Rongting Huang

Postdoctoral Scholar, Pathology

Bio

BIO

Dr. Huang is a computational biologist with academic interests in cancer genomics and spatial biology, particularly in the field of gynecologic cancers. During her Ph.D. under the mentorship of Dr. Yuanhua Huang, she developed statistical methods to detect allele-specific somatic copy number variations from single-cell and spatial transcriptomic data, aiming to understand genetic diversity in biological systems. Currently, her research focuses on advancing gynecologic cancer studies and women’s health through spatial technology platforms, computational modeling, and innovative data visualizations to uncover meaningful insights.

Outside of research, she enjoys hiking, rock climbing, and calligraphy, which help her stay creative and balanced.

HONORS AND AWARDS

- CRI Immuno-Informatics Postdoctoral Fellow, CRI (2025-2028)
- Bau Tsu Zung Bau Kwan Yeu Hing Research and Clinical Fellowship, The University of Hong Kong (2023-2024)
- Hui Pun Hing Memorial Postgraduate Fellowships, The University of Hong Kong (2020-2021)
- JXTX Scholarship winner of 2023 CSHL Genomic Informatics Conference, Cold Spring Harbor Laboratory (2023)
- Silver Presentation Award, Single-Cell Data Science Workshop, Hong Kong (2022)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Associate Membership, American Association for Cancer Research (AACR) (2025 - 2025)
- Member, International Society for Computational Biology (ISCB) (2021 - 2024)

PROFESSIONAL EDUCATION

- Doctor of Philosophy, University Of Hong Kong (2025)
- Master of Science, Peking University (2020)
- Bachelor of Engineering, Xiamen University (2017)
- Ph.D., The University of Hong Kong , Computational Biology, Cancer Genomics (2025)
- Mphil., Peking University , Bioinformatics, Molecular Biology (2020)
- B.Eng., Xiamen University , Automation (2017)

STANFORD ADVISORS

- Brooke Howitt, Postdoctoral Faculty Sponsor

LINKS

- Personal Site: https://rongtingting.github.io/
- GitHub: https://github.com/Rongtingting
- Twitter: https://x.com/RongtingHuang
- Linkedin: https://www.linkedin.com/in/rongting-huang-502ab0131/

Research & Scholarship

LAB AFFILIATIONS

- Brooke Howitt, Brooke Howitt Lab (3/24/2025)

Publications

PUBLICATIONS

- **Informatics-driven spatial-omics for cancer immunotherapy discovery in gynecologic cancers.**
  Huang, R., Libert, D., Kasimov, A., Kingsley, L., Nasr, S., Al-Humadi, R., Finch, L. A., Diver, E., Reddy, R. A., Litkouhi, B., Bixel, K., Jiang, S., Howitt, et al
  AMER ASSOC CANCER RESEARCH.2026
- **Same-Slide Spatial Multi-Omics Integration with IN-DEPTH Reveals Tumor Virus-Linked Spatial Reorganization of the Tumor Microenvironment.** *Cancer discovery*
  Yiu, S. P., Chang, Y., Yeo, Y. Y., Qiu, H., Wu, W., Michel, H. A., Jin, X., Huang, R., Kure, S., Parmelee, L., Luo, S., Cramer, P., Lee, et al
  2026
- **Robust analysis of allele-specific copy number alterations from scRNA-seq data with XClone.** *Nature communications*
  Huang, R., Huang, X., Tong, Y., Yan, H. Y., Leung, S. Y., Stegle, O., Huang, Y.
  2024; 15 (1): 6684
- **PhosMap: An ensemble bioinformatic platform to empower interactive analysis of quantitative phosphoproteomics.** *Computers in biology and medicine*
  Tong, M., Liu, Z., Li, J., Wei, X., Shi, W., Liang, C., Yu, C., Huang, R., Lin, Y., Wang, X., Wang, S., Wang, Y., Huang, et al
  2024; 174: 108391
- **MQuad enables clonal substructure discovery using single cell mitochondrial variants.** *Nature communications*
  Kwok, A. W., Qiao, C., Huang, R., Sham, M. H., Ho, J. W., Huang, Y.
  2022; 13 (1): 1205
- **Crosstalk of intracellular post-translational modifications in cancer.** *Archives of biochemistry and biophysics*
  Wu, Z., Huang, R., Yuan, L.
  2019; 676: 108138
- **Systematic characterization and prediction of post-translational modification cross-talk between proteins.** *Bioinformatics (Oxford, England)*
  Huang, R., Huang, Y., Guo, Y., Ji, S., Lu, M., Li, T.
  2019; 35 (15): 2626-2633
- **Genome-wide characterization of intergenic polyadenylation sites redefines gene spaces in Arabidopsis thaliana.** *BMC genomics*
  Wu, X., Zeng, Y., Guan, J., Ji, G., Huang, R., Li, Q. Q.
  2015; 16 (1): 511

PRESENTATIONS

- XClone: Robust analysis of allele-specific copy number variations from scRNA-seq data - ISMB/ECCB2023 VarI COSI (July 23, 2023 - July 27, 2023)