20'+10']

Presenter affiliation: King's College London, London, United Kingdom.

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Single-cell sequencing reveals genetic and dietary influences on the oocyte epigenome

Antonio Galvao, Hannah Demond, Erika Herrera-Puerta, Stephen J. Clark, Zahra Anvar, Gavin Kelsey [20'+10']

Presenter affiliation: The Babraham Institute, Cambridge, United Kingdom; University of Cambridge, Cambridge, United Kingdom.

4

Mapping the mouse cell atlas by Microwell-seq

Guoji Guo [20'+10']

Presenter affiliation: Center for Stem Cell and Regenerative Medicine, Hangzhou, China.

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Single-cell RNA sequencing analysis reveals sequential cell fate transition during human spermatogenesis

Yidong Chen, Xixi Liu, Jie Qiao, Fuchou Tang [20'+10']

Presenter affiliation: Peking University, Beijing, China.

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A single-cell analysis of mouse vascular cells

Dongxu He, Aiqing Mao, Hao Kan, Ka Zhang, Zhiming Zhang, Lei Feng, Xin Ma [10'+5']

Presenter affiliation: Jiangnan University, Wuxi, China.

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Single cell RNA-seq and biology of oocyte maturation and early embryo development in pigs

Cai-Xia Yang [10'+5']

Presenter affiliation: Northeast Agricultural University, Harbin, China.

8

Molecular regulation and adapted differentiation trajectories in hematopoietic stem and progenitor cells after irradiation and sepsis

Xi Wang, Ann-Kathrin Schuon, Qin Zhang, Alessandro Greco, Katrin Busch, Hans-Reimer Rodewald, Thomas Höfer [10'+5']

Presenter affiliation: German Cancer Research Center, Heidelberg, Germany; University of Heidelberg, Heidelberg, Germany.

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Defining a lineage roadmap for endocrine and exocrine pancreatic development at single-cell resolution

Xin-Xin Yu, Wei-Lin Qiu, Liu Yang, Yu Zhang, Cheng-Ran Xu [10'+5']

Presenter affiliation: Peking University, Beijing, China.

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SESSION 3 POSTER SESSION

- Tagmentation on microbeads—Restore long-range DNA sequence information using surface-immobilized transposomes**
He Chen, Jiacheng Yao, Yusi Fu, Yuhong Pang, Jiangbin Wang, Yanyi Huang
Presenter affiliation: Peking University, Beijing, China. 11
- Single molecule fluorescence in situ hybridization (smFISH) analysis in budding yeast vegetative growth and meiosis**
Jingxun Chen, David McSwiggen, Elçin Ünal
Presenter affiliation: UC Berkeley, Berkeley, California. 12
- Single-molecule single-cell sequencing identifies ongoing copy number evolution and clonal origins in hereditary breast cancers**
Darlan Conterno Minussi, Alexander Davis, Cheng Peng, Haowei Du, Kaile Wang, Emi Sei, Min Hu, Shanshan Bai, Banu Arun, Angelica Barrera, Nicholas Navin
Presenter affiliation: The University of Texas MD Anderson Cancer Center, Houston, Texas. 13
- Single-cell RNA-seq reveals distinct endothelial EndMT subpopulations in cerebral cavernous malformation**
Lei L. Conze, Sara I. Cunha, Johan Brännström, Petra Magnusson, Elisabetta Dejana
Presenter affiliation: Uppsala University, Uppsala, Sweden. 14
- Single cell transcriptome analysis of pituitary adenomas**
Yueli Cui, Shu Zhang, Chao Li, Dabiao Zhou, Fuchou Tang
Presenter affiliation: College of Life Sciences, Peking University, Beijing, China. 15
- Determinants of the accuracy of integer copy number inference from single cell genome sequencing data**
Alexander Davis, Nicholas Navin
Presenter affiliation: The University of Texas MD Anderson Cancer Center, Houston, Texas. 16

