

YIGE WU, PhD

CANCER GENOMICS AND BIOINFORMATICS EXPERT

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SUMMARY

Innovative computational biology expert with PhD and 2 years of industry experience. Specializes in multi-omics integration, biomarker discovery, and CRISPR/Cas9 therapy support. Proven track record in developing scalable bioinformatics pipelines and translating complex data into actionable insights for precision medicine and immune-oncology research.

CORE COMPETENCIES

Programming: R, Python, Shell, Linux, MATLAB, C++, Conda, and Parallel Computing.

Bioinformatics: NGS data analysis (exome/genome sequencing, somatic/germline variants, CNVs), scRNA-seq, snATAC-seq, spatial transcriptomics, and proteomics/phosphoproteomics/ metabolomics processing.

Data Analysis: Statistical modeling, machine learning, multimodal data integration, biomarker discovery, and data visualization.

Pipeline Development: Scalable/reproducible workflows, cloud computing (AWS, Google Cloud), containerization (Docker), and version control (Git).

Leadership: Project management, mentoring, and cross-functional collaboration.

Communication: Scientific writing, presentations, and technical documentation.

RESEARCH EXPERIENCE

INTELLIA THERAPEUTICS. Cambridge, MA

01/2023 – 01/2025

Computational Scientist

- Engineered scalable bioinformatics pipelines for single-cell and bulk RNA-seq data analysis, improving reproducibility and efficiency.
- Spearheaded multi-omics analyses, enabling insights into tumor microenvironment contexture.
- Orchestrated cross-functional collaborations, delivering actionable insights for research goals.
- Championed reproducibility through version control systems and comprehensive documentation.

WASHINGTON UNIVERSITY IN ST. LOUIS, St. Louis, MO

08/2016 – 01/2023

Postdoctoral Research Associate, Ding lab, Department of Medicine (05/2022 – 01/2023)

- Investigated novel drug combination efficacy using patient-derived xenograft models for renal cancer.

PhD Student, Ding Lab, Department of Medicine (09/2016 – 05/2022)

- Constructed somatic CNV pipeline, processing 1,300+ the Clinical Proteomic Tumor Analysis Consortium (CPTAC) cases across seven cancer types. (project code: <https://github.com/ding-lab/BICSEQ2>)
- Architected cloud-based pipelines, validating rare germline copy number variations (CNVs) across 10,389 tumors for The Cancer Genome Atlas (TCGA). (project code: https://github.com/yigewu/xhmm_google_cloud)
- Pioneered multimodal data analysis (genomics, proteomics, epigenetics) of clear cell renal cell carcinomas (ccRCC), revealing tumor heterogeneity and therapeutic targets. (project code: https://github.com/yigewu/ccRCC_sn_publication)
- Spearheaded large-scale collaborative study, coordinating 30+ team members across 150+ conferences.
- Established mutational impact analysis pipeline for proteome studies in Cell publications.
- Secured U.S. Patent application for cancer treatment methods (Patent 17/231,273).

PEKING UNIVERSITY, Beijing, China

09/2014 – 05/2016

Research Assistant, Wei Lab, School of Life Sciences

Conceptualized quantitative model and engineered programs for joint attention visual behavior detection.

EDUCATION

Doctor of Philosophy (Ph.D.), Human Statistical Genetics, WASHINGTON UNIVERSITY IN ST. LOUIS, St. Louis, MO (2022)

Bachelor of Science (B.Sc.), Life Science, PEKING UNIVERSITY, Beijing, China (2016)

Bachelor of Science (B.Sc.), Psychology, PEKING UNIVERSITY, Beijing, China (2016)

