

Rongting Huang

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Education/Experience

- 2025– **Postdoctoral Scholar**, *Stanford University*, Department of Pathology, Stanford, CA, U.S.
Mentor: Dr. Brooke Howitt
- 2025– **Postdoctoral Scholar**, *Harvard Medical School*, BIDMC, Boston, MA, U.S.
Mentor: Dr. Sizun Jiang
- 2020–2024 **Ph.D. in Cancer Genomics/Computational biology**, *The University of Hong Kong*, School of Biomedical Sciences, Li Ka Shing Faculty of Medicine, Hong Kong.
Supervisor: Dr. HUANG Yuanhua
- 2023–2024 **Visiting PhD Student in Spatial Biology**, *Harvard Medical School*, Laboratory of Systems Pharmacology, Harvard Program in Therapeutic Science, Boston, MA, U.S.
Supervisor: Dr. Ajit Johnson Nirmal
- 2017–2020 **MPhil in Bioinformatics**, *Peking University*, School of Basic Medical Sciences, Beijing, China.
Supervisor: Prof. Li Tingting
- 2013–2017 **B.Eng. in Automation**, *Xiamen University*, Department of Automation, Xiamen, China.

Publications

Notations for all below: *: Corresponding authors; †: Joint first authors

- 2024 **Huang R.**[†], Huang, X.[†], Tong, Y., Yan, H.Y., Leung, S.Y., Stegle, O. and Huang, Y.* "Robust analysis of allele-specific copy number alterations from scRNA-seq data with **XClone**.", **Nature Communications**, 15, 6684 (2024).
- 2022 Kwok, A.W.C., Qiao, C., **Huang R.**, Sham, M.H., Ho, J.W.* and Huang, Y.* "**MQuad** enables clonal substructure discovery using single cell mitochondrial variants.", **Nature Communications**, 13(1), p.1205.
- 2024 Tong, M., Liu, Z., Li, J., Wei, X., Shi, W., Liang, C., Yu, C., **Huang R.**, Lin, Y., Wang, X., ... Ji, Z.* "**PhosMap**: An ensemble bioinformatic platform to empower interactive analysis of quantitative phosphoproteomics.", **Computers in Biology and Medicine**, p.108391.
- 2019 Wu Z.^{†,*}, **Huang R.**[†] and Yuan L. "Crosstalk of Intracellular Post-translational Modifications in Cancer", **Archives of Biochemistry and Biophysics**, 10.1016/j.abb.2019.108138
- 2018 **Huang R.**[†], Huang Y.[†], Guo Y.[†], Ji S., Lu M., and Li T*. "Systematic characterization and prediction of post-translational modification cross-talk between proteins", **Bioinformatics**, 2019 35(15):2626-2633
- 2015 Wu X.*, Zeng Y., Guan J., Ji G., **Huang R.** and Li Q. "Genome-wide characterization of intergenic polyadenylation sites redefines gene spaces in *Arabidopsis thaliana*", **BMC Genomics**, 2015, 16(1), 511

Academic Ability

- Research Interests** Cancer clonal evolutionary tree reconstruction from single cell multi-omics, Super-resolved spatial transcriptomics generation, tumor microenvironment analysis based on CNVs, Spatial Biology
- Bioinformatics** NGS, Single-cell Genomics, Cancer evolution, CNV, Proteomics and Phosphoproteomics, Spatial transcriptomic, Highly multiplexed image analysis

Data Science Statistical Modelling, single-cell genomic data analysis
Programming Python (daily use, 7 years), R, Shell, \LaTeX , Matlab, C, HTML, CSS, etc

Research Projects

- 2023-present **Morphology detection in High-plex immunofluorescence image (CyclIF) via autoencoder**, *Method*, Harvard Medical School.
- 2023-present **Exploring the detection of copy number variations from single-cell spatial transcriptomic data and histological images**, *Method*, The University of Hong Kong.
- 2020-present **Detection of allele-specific subclonal copy number variations from single-cell transcriptomic data**, *Method*, The University of Hong Kong.
- 2020-2021 **B allele frequency and copy number variations analysis in single-cell mitochondrial data**, *Analysis*, The University of Hong Kong.
- 2018-2020 **Exploring the post-translational modification(PTM) clusters based on proteomics mass spectrometry and structure data, further combining the somatic mutations clusters in diseases**, *Collaboration with National Center for Protein Sciences in Beijing, China*.
- 2017-2018 **Cross-talk prediction of Post-translational modification**, *Collaboration with EMBL-EBI in Cambridge, UK*.

Academic Activities

Presentations and posters

- 2023.12 **Poster**, *Genome Informatics 2023, Cold Spring Harbor Conference*, Computational analysis of copy number variations in spatial transcriptomics data.
○ JXTX Scholarship winner for the 2023 CSHL Genomic Informatics Conference
- 2023.07 **Oral&Poster**, *ISMB/ECCB2023 VarI COSI, Lyon, France*, XClone: Robust analysis of allele-specific copy number variations from scRNA-seq data .
- 2022.11 **Poster**, *27th-LKS-Research Postgraduate Symposium, HKU*, XClone: detection of allele-specific subclonal copy number variations from single-cell transcriptomic data.
- 2022.07 **Poster**, *ISMB2022*, XClone: Statistical modelling of copy number variations in single cells.
- 2022.06 **Oral**, *Single-Cell Data ScienceWorkshop, HK*, XClone: Statistical modelling of copy number variations in single cells.
○ 2nd Best Flash Talk, Sliver Presentation Award
- 2019.01 **Invited talk**, the 10th Multidisciplinary Conference on New ideas and New Technologies in Health Science Center, PKU: Systematic characterization and prediction of post-translational modification cross-talk between proteins.

Scholarships and Awards

- Sep. 2023-24 **Bau Tsu Zung Bau Kwan Yeu Hing Research and Clinical Fellowship** *HKU*
- Sep. 2020 **Hui Pun Hing Memorial Postgraduate Fellowships** *University of Hong Kong*
- Sep. 2020-24 **Postgraduate Scholarships, University Postgraduate Fellowships** *University of Hong Kong*
- June. 2020 **Outstanding Graduate Award** *Peking University*
- Nov. 2019 **National Scholarship for Graduates** *Ministry of Education, China*
- Dec. 2017 **First Academic Excellence Scholarship** *Peking University*
- Nov. 2014-16 **National Scholarship for Undergraduates, three times** *Ministry of Education, China*
○ Top 1% in candidates
- Apr. 2016 **"WenQing" Principal's Scholarship** *Xiamen University*
○ Top 6 Undergraduates per year