Single-cell RNA-seq analysis unveils a prevalent epithelial/mesenchymal hybrid state during mouse organogenesis	
<u>Ji Dong</u> , Yuqiong Hu, Xiaoying Fan, Xinglong Wu, Fuchou Tang Presenter affiliation: Peking University, Beijing, China.	17
Regional different regulations in development of human cortex revealed by single cell transcriptome analysis	
<u>Xiaoying Fan</u> , Shu Zhang, Yuanyuan Fu Presenter affiliation: Peking University, Beijing, China.	18
Automated single-cell isolation and dispensing technology for rare cell samples	
Guilhem Tourniaire, Arielle L. Greenfield, Joshua Cantlon, Ophelie I. Berthuy, Eric Cheng, <u>Alessandra Fischetti</u> , Derek B. Bogdanoff, Erica L. Eggers, Michael R. Wilson Presenter affiliation: SCIENION Inc., Monmouth Junction, New Jersey.	19
High-throughput single-cell whole-genome amplification through centrifugal emulsification and eMDA	
<u>Yusi Fu</u> , Fangli Zhang, Xiannian Zhang, Junlong Zhang, Meijie Du, Mengcheng Jiang, Lu Liu, Jie Li, Yanyi Huang, Jianbin Wang Presenter affiliation: School of Life Sciences, Peking University, Beijing, China.	20
Cell fate determining molecular switches and signaling pathway in Pax7-expressing somitic mesoderm	
<u>Cheuk Wang Fung</u> , Han Zhu, Shaopu Zhou, Angela R. Wu, Zhenguo Wu Presenter affiliation: Hong Kong University of Science and Technology, Hong Kong.	21
Single-cell multi-omics sequencing of human early embryos	
Lin Li, Fan Guo, <u>Yun Gao</u> , Yixin Ren, Fuchou Tang, Jie Qiao Presenter affiliation: Peking University, Beijing, China, China.	22
Single-cell chromatin accessibility landscapes of growing mouse oocytes	
<u>Chan Gu</u> , Fan Guo Presenter affiliation: Sichuan University, Chengdu, China.	23

A highly sensitive and reliable transcriptome profiling method for single-cell or low input RNA

Yanxia Bei, Keerthana Krishnan, Janine Borgaro, Timur Shtatland, Brad Langhorst, Tom Evans, Eileen Dimalanta, Nicole Nichols, Shengxi Guan

Presenter affiliation: New England Biolabs, Ipswich, Massachusetts. 24

The adult human testis transcriptional cell atlas

Jingtao Guo, Edward J. Grow, James M. Hotaling, Bradley R. Cairns
Presenter affiliation: Howard Hughes Medical Institute, University of Utah School of Medicine, Salt Lake City, Utah; University of Utah Health Sciences Center, Salt Lake City, Utah. 25

Higher evolutionary constraints in neurons revealed by single cell transcriptomics

Ganlu Hu

Presenter affiliation: CAS-MPG Partner Institute for Computational Biology, Shanghai, China. 26

Dissecting the transcriptome landscape of the human fetal neural retina and retinal pigment epithelium by single-cell RNA-seq analysis

Yuqiong Hu, Xiaoye Wang, Boqiang Hu, Yunuo Mao, Yidong Chen, Jie Qiao, Fuchou Tang

Presenter affiliation: College of Life Sciences, Peking University, Third Hospital, Beijing, China. 27

Single-cell analysis reveals reprogramming of the cancer and associated microenvironment during lung adenocarcinoma progression

Nayoung Kim, Yourae Hong, Woong-Yang Park, Myung-Ju Ahn, Hae-Ock Lee

Presenter affiliation: Samsung Medical Center, Seoul, South Korea; Sungkyunkwan University School of Medicine, Suwon, South Korea. 28

Towards a human breast cell atlas of normal cell types

Tapsi Kumar, Shanshan Bai, Kaile Wang, Min Hu, Emi Sei, Anita Wood, Jie Wiley, Hui Chen, Alejandro Contreras, Mediget Teshome, Ken Chen, Kai Kessenbrock, Devon Lawson, Bora Lim, Nicholas E. Navin

Presenter affiliation: The University of Texas MD Anderson Cancer Center, Houston, Texas. 29

