Yang CUI

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Department of Computational Biology and Medical Sciences
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Summary

- Motivated researcher interested in the field of single-cell and spatial multi-omics.
- Knowledgeable in cancer biology, molecular biology and bioinformatics.
- Experienced in applying computational methods to multi-omics projects.
- Proficient in **R** and **Python**, skilled in establishing analysis pipelines.

Education

- **University of Tokyo** Apr 2022 - Mar 2025
  Doctor of Philosophy, Department of Computational Biology and Medical Sciences

- **Tokyo Medical and Dental University** Apr 2020 - Mar 2022
  Master of Medical Science, Department of Immunology

- **East China University of Science and Technology** Sep 2013 - Jul 2017
  Bachelor of Engineering, Department of Biotechnology

Scholarships

- Fostering Advanced Human Resources to Lead Green Transformation (**SPRING-GX**), University of Tokyo (Grant Number JPMJSP2108, 2024 - 2025)

Dissertations

- Yang CUI, Computational Analysis Reveals MHC-II-expressing Tumor Cells Influence Immune Surveillance and Prognostic Outcomes in Triple-Negative Breast Cancer. **[Doctoral dissertation]** University of Tokyo, Department of Computational Biology and Medical Sciences. 2025
- Yang CUI, Confirmation of Humanized PD-L1 Mice and the Role of Prolonged NADPH Oxidase-dependent Reactive Oxygen Species Production in B Cell Activation. **[Master's dissertation]** Tokyo Medical and Dental University, Department of Immunology, 2022.

Publications

- Cui, Y.*, **Cui, Y.***, Wang, R., Zhu, Z., Zeng, X., Nakai, K., Cui, F., Zhang, Z., Shi, H., Chen, Y., Ye, X., Sakurai, T., & Wei, L. (2025). DiffusionST: a deep generative diffusion model-based framework for enhancing spatial transcriptomics data quality and identifying spatial domains. ***Briefings in bioinformatics***, 26(4), bbaf390. (*Co-first author)
- Cui, Y.*, **Cui, Y.***, Ding, Y., Nakai, K., Wei, L., Le, Y., Ye, X., & Sakurai, T. (2025). OmniClust: A versatile clustering toolkit for single-cell and spatial transcriptomics data. ***Methods*** (San Diego, Calif.), 238, 84–94. (*Co-first author)
- Yang, Y., **Cui, Y.**, Zeng, X., Zhang, Y., Loza, M., Park, S. J., & Nakai, K. (2025). STAIG: Spatial transcriptomics analysis via image-aided graph contrastive learning for domain exploration and alignment-free integration. ***Nature communications***, 16(1), 1067.
- Zeng, X., Gyoja, F., **Cui, Y.**, Loza, M., Kusakabe, T. G., & Nakai, K. (2024). Comparative single-cell transcriptomic analysis reveals putative differentiation drivers and potential origin of vertebrate retina.

NAR genomics and bioinformatics, 6(4), lqae149.

- **Cui, Y.**, Zhang, W., Zeng, X., Yang, Y., Park, S. J., & Nakai, K. (2024). Computational analysis of the functional impact of MHC-II-expressing triple-negative breast cancer. ***Frontiers in immunology***, 15, 1497251.
- Zhang, W., **Cui, Y.**, Liu, B., Loza, M., Park, S. J., & Nakai, K. (2024). HyGAnno: hybrid graph neural network–based cell type annotation for single-cell ATAC sequencing data. ***Briefings in Bioinformatics***, 25(3), bbae152.

Manuscripts in Progress

- Cui, Y., Wang, R., Zeng, X., **Cui, Y.**, Zhu, Z., Nakai, K., … & Wei, L. (2024). DenoiseST: A dual-channel unsupervised deep learning-based denoising method to identify spatial domains and functionally variable genes in spatial transcriptomics. ***bioRxiv***, 2024-03.

Poster Presentation

- **Cui, Y.**, Zhang, W., Zeng, X., Yang, Y., Park, S. J., & Nakai, K., Computational Transcriptomic Analysis Reveals MHC-II Expressing Tumor Cells Influence Immune Surveillance and Prognostic Outcomes in the Tumor Microenvironment of Triple-Negative Breast Cancer, ***1st Asia & Pacific Bioinformatics Joint Conference (APBJC2024)***, 2024 Oct.22-25, Japan, Okinawa.
- **Cui, Y.**, Nakai, K. Computational Transcriptomic Analysis Identifies a Novel Immune-dysregulated TNBC Subtype Regulated by STAT3, ***The 47th Annual Meeting of the Molecular Biology Society of Japan (MBSJ2023)***, 2023. Dec.6-8, Japan, Kobe.
- **Cui, Y.**, Nakai, K. Unveiling a Distinct Immunological Characteristic and a Prognostic Prediction Model in Breast Cancer through Integrated Transcriptomic Analysis, ***The 21st Awaji International Forum on Infection and Immunity***, 2023. Sep3-6, Japan, Karuizawa.

Languages

- Proficient in English
- Proficient in Japanese (JLPT N1)
- Native in Chinese

Hobbies

- Recreational camping and hiking