PUBLICATIONS

- **Wu, Y.**, Terekhanova, N. V., Caravan, W., Naser Al Deen, N., Lal, P., Chen, S., Mo, C.-K., Cao, S., Li, Y., Karpova, A., Liu, R., Zhao, Y., Shinkle, A., Strunilin, I., Weimholt, C., Sato, K., Yao, L., Serasanambati, M., Yang, X., ... Chen, F. (2023). Epigenetic and transcriptomic characterization reveals progression markers and essential pathways in clear cell renal cell carcinoma. *Nature Communications*, 14(1), Article 1. <https://doi.org/10.1038/s41467-023-37211-7>
- **Wu, Y.**, Chen, S., Yang, X., Sato, K., Lal, P., Primeau, T., Wang, Y., Mudd, J., Hoog, J., Zhao, Y., Gould, A., Shinkle, A., Sun, H., Herndon, J., Davis, S., Wendl, M., Evrard, Y., Wellem, B., Lewis, ..., Ding, L., & Chen, F. (2023). Combining the tyrosine kinase inhibitor cabozantinib and the mTORC1/2 inhibitor sapanisertib blocks ERK pathway activity and suppresses tumor growth in renal cell carcinoma. *Cancer Research*, 83(24), 4161-4178. <https://doi.org/10.1158/0008-5472.CAN-23-0604>
- Huang, K., Mashl, R. J., **Wu, Y.**, Ritter, D. I., Wang, J., Oh, C., Paczkowska, M., Reynolds, S., Wyczalkowski, M. A., Oak, N., Scott, A. D., Krassowski, M., Cherniack, A. D., Houlahan, K. E., Jayasinghe, R., Wang, L.-B., Zhou, D. C., Liu, D., Cao, S., ... Ding, L. (2018). Pathogenic germline variants in 10,389 adult cancers. *Cell*, 173(2), 355-370.e14. <https://doi.org/10.1016/j.cell.2018.03.039>
- Huang, K.-L., **Wu, Y.**, Primeau, T., Wang, Y.-T., Gao, Y., McMichael, J. F., Scott, A. D., Cao, S., Wendl, M. C., Johnson, K. J., Ruggles, K., Held, J., Payne, S. H., Davies, S., Dar, A., Kinsinger, C. R., Mesri, M., Rodriguez, H., Ellis, M. J., ... Ding, L. (2019). Regulated phosphosignaling associated with breast cancer subtypes and druggability. *Molecular & Cellular Proteomics: MCP*, 18(8), 1630–1650. <https://doi.org/10.1074/mcp.RA118.001243>
- Wang, L.-B., Karpova, A., Gritsenko, M. A., Kyle, J. E., Cao, S., Li, Y., Rykunov, D., Colaprico, A., Rothstein, J. H., Hong, R., Stathias, V., Cornwell, M., Petralia, F., **Wu, Y.**, Reva, B., Krug, K., Pugliese, P., Kawaler, E., Olsen, L. K., ... Zhu, J. (2021). Proteogenomic and metabolomic characterization of human glioblastoma. *Cancer Cell*, 39(4), 509-528.e20. <https://doi.org/10.1016/j.ccr.2021.01.006>
- Clark, D. J., Dhanasekaran, S. M., Petralia, F., Pan, J., Song, X., Hu, Y., Leprevost, F. da V., Reva, B., Lih, T.-S. M., Chang, H.-Y., Ma, W., Huang, C., Ricketts, C. J., Chen, L., Krek, A., Li, Y., Rykunov, D., Li, Q. K., Chen, L. S., Ozbek, U., Vasaikar, S., **Wu, Y.**, ... Tu, Z. (2019). Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. *Cell*, 179(4), 964-983.e31. <https://doi.org/10.1016/j.cell.2019.10.007>
- Dou, Y., Kawaler, E. A., Cui Zhou, D., Gritsenko, M. A., Huang, C., Blumenberg, L., Karpova, A., Petyuk, V. A., Savage, S. R., Satpathy, S., Liu, W., **Wu, Y.**, Tsai, C.-F., Wen, B., Li, Z., Cao, S., Moon, J., Shi, Z., Cornwell, M., ... Clinical Proteomic Tumor Analysis Consortium. (2020). Proteogenomic Characterization of Endometrial Carcinoma. *Cell*, 180(4), 729-748.e26. <https://doi.org/10.1016/j.cell.2020.01.026>