Wnt signalling as therapeutic target for overcoming taxane resistance in breast cancer	
<u>Kee Wah Lee</u> , Muhammad Sufyan bin Masroni, Karen Meiling Tan, Mo-Huang Li, Lihan Zhou, Steven Tucker, Lynette Su Mien Ngo, Chan Fong Chang, Boon Huat Bay, Soo Yong Tan, Mikael Hartman, Victor Kwan Min Lee, Huiwen Chua, Tze Ping Loh, Sai Mun Leong, Evelyn Siew-Chuan Koay	
Presenter affiliation: National University of Singapore, Singapore.	30
APEC—Accession based method for single cell chromatin accessibility analysis	
<u>Bin Li</u> , Yang Li, Qiaoni Yu, Kun Li, Kun Qu	
Presenter affiliation: University of Science and Technology of China, Hefei, China.	31
A hand-held microfluidic device for single cell RNA-Seq	
I-Jane Chen, Tao Wu, Michael Junkin, Lei Wang, <u>Guibo Li</u>	
Presenter affiliation: BGI-Shenzhen, Shenzhen, China; China National GeneBank, Shenzhen, China.	32
Single cell RNA sequencing of Pax7 muscle stem cells defines their heterogeneity mediated by aging- and metabolic niche in mice	
<u>Hu Li</u> , Qian Chen, Changyin Li, Ran Zhong, Yixia Zhao, Dahai Zhu, Yong Zhang	
Presenter affiliation: Chinese Academy of Medical Sciences and School of Basic Medicine, Beijing, China.	33
Tracing the temporal-spatial transcriptome landscapes of the human fetal digestive tract using single-cell RNA-sequencing	
Shuai gao, Rui Wang, <u>Jingyun Li</u> , Fuchou Tang	
Presenter affiliation: Peking university, Beijing, China.	34
Dissecting the epigenomic dynamics of human fetal germ cell development at single-cell resolution	
<u>Li Li</u> , Lin Li, Qingqing Li, Xixi Liu, Xinyi Ma, Jun Yong, Shuai Gao, Xinglong Wu, Jie Qiao, Liying Yan, Fuchou Tang	
Presenter affiliation: College of Life Sciences, Peking University, Beijing, China.	35
Single-cell transcriptomic analyses reveal distinct dorsal/ventral pancreatic programs	
<u>Lin-Chen Li</u> , Wei-Lin Qiu, Yu-Wei Zhang, Zi-Ran Xu, Yi-Ni Xiao, Caiying Hou, Lamao Qiezhong, Peng Yu, Xin Cheng, Cheng-Ran Xu	
Presenter affiliation: Peking University, Beijing, China.	36

- Comprehensive transcriptomic profiles of non-small cell lung cancer by single-cell RNA-seq**
Qingqing Li, Rui Wang, Zhenlin Yang, Lu Wen, Jie Wang, Fuchou Tang
 Presenter affiliation: Biomedical Pioneering Innovation Center, Beijing, China. 37
- Network embedding-based representation learning for single cell RNA-seq data**
Xiangyu Li, Weizheng Chen, Yang Chen, Xuegong Zhang, Jin Gu, Michael Q. Zhang
 Presenter affiliation: Tsinghua University, Beijing, China. 38
- Comprehensive molecular profiling of B cells at single cell resolution enables the diagnosis of ocular malignancie**
 Wei Jian Tan, Mona Wang Meng, Paola Ricciardi-Castagnoli, Anita Chan Sook Yee, Tong Seng Lim
 Presenter affiliation: A. Menarini Biomarkers Singapore Pte Ltd, Singapore. 39
- Inferring cellular metabolic activities during the cell cycle using scRNA-seq data**
Haiyue Liu, Daniel Schwabe, Sara Formichetti, Martin Falcke, Nikolaus Rajewsky
 Presenter affiliation: Max-Delbrück Center for Molecular Medicine, Berlin, Germany. 40
- Genome-scale DNA methylation method for investigating non-hematopoietic tissue-of-origin of plasma cfDNA**
Xiaomeng Liu, Jie Ren, Nan Luo, Yuhan Liao, Fuchou Tang, Jirun Peng, Lu Wen
 Presenter affiliation: Peking University, Beijing, China; University of Electronic Science and Technology of China, Chengdu, China. 41
- Development of a single cell adhesion assay using capillary based cell and tissue acquisition system**
Zhongcai Ma, David Ma, Lili C. Kudo, Stanislav L. Karsten
 Presenter affiliation: NeuroInDx, Inc., Torrance, California. 42
- Projection of colorectal cancer progression by single cell RNA sequencing**
Jae-Woong Min, Hae-Ock Lee, Yourae Hong, Nayoung Kim, Hye Hyeon Eum, Woosung Chung, Woong-Yang Park
 Presenter affiliation: Samsung Genome Institute, Seoul, South Korea. 43

