Joint Bioconductor Asia - Hong Kong Bioinformatics Symposium

Website: https://biocasia2023.bioconductor.org/
Venue: Boardroom, 1/F, Faculty Administration Wing (FAW), LKS Faculty of Medicine, 21 Sassoon Road
Programme drafted on 13/10/2023

R/Bioconductor workshops

Oct 15 (Sun), 09:30-17:30	RNA-seq analysis with R/Bioconductor *Dr David Shih, Mr Jonathan Tse and Ms Noel Yue*, *The University of Hong Kong* Seminar Room 2, 4/F, No. 3 Sassoon Road
Oct 16 (Mon), 14:30-17:30	SCDNEY: Unlocking insights for single-cell and spatial data with scFeatures *Dr Yue Cao and Mr Andy*, *University of Sydney* Lecture Theatre 2, G/F, William M.W. Mong Block, 21 Sassoon Road
Oct 16 (Mon), 14:30-17:30	Analysing CRISPR screens with MAGeCK and edgeR *Dr Göknur Giner*, *Walter and Eliza Hall Institute of Medical Research (WEHI) & U Melbourne* Lecture Theatre 3, G/F, William M.W. Mong Block, 21 Sassoon Road

Monday, 16 Oct 2023 (HKT)

09:00 - 09:05	**Welcome**
09:05 - 10:05	**Session 1: Statistical modelling** - chaired by Dr Yuanhua Huang
09:05 - 09:35	Evolving an ecosystem for scalable genomic data science *Prof Vincent Carey*, *Harvard University*
09:35 - 09:50	Improved Estimation of Functional Enrichment in SNP Heritability Using Feasible Generalized Least Squares *Mr Zewei Xiong*
09:50 - 10:05	Systems approach for congruence and selection of cancer models towards precision medicine *Dr Jian Zou*, *Chongqing Medical University*
10:05 - 10:20	Coffee Break
10:20 - 11:20	**Session 2: Statistical genetics** - chaired by Dr Yingying Wei
10:20 - 10:50	High-Dimensional Causal Mediation in Imaging Genetics Study *Prof George Tseng*, *University of Pittsburgh*
10:50 - 11:05	A statistical method for Cross-population fine-mapping by leveraging genetic diversity and accounting for confounding bias *Dr Mingxuan Cai*, *City University of Hong Kong*
11:05 - 11:20	Functional Adaptive Double-Sparsity Estimator for Functional Linear Regression with Application in Wearable Sensor Data Analysis *Dr Xinyue Li*, *City University of Hong Kong*
11:20 - 11:35	Coffee Break
11:35 - 12:50	**Session 3: Cancer and Therapeutics** - chaired by Dr David Shih
11:35 - 11:50	Identifying predictors of glioma evolution from longitudinal sequencing *Dr Quanhua Mu*, *The Hong Kong University of Science and Technology*
11:50 - 12:05	Epigenetic cancer drug facilitates the proteogenomics discovery of immunotherapy targets *Dr Stephen Li*, *The University of Hong Kong*
12:05 - 12:20	Unmasking LUAD's Vulnerabilities: Targeting AURKA-TPX2 Interaction for Innovative Therapeutics *Dr MUKUNTHAN KS*, *Manipal Institute of Technology*
12:20 - 12:35	Integrative Epigenomics and Transcriptomics Analysis to Identify Signature Biomarkers of Lung Adenocarcinoma *Mr Arnab Mukherjee*, *Manipal Institute of Technology*

12:35 - 12:50 (flash talks)	(1) Epigenetic clock CpGs are associated with chromatin and are enriched at enhancers *Mr Yik Chai Charles Lau* (2) Copy number state minimum evolutionary path algorithm for inferring whole genome doublings *Mr Wai Tung Jonathan Tse* (3) Transcriptomic analysis of cisplatin resistance in ovarian cancer *Ms Noel Yue* (4) Comprehensive genomic characterization of EBV-associated carcinomas *Ms Yucan Chen*
12:50 - 14:30	Lunch
14:30 - 17: 30	**Hiking**

Tuesday, 17 Oct 2023 (HKT)

