

Programme | NSFC/RGC Workshop on Single-Cell Data Science

Website: <https://singlecell2022.hku.hk/>

Wednesday, 1 June 2022 (HKT)

09:05 - 09:10	Welcome
09:10 - 09:50	Keynote Speaker 1 - chaired by Dr. Joshua Ho Large scale single-cell multi-sample multi-condition data integration <i>Prof Jean Yang, University of Sydney</i>
09:50 - 10:30	Session 1: Large-scale Approaches - chaired by Dr. Yuanhua Huang A comparison of computational methods for selecting marker genes in single-cell RNA sequencing data <i>Dr Daivs McCarthy, University of Melbourne</i>
10:10 - 10:30	hECA: Human Ensemble Cell Atlas as a Virtual Body for "In Data" Cellular Experiments <i>Prof Xuegong Zhang, Tsinghua University</i>
10:40 - 12:00	Session 2: Statistical Modelling - chaired by Dr. Zhixiang Lin
10:40 - 11:00	Differential Inference for Single-cell RNA-sequencing Data <i>Dr Yingying Wei, CUHK</i>
11:00 - 11:20	Cell clustering for spatial transcriptomics data with graph neural network <i>Dr Ye Yuan, Shanghai Jiaotong University</i>
11:20 - 11:40	The Graphical R2D2 Estimator for the Biological Networks <i>Dr Dora Zhang, HKU</i>
11:40 - 12:00 (flash talks)	(1) Sample demultiplexing, multiplet detection, cell-type classification and verification in large-scale single cell sequencing <i>Dr Lian Qiuyu</i> (2) FlowGrid: A python package for fast clustering for millions of single cell transcriptomic profiles <i>Ms Fang Xiunan</i> (3) UniTelo: temporally unified RNA velocity reinforces single-cell trajectory inference <i>Mr Gao Mingze</i> (4) Differential composition analysis of single-cell data <i>Ms Lin Xinyi</i>
14:00 - 15:20	Session 3: Omics Technology - chaired by Dr. Wenfei Jin
14:00 - 14:20	Measuring Protein-DNA Interaction for Decoding Epigenome in Single Cells <i>Prof Aibin He, Peking University</i>
14:20 - 14:40	scONE-seq: A one-tube single-cell multi-omics method enables simultaneous dissection of molecular phenotype and genotype heterogeneity from frozen tumors <i>Prof Angela Wu, HKUST</i>
14:40 - 15:00	ISSAAC-seq enables sensitive and flexible multimodal profiling of chromatin accessibility and gene expression in single cells <i>Dr Xi Chen, SUSTech</i>
15:00 - 15:20	Inferring genetic models from cell landscapes <i>Dr Guoji Guo, Zhejiang University</i>

15:30 - 17:30	Session 4: Atlas & Development - chaired by Dr. Xi Chen
15:30 - 15:50	Cellular and microbial niches of the human intestinal tract <i>Prof Kylie James, Garvan Institute</i>
15:50 - 16:10	A human embryonic limb cell atlas resolved in space and time <i>Prof Hongbo Zhang, Sun-Yatsen University</i>
16:10 - 16:30	Integrative Spatial Transcriptome Analysis for Embryo Development <i>Dr Guangdun Peng, GIBH, CAS</i>
16:30 - 16:50	From one to many: the making of multi-ciliated cells <i>Dr Mu He, HKU</i>
16:50 - 17:10	Cells of the developing human lung <i>Dr Peng He, EMBL-EBI & Sanger Institute</i>
17:10 - 17:30 (flash talks)	(1) Spatial-temporal transcriptomics analysis of Mesodermal Lineage Organoids (MLOs) reveals human developmental hematopoiesis <i>Mr Xiang Yang</i>
	(2) Single cell analysis reveals CHOP as an early marker for conventional chondrosarcoma <i>Dr Su Zezhuo</i>
	(3) Single-cell RNA sequencing of lung adenocarcinoma patients reveals age-dependent tumour microenvironment alterations that facilitate response to immunotherapy <i>Mr Zhu Xiaoqiang</i>
	(4) Investigation of Thymic Nursing Cell Complexes by Single-Cell RNA Sequencing <i>Mr Velayutham Sampath Kannan</i>