- A sub-group of neutrophils causing organ damage in sepsis mouse model**
Hengxiao Ni
 Presenter affiliation: Xiamen University, Xiamen, China. 44
- Functional heterogeneity using single cell lineage tracing towards a phenotype-genotype map of chemo-resistance in pancreatic cancer**
Sahil Seth, Chieh-Yuan Li, I-Lin Ho, Denise Corti, Andrew Futreal, Giulio Draetta, Alessandro Carugo, Andrea Viale
 Presenter affiliation: MD Anderson Cancer Center, Houston, Texas. 45
- Single-cell RNA-Seq analysis reveals transcriptomic features of a rare prostate basal cell carcinoma**
Xianbin Su, Guoliang Yang, Jian-Jun Sha, Ze-Guang Han
 Presenter affiliation: Shanghai Jiao Tong University, Shanghai, China. 46
- Integrated single-cell exome sequencing of synchronous liver-limited metastatic colorectal cancer reveals distinct tumor evolution and heterogeneity**
Jie Tang, Haoxuan Jin, Heran Wang, Keying Lu, Lei Wang, Xiaoling Liu, Shichen Dong, Lie Yang, Zongguang Zhou, Guibo Li, Dan Xie
 Presenter affiliation: West China Hospital, Sichuan University, Cheng Du, China. 47
- A favorable clinical outcome to influenza infection in neonates is linked to reprogramming of monocytes towards a less inflammatory phenotype with metabolic shift**
Thomas Ulas, Anna M. Heinemann, Sabine Pirr, Joachim L. Schultze, Dorothee Viemann
 Presenter affiliation: LIMES, Bonn, Germany. 48
- FASTGenomics—An analytical ecosystem for single-cell RNA sequencing data**
Thomas Ulas, Claus J. Scholz, Stefanie Herresthal, Kathrin Heikamp, Christina Kratsch, Joachim L. Schultze
 Presenter affiliation: LIMES, Bonn, Germany; PRECISE, Bonn, Germany. 49
- Heterogeneity of malignant and tumor infiltrated cells from diffuse large B cell lymphoma revealed by single cell RNA sequencing**
Lei Wang, Xiaofei Ye, Yongtian Zhao, Man Nie, Shichen Dong, Cuijuan Zhang, Guibo Li, Zhiming Li, Kui Wu, Qiang Pan-Hammarström
 Presenter affiliation: BGI-Shenzhen, Shenzhen, China; China National GeneBank, Shenzhen, China. 50

Stepwise cellular remodeling along cardiac hypertrophy revealed by single-cell RNA sequencing

Zongna Ren, Peng Yu, Dandan Li, Zheng Li, Yingnan Liao, Yin Wang, Bingying Zhou, Li Wang

Presenter affiliation: Fuwai Hospital, National Center for Cardiovascular Diseases, CAMS and PUMC, Beijing, China.

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Dissecting the global dynamic molecular profiles of human fetal kidney development by single-cell RNA sequencing

Ping Wang, Yidong Chen, Jun Yong, Yueli Cui, Rui Wang, Ping Lu, Lu Wen, Jie Qiao, Fuchou Tang

Presenter affiliation: Peking University, Beijing, China.

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High-throughput single-cell CNV detection reveals tumor clonal subtypes in hepatocellular carcinoma

Yuzhou Wang, Miaomiao Jiang, Zhikun Zhao, Liang Wu, Shiping Liu

Presenter affiliation: BGI-Shenzhen, Shenzhen, China.

