

# 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](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](https://github.com/yigewu/ccRCC_sn_publication))
- 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., Welm, 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.ccell.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>