Thursday, 2 June 2022 (HKT)

09:05 - 09:10	Welcome
09:10 - 10:30	Session 5: Integrative Analysis - chaired by Dr. Yingying Wei
09:10 - 09:30	Population genetics meets cellular genomics <i>Prof Joseph Powell, Garvan Institute</i>
09:30 - 09:50	CoSpar identifies early cell fate biases from single cell transcriptomic and lineage information <i>Prof Shouwen Wang, Westlake & Harvard University</i>
09:50 - 10:10	Adversarial domain translation networks for integrating large-scale atlas-level single-cell datasets <i>Prof Can Yang, HKUST</i>
10:10 - 10:30	Profiling of transcribed cis-regulatory elements in single cells <i>Dr Chung-chau Hon, RIKEN</i>
10:40 - 12:00	Session 6: Cellular Data Insights - chaired by Dr. Heidi Ling
10:40 - 11:00	Tracing T cell development and T cell activation using single cell RNA-seq <i>Dr Wenfei Jin, SUSTech</i>
11:00 - 11:20	Identification and characterization of pathogen-specific T cells in paired single-cell RNA and TCR sequencing data <i>Dr David Shih, HKU</i>
11:20 - 11:40	Tumor-associated monocytes promote glioma progression via EGFR signaling <i>Prof Jiguang Wang, HKUST</i>
11:40 - 12:00 (flash talks)	(1) Single cell mitochondrial DNA mutations enable clonal tracking in osteosarcoma <i>Dr Xue Yan</i>
	(2) Single-cell computational analysis of CRISPR/Cas9-based cellular lineage tracing system <i>Ms Chao Yiming</i>
	(3) XClone: Statistical modelling of copy number variations in single cells <i>Ms Huang Rongting</i>
	(4) MQuad enables clonal substructure discovery using single cell mitochondrial variants <i>Mr Kwok Aaron Wing Cheung</i>

14:00 - 15:20	Session 7: Emerging Technology & Application - chaired by Dr. Joshua Ho
14:00 - 14:20	Microfluidics for single-cell printing and live-cell elasticity measurement <i>Dr Huaying Chen, HIT-Shenzhen</i>
14:20 - 14:40	Massive single-cell image-based profiling and analytics: Expect the unexpected <i>Prof Kevin KM Tsia, HKU</i>
14:40 - 15:00	Live single-cell imaging reveals a polyploid tumour cell subset upon bidirectional tumour-macrophage interaction <i>Prof Alice Wong, HKU</i>
15:00 - 15:20	Histology image-based spatial characterizations of tumor microenvironment for cancer diagnosis, prognosis and molecular subtyping <i>Dr Xin Wang, CUHK</i>
15:30 - 16:50	Session 8: Cancer Genetics - chaired by Dr. David Shih
15:30 - 15:50	Decitabine response in acute myeloid leukemia <i>Dr Asif Javed, HKU</i>
15:50 - 16:10	Multomic single-cell analysis of the differentiation trajectories of acute myeloid leukemia <i>Prof Feng Liu, Ruijing Hospital & Shanghai Jiaotong U</i>
16:10 - 16:30	Mutational landscapes to identify the origin of cancers at single cell resolution <i>Dr Jason Wong, HKU</i>
16:30 - 16:50	Clustering single-cell RNA sequencing data using copy number alterations without an healthy reference <i>Mr Salvatore Milite, Human Technopole</i>
17:00 - 17:40	Keynote Speaker 2 - chaired by Dr. Yuanhua Huang From genotype to phenotype with single-cell resolution <i>Prof Oliver Stegle, EMBL & DKFZ</i>
17:40 - 17:45	Remarks & Prizes