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Multi-omics analysis for the elucidation of tumor heterogeneity by simultaneous analysis of genome and transcriptome in individual single cells

Jeongmin Woo, Taeseob Lee, Kyung Yeon Han, Daeun You, Yisun Jung, Hee Jun Choi, Sangmin Kim, Jeong Eon Lee, Jinho Kim, Donghyun Park

Presenter affiliation: Sungkyunkwan University, Seoul, South Korea; Samsung Medical Center, Seoul, South Korea.

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A local alignment strategy increases data efficiency with precise DNA methylation estimation in analyzing single-cell bisulfite sequencing data

Peng Wu, Ping Zhu

Presenter affiliation: Chinese Academy of Medical Sciences, Institute of Hematology and Blood Disease Hospital, Tianjin, China.

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Holo-Seq—Single-cell sequencing of holo-transcriptome

Zhengyun Xiao, Guo Cheng, Yang Jiao, Chen Pan, Ran Li, Danmei Jia, Jing Zhu, Chao Wu, Min Zheng, Junling Jia

Presenter affiliation: Zhejiang University, Hangzhou, China.

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Single-cell transcriptomic landscape of nucleated cells in umbilical cord blood

Yi Zhao, Xiao Li, Weihua Zhao, Jingwan Wang, Ziyun Wan, Shiping Liu, Xie Wang, Yong Hou, Xiao Liu

Presenter affiliation: BGI-Shenzhen, Shenzhen, China; South China University of Technology, Guangzhou, China.

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Exploring T cell heterogeneity in human peripheral blood with massively parallel single cell multimodal data <u>Shiwei Zheng</u> , Marlon Stoeckius, Stephanie Hao, Eleni Mimitou, Peter Smibert, Rahul Satija Presenter affiliation: New York Genome Center, New York, New York; New York University, New York, New York.	58
The placenta is a site for definitive HSC emergence <u>Chunyu Zhou</u> Presenter affiliation: Chinese Academy of Sciences, Shanghai, China.	59
The transcriptome landscape of human early post-implantation embryos <u>Fan Zhou</u> , Rui Wang, Peng Yuan, Yixin Ren, Yunuo Mao, Rong Li, Ying Lian, Junsheng Li, Lu Wen, Liying Yan, Jie Qiao, Fuchou Tang Presenter affiliation: Third Hospital, College of Life Sciences, Peking University, Beijing, China.	60
A local alignment strategy increases data efficiency with precise DNA methylation estimation in analyzing single-cell bisulfite sequencing data Peng Wu, <u>Ping Zhu</u> Presenter affiliation: Chinese Academy of Medical Sciences, Institute of Hematology and Blood Disease Hospital, Tianjin, China.	61
Immune landscape of triple-negative breast cancer revealed by single-cell sequencing Si Qiu, Ruoxi Hong, <u>Zhenkun Zhuang</u> , Linnan Zhu, Yuan Li, Shang Liu Presenter affiliation: BGI Genomics, Shenzhen, China.	62
Two novel statistical algorithms for single-cell RNA-seq data analyses <u>Xin Zou</u> , Jie Hao, Ze-Guang Han Presenter affiliation: Shanghai Jiao Tong University, Shanghai, China.	63

TUESDAY, November 6—4:30 PM

Chinese Tea and Beer Tasting

SESSION 4 APPLICATIONS FOR NEUROBIOLOGY AND OTHER
FIELDS

Chairperson: **Zemin Zhang**, Peking University, Beijing, China

**Comparative analysis of tumor-infiltrating T cells across multiple
tumor indications**

Liangtao Zheng, Yuanyuan Zhang, Lei Zhang, Zemin Zhang [20'+10']
Presenter affiliation: Peking University, Beijing, China. 64

Towards building single-cell multi-omics maps for human organs

Kun Zhang [20'+10']
Presenter affiliation: UCSD, La Jolla, California. 65

Zorina Galis [20'+10']

Presenter affiliation: National Institutes of Health, Bethesda, Maryland.

Xiaoqun Wang [10'+5']

Presenter affiliation: Institute of Biophysics, CAS, Beijing, China.