Time	Event
09:00 - 09:05	**Welcome**
09:05 - 10:05	**Session 4: Single-cell dynamics** - chaired by Dr Yuanhua Huang
09:05 - 09:35	Exploring Cell Fate and Memory through Single-Cell Multi-Omic Lineage Tracing *Dr Shou-Wen Wang*, *Westlake University*
09:35 - 09:50	Covidscope: An atlas scale COVID‚Äì19 resource for single-cell meta analysis at sample and cellular levels *Ms Danqing (Angela) Yin*, *The University of Hong Kong*
09:50 - 10:05	Temporal preserved representation learning from time-series single-cell transcriptomics data *Ms Yijun Liu*, *The University of Hong Kong*
10:05 - 10:20	Coffee Break
10:20 - 11:20	**Session 5: Single-cell genomics** - chaired by Dr Jiguang Wang & Prof Jean Yang
10:20 - 10:50	Identification of potential neural precursor cell populations using atlas-level single-cell data *Prof Zhichao Miao*, *Guangzhou National Laboratory*
10:50 - 11:05	Annotating and discovering cell types from single cell RNA-seq data using machine learning *Dr Yu Li* , *The Chinese University of Hong Kong*
11:05 - 11:20	JSNMF enables effective and accurate integrative analysis of single-cell multiomics data *Prof Zhixiang Lin*, *The Chinese University of Hong Kong*
11:20 - 11:35	Coffee Break
11:35 - 12:20	**Session 6: Single-cell analytics** - chaired by Dr Zhixiang Lin
11:35 - 11:50	Differential inference for single-cell RNA-sequencing data *Dr Fangda Song*, *The Chinese University of Hong Kong, Shenzhen*
11:50 - 12:05	Spatiotemporal transcriptomic and genomic analysis reveals waves of hematopoiesis in human embryonic organoids *Ms Yiming Chao*, *1. The University of Hong Kong, HKSAR 2. Centre for Translational Stem Cell Biology, HKSAR 3. Wellcome-MRC Cambridge Stem Cell Institute, UK*
12:05 - 12:20 (flash talks)	(1) Unveiling the Complexity: The Current State of Single-Cell Benchmarking *Dr Yue Cao* (2) Deep autoencoder for interpretable tissue-adaptive deconvolution and cell-type-specific gene analysis *Ms Yixuan Wang* (3) Deciphering sequence-informed regulatory patterns from single-cell multi-omics *Ms Fangxin Cai* (4) Con-AAE: contrastive cycle adversarial autoencoders for single-cell multi-omics alignment and integration *Mr Xuesong Wang*
12:20 - 12:50	**Session 7: Hong Kong Bioinformatics Community Forum** - chaired by Dr Joshua Ho
	Discuss the development of bioinformatics community in Hong Kong, Open forum hosted by Dr Joshua Ho for all participants, including bioinformatics researchers and students
12:50 - 14:00	Lunch

14:00 - 15:10	**Session 8: Spatial transcriptomics and imaging** - chaired by Dr Can Yang / Dr Lequan Yu
14:00 - 14:15	Biologically-informed self-supervised learning for segmentation of subcellular spatial transcriptomics data *Dr Xiaohang Fu, The University of Sydney*
14:15 - 14:30	Benchmarking translational potential of spatial transcriptomics imputation from histology images *Ms Chuhan Wang, The University of Sydney*
14:30 - 14:45	Systematic comparison of sequencing-based spatial transcriptomic methods *Dr Luyi Tian, Guangzhou Laboratory*
14:45 - 15:00	CellContrast: Reconstructing Spatial Relationships in Single-Cell RNA Sequencing Data via Deep Contrastive Learning *Dr Shumin Li, The University of Hong Kong*
15:00 - 15:10 (flash talks)	(1) Decoding Fine-grained Cellular Architectures from Histology Images *Mr Weiqin Zhao* (2) Towards the Visual-Transcriptomics Foundation Model for Spatial Transcriptomics Analysis *Ms Zhuo Liang* (3) Multi-task learning for Blastocyst Quality Assessment *Ms Lu Yu*
15:10 - 15:25	Coffee Break
15:25 - 16:30	**Session 9: Biotechnology computation**- chaired by Dr Joshua Ho
15:25 - 15:55	Experiment-guided clustering to unravel complex drug-diet interactions in nutriomics data *Prof Jean Yang, University of Sydney*
15:55 - 16:10	Cell-type aware CRISPR editing outcomes prediction *Mr Weizhong Zheng, The University of Hong Kong*
16:10 - 16:25	Integrating long-read RNA sequencing improves locus-specific quantification of transposable element expression *Ms Sojung Lee, The University of Hong Kong*
16:25 - 16:30 (flash talks)	(1) Improving long-read scRNA-seq data analysis with FLAMES *Mr Changqing Wang*
16:30 - 16:45	Coffee Break
16:45 - 17:45	**Session 10: General bioinformatics** - chaired by Dr Jason Wong
16:45 - 17:15	Biodiversity Genomics - From evolution to conservation policy *Prof Jerome Hui, The Chinese University of Hong Kong*
17:15 - 17:30	Lipidomic signatures of resilience to coronary artery disease learnt from chimpanzees *Mr Andy Tran, University of Sydney*
17:30 - 17:45	TDbasedUFE and TDbasedUFEadv: bioconductor packages to perform tensor decomposition based unsupervised feature extraction *Prof Y-h. Taguchi, Chuo University*
17:45 - 18:00	**Remarks**