**Single-cell RNA-seq analysis identifies markers of resistance to
targeted BRAF inhibitors in melanoma cell populations**

Yu-Jui Ho, Naishitha Anaparthi, David Molik, Grinu Mathew, Toby
Aicher, Ami Patel, James Hicks, Molly G. Hammell [10'+5']
Presenter affiliation: Cold Spring Harbor Laboratory, Cold Spring
Harbor, New York. 66

**The *Hand2as* locus precisely controls the spatial expression of
HAND2 and heart lineage development**

Xue Han, Jiejie Zhang, Yaxi Liu, Xiaoying Fan, Shanshan Ai, Yingjie
Luo, Sai Luo, Hui Zheng, Yanzhu Yue, Zai Chang, Fuchou Tang,
Zhongzhou Yang, Aibin He, Xiaohua Shen [10'+5']
Presenter affiliation: Tsinghua University, Beijing, China. 67

SESSION 5 NEW TECHNOLOGIES I

Chairperson: **Jianbin Wang**, Tsinghua University, Beijing, China

Single-cell multi-omics to study DNA mutation, genetic heterogeneity and disease

Thierry Voet [20'+10']

Presenter affiliation: University of Leuven, KU Leuven, Leuven, Belgium; Wellcome Sanger Institute, Hinxton, United Kingdom. 68

Single-cell epigenomics using combinatorial indexing

Andrew C. Adey, Ryan M. Mulqueen, Kristof A. Torkenczy [20'+10']

Presenter affiliation: Oregon Health & Science University, Portland, Oregon. 69

Long Cai [20'+10']

Presenter affiliation: California Institute of Technology, Pasadena, California.

Standardized oligo barcode antibody conjugates for highly-multiplexed immunophenotyping by single-cell sequencing

Bertrand Z. Yeung, Michael C. Li, Kristopher Nazor, Xifeng Yang [20'+10']

Presenter affiliation: BioLegend Inc, San Diego, California. 70

Comparative analysis of droplet-based ultra-high-throughput single-cell RNA-seq systems

Jianbin Wang [10'+5']

Presenter affiliation: Tsinghua University, Beijing, China. 71

Microfluidics for imaging and sequencing single cells

Aaron Streets, Nicolas Altemose [10'+5']

Presenter affiliation: University of California Berkeley, Berkeley, California; Chan-Zuckerberg Biohub, San Francisco, California. 72

Single-cell chromatin accessibility landscapes of mammalian germ cells and early embryos

Fan Guo [10'+5']

Presenter affiliation: Sichuan University, Chengdu. 73

High throughput immune profiling using integrated single cell multi-omics analyses

Anjana S. Narayanan, Darisha Jhutti, Yifeng Yin, Solongo Ziraldo, Jerald Sapida, Julia Lau, Luz Montesclares, Geoffrey McDermott, Francesca Meschi, John Chevillet, Corey Nemec, Jean Wang, Paul Giresi, Brett Olsen, Preyas Shah, Li Wang, Alvaro Gonzalez, Grace Zheng [20'+10']

Presenter affiliation: 10X Genomics, Inc., Pleasanton, California.

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WEDNESDAY, November 7—1:30 PM

Visit to Old Suzhou

WEDNESDAY, November 7—7:00 PM

SESSION 6 NEW TECHNOLOGIES II

Chairperson: **Orit Rozenblatt-Rozen**, Broad Institute, Cambridge, Massachusetts, USA

KEYNOTE SPEAKER

Stephen Quake [35'+10']
Stanford University, Stanford, California

High-throughput single-cell whole-genome amplification through centrifugal emulsification and MDA

Yanyi Huang [20'+10']

Presenter affiliation: Peking University, Beijing, China.

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Detection of metabolically active tumor cells in pleural effusion and peripheral blood of lung cancer patients

Qihui Shi, Ziming Li, Yin Tang, Zhuo Wang, Wei Wei, Shun Lu [10'+5']

Presenter affiliation: Fudan University, Shanghai, China.

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A single-cell resolution spatial and temporal roadmap of gastrula mouse embryo

Ran Wang, Jonathan Griffiths, Liantang Wang, Guizhong Cui, Guangdun Peng, John Marioni, Naihe Jing [10'+5']
Presenter affiliation: Shanghai Institute of Biochemistry and Cell Biology, Shanghai, China; Cancer Research UK Cambridge Institute, Cambridge, United Kingdom; EMBL-European Bioinformatics Institute (EMBL-EBI), Cambridge, United Kingdom.

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Diverse modes of clonal evolution in HBV-related hepatocellular carcinoma revealed by single-cell genome sequencing

Qiang Gao, Jia Fan [10'+5']
Presenter affiliation: Liver Cancer Institute, Zhongshan Hos., Fudan University, Shanghai, China.

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THURSDAY, November 8—9:00 AM

SESSION 7 COMPUTATIONAL METHODS

Chairperson: John Marioni, EMBL-EBI, Hinxton, United Kingdom

Using single-cell RNA-sequencing to provide insight into cell fate

John Marioni [20'+10']
Presenter affiliation: University of Cambridge, Cambridge, United Kingdom; European Molecular Biology Laboratory, European Bioinformatics Institute (EMBL-EBI), Hinxton, United Kingdom; Wellcome Trust Sanger Institute, Hinxton, United Kingdom.

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Comprehensive integration of single cell data

Rahul Satija [20'+10']
Presenter affiliation: New York Genome Center, New York, New York.

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Single-cell transcriptomics—Applying new methods to lung and colorectal cancer

Shyam Prabhakar [20'+10']
Presenter affiliation: Genome Institute of Singapore, Singapore.

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Exploring the analysis landscape of single-cell RNA-seq

Alicia Oshlack [20'+10']
Presenter affiliation: Murdoch Children's Research Institute, Parkville, Australia.

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Identification of cancer stem cells from single-cell RNA-Seq data
Andrew E. Teschendorff, Weiyang Chen, Tariq Enver [10'+5']
Presenter affiliation: SIBS, Shanghai, China; UCL, London, United Kingdom. 83

Starfish—Developing a computational platform for image-based transcriptomics and proteomics
Shannon Axelrod, Ambrose J. Carr, Jeremy Freeman, Deep Ganguli, Brian Long, Tony Tung, The SpaceTx Consortium [10'+5']
Presenter affiliation: The Chan Zuckerberg Initiative, San Francisco, California. 84

Single cell DNA methylation landscapes of human early embryos and bioinformatics strategies for data analysis and visualization
Ping Zhu, Hongshan Guo, Yu Hou, Weilong Guo, Peng Wu, Liying Yan, Jie Qiao, Fuchou Tang [10'+5']
Presenter affiliation: Institute of Hematology and Blood Disease Hospital, Tianjin, China. 85

bayNorm—Bayesian gene expression recovery, imputation and normalisation for single cell RNA-sequencing data
Wenhao Tang, François Bertaux, Philipp Thomas, Claire Stefanelli, Malika Saint, Samuel Marguerat, Vahid Shahrezaei [10'+5']
Presenter affiliation: Imperial College London, London, United Kingdom. 86

THURSDAY, November 8—2:00 PM

SESSION 8 APPLICATIONS FOR IMMUNITY AND OTHER FIELDS

Chairperson: **Haeock Lee**, Sungkyunkwan University School of Medicine, Seoul, Korea

Tracking the tumor microenvironment during lung adenocarcinoma progression
Nayoung Kim, Yourae Hong, Woong-Yang Park, Myung-Ju Ahn, Hae-Ock Lee [20'+10']
Presenter affiliation: Samsung Medical Center, Sungkyunkwan University School of Medicine, Seoul, South Korea. 87

- Learning and annotating single cell manifolds—Methods, software and an application to studying autoimmunity**
 Romain Lopez, Jeffrey Regier, Michael Cole, David Detomaso, Matthew Jones, Meena Subramaniam, Chenling Xu, Jimmie Ye, Michael Jordan, Nir Yosef [20'+10']
 Presenter affiliation: University of California Berkeley, Berkeley, California. 88
- Comprehensive single-cell landscape of colon cancer**
Woong-Yang Park, Hae-Ock Lee, Jae-Woong Min [20'+10']
 Presenter affiliation: Samsung Medical Center, Seoul, South Korea. 89
- Chromatin mapping and single-cell immune profiling define the temporal dynamics of ibrutinib drug response in chronic lymphocytic leukemia**
Andre F. Rendeiro, Thomas Krausgruber, Nikolaus Fortelny, Fangwen Zhao, Thomas Penz, Matthias Farlik, Linda C. Schuster, Amelie Nemic, Szabolcs Tasnády, Marienn Réti, Zoltan Matrai, Donat Alpar, Csaba Bodor, Christian Schmidl, Christoph Bock [10'+5']
 Presenter affiliation: CeMM Research Center for Molecular Medicine of the Austrian Academy of Sciences, Vienna, Austria. 90
- Transcriptional analysis of cardiac differentiation from human pluripotent stem cells at single cell resolution**
 Clayton Friedman, Quan Nguyen, Joseph Powell, Nathan Palpant [10'+5']
 Presenter affiliation: The University of Queensland, Brisbane, Australia. 91
- Mapping the human immune landscape in the alveolar space of healthy donors and COPD patients**
Kevin Bassler, Wataru Fujii, Theodoros Kapellos, Dirk Skowasch, Joachim L. Schultze [10'+5']
 Presenter affiliation: Life and Medical Sciences (LIMES) Institute, Bonn, Germany. 92
- Chromatin accessibility and single-cell transcriptome analysis reveal novel regulatory CD4⁺ T cell subsets in systemic lupus erythematosus patients**
 Chuang Guo, Qian Liu, Dandan Zong, Zuqi Zuo, Qiaoni Yu, Pengcheng Du, Qing Sha, Quan Wu, Jinhui Tao, Xiaomei Li, Kun Qu [10'+5']
 Presenter affiliation: School of Life Sciences, University of Science and Technology of China, Hefei, China. 93

Single cell transcriptome analysis and function genomics in β cell biology

Zhou Fang, Chen Weng, Haiyan Li, Jiajia Xi, Peter Arvan, Yun Li, Yanxin Pei, Fulai Jin, Yan Li [10'+5']

Presenter affiliation: Case Western Reserve University, Cleveland, Ohio.

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Deciphering modulation of cellular identity in human pancreatic islets using single-cell sequencing

Brenda Marquina Sanchez, Nikolaus Fortelny, Matthias Farlik, Stefan Kubicek [10'+5']

Presenter affiliation: CeMM, Vienna, Austria.

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Cell fate determination in the human placenta

Hongmei Wang [10'+5']

Presenter affiliation: Institute of Zoology, Chinese Academy of Sciences, Beijing, China.

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THURSDAY, November 8—6:00 PM

COCKTAILS and BANQUET

FRIDAY, November 9—9:00 AM

SESSION 9 APPLICATIONS FOR CANCER

Chairperson: **Fan Bai**, Peking University, Beijing, China

Delineating clonal evolution in breast cancer with single cell genomics

Ruli Gao, Nick Navin [20'+10']

Presenter affiliation: UT MD Anderson Cancer Center, Houston, Texas.

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Single-cell RNA sequencing in pathogenic bacteria and virus infection

Fan Bai [20'+10']

Presenter affiliation: Peking University, Beijing, China.

Accurate genomic variant detection in single cells with primary template-directed amplification	
Veronica Gonzalez, Sivaraman Natarajan, Robert Carter, Kavya Annu, Xiang Chen, John Easton, <u>Charles Gawad</u> [20'+10']	
Presenter affiliation: St. Jude Children's Research Hospital, Memphis, Tennessee..	98
Breast cancer metastasis in single cell resolution	
Ryan T. Davis, Kerrigan Blake, Dustin Maurer, Eric Mjolsness, zena Werb, <u>Devon A. Lawson</u> [20'+10']	
Presenter affiliation: University of California, Irvine, Irvine, California.	99
The operation of Muller's ratchet in cancer cell populations	
<u>Xuemei Lu</u> [10'+5']	
Presenter affiliation: Beijing Institute of Genomics, Beijing, China; Kunming Institute of Zoology, Kunming, China.	100
Diverse clonal hematopoiesis in childhood cancer survivors revealed by single-cell genome sequencing	
<u>Robert Carter</u> , Sivaraman Natarajan, Veronica Gonzalez, Les Robison, Charles Gawad [10'+5']	
Presenter affiliation: St. Jude Children's Research Hospital, Memphis, Tennessee.	101