



Weiruo Zhang

Research Engineer, Biomedical Data Science

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BIO

Dr. Zhang is currently a Research Engineer at the Department of Biomedical Data Science and the Center for Cancer Systems Biology, Stanford School of Medicine.

Dr. Zhang obtained her M.S. and Ph.D. in Electrical Engineering, both from Stanford University. Her Ph.D. studies focused on developing computational algorithms for metabolomics data analysis, in which she received Young Scientist Award from the Metabolomics Society for her algorithm on metabolic network analysis delineating the effects of genetic mutants and drug treatment on the metabolome. Her postdoctoral studies at the Department of Radiology, Stanford School of Medicine, integrated radiomic data and genomic data that identified a prognostic metabolic regulation biomarker for non-small cell lung cancer. Her current research primarily focuses on developing and implementing novel computational methods to integrate and analyze single-cell multi-omics data, such as single-cell RNA sequencing, spatial proteomics and spatial transcriptomics. She has developed algorithms to solve computational challenges of spatial omics data and to identify mediators for cell-cell interactions associated with metastasis that was featured in Stanford Medicine Magazine. Dr. Zhang has authored and co-authored publications including Nature, Cell, Nature Methods etc. Her research aims at bridging multi-omics, imaging, machine learning, artificial intelligence to better understand biology for cancer progression and immunosuppression.

HONORS AND AWARDS

- University Biomedical Informatics Research Training Award, NLM, National Institutes of Health (2020)
- Young Scientist Award, The Metabolomics Society (2013)
- First Class Honor, National University of Singapore (2009)

EDUCATION AND CERTIFICATIONS

- BE, National University of Singapore , Electrical Engineering (2009)
- MS, Stanford University , Electrical Engineering (2011)
- PhD, Stanford University , Electrical Engineering, Bioinformatics (2015)

SERVICE, VOLUNTEER, AND COMMUNITY WORK

- Staff representative, JEDI (Justice, Equity, Diversity, and Inclusion) committee (2022)

Publications

PUBLICATIONS

- **The colocalome as a spatial -omic reveals shared microenvironment features between tumour-stroma assembloids and human lung cancer.** *bioRxiv : the preprint server for biology*
Bouchard, G., Zhang, W., Li, I., Ilertsen, I., Bhattacharya, A., Li, Y., Trope, W., Shrager, J. B., Kuo, C., Tian, L., Giaccia, A. J., Plevritis, S. K.
2023

- **Galectin-1 mediates chronic STING activation in tumors to promote metastasis through MDSC recruitment.** *Cancer research*
Nambiar, D. K., Viswanathan, V., Cao, H., Zhang, W., Guan, L., Chamoli, M., Holmes, B., Kong, C., Hildebrand, R., Koong, A. J., von Eyben, R., Plevritis, S., Li, et al
2023
- **Organization of the human intestine at single-cell resolution.** *Nature*
Hickey, J. W., Becker, W. R., Nevins, S. A., Horning, A., Perez, A. E., Zhu, C., Zhu, B., Wei, B., Chiu, R., Chen, D. C., Cotter, D. L., Esplin, E. D., Weimer, et al
2023; 619 (7970): 572-584
- **NFE2L2 mutations enhance radioresistance in head and neck cancer by modulating intratumoral myeloid cells.** *Cancer research*
Guan, L., Nambiar, D. K., Cao, H., Viswanathan, V., Kwok, S., Hui, A. B., Hou, Y., Hildebrand, R., von Eyben, R., Holmes, B. J., Zhao, J., Kong, C. S., Wamsley, et al
2023
- **Identification of cell types in multiplexed in situ images by combining protein expression and spatial information using CELESTA.** *Nature methods*
Zhang, W., Li, I., Reticker-Flynn, N. E., Good, Z., Chang, S., Samusik, N., Saumyaa, S., Li, Y., Zhou, X., Liang, R., Kong, C. S., Le, Q., Gentles, et al
2022
- **Lymph node colonization induces tumor-immune tolerance to promote distant metastasis.** *Cell*
Reticker-Flynn, N. E., Zhang, W., Belk, J. A., Basto, P. A., Escalante, N. K., Pilarowski, G. O., Bejnood, A., Martins, M. M., Kenkel, J. A., Linde, I. L., Bagchi, S., Yuan, R., Chang, et al
2022
- **Multi-omics analysis of spatially distinct stromal cells reveals tumor-induced O-glycosylation of the CDK4-pRB axis in fibroblasts at the invasive tumor edge.** *Cancer research*
Bouchard, G., Garcia-Marques, F. J., Karacosta, L. G., Zhang, W., Bermudez, A., Riley, N. M., Varma, S., Mehl, L. C., Benson, J. A., Shrager, J. B., Bertozzi, C. R., Pitteri, S. J., Giaccia, et al
2021
- **Lymph node colonization promotes distant tumor metastasis through the induction of tumor-specific immunosuppression**
Reticker-Flynn, N. E., Basto, P. A., Zhang, W., Martins, M. M., Chang, S., Gentles, A. J., Sunwoo, J. B., Plevritis, S. K., Engleman, E. G.
AMER ASSOC CANCER RESEARCH.2020
- **Lymph node colonization promotes distant tumor metastasis through the induction of tumor-specific immunosuppression.**
Reticker-Flynn, N. E., Basto, P. A., Zhang, W., Bejnood, A., Kenkel, J. A., Martins, M. M., Chang, S., Gentles, A. J., Sunwoo, J. B., Plevritis, S. K., Engleman, E. G.
AMER ASSOC CANCER RESEARCH.2020: 25–26
- **Lymph node colonization promotes distant tumor metastasis through the induction of systemic immune tolerance**
Reticker-Flynn, N. E., Martins, M. M., Basto, P. A., Zhang, W., Bejnood, A., Gentles, A. J., Sunwoo, J. B., Plevritis, S. K., Engleman, E. G.
AMER ASSOC CANCER RESEARCH.2019
- **A radiogenomic dataset of non-small cell lung cancer.** *Scientific data*
Bakr, S., Gevaert, O., Echegaray, S., Ayers, K., Zhou, M., Shafiq, M., Zheng, H., Benson, J. A., Zhang, W., Leung, A. N., Kadoch, M., D Hoang, C., Shrager, et al
2018; 5: 180202
- **A radiogenomic dataset of non-small cell lung cancer** *SCIENTIFIC DATA*
Bakr, S., Gevaert, O., Echegaray, S., Ayers, K., Zhou, M., Shafiq, M., Zheng, H., Benson, J., Zhang, W., Leung, A. C., Kadoch, M., Hoang, C. D., Shrager, et al
2018; 5
- **Studying tumor metabolic reprogramming through integration of metabolomics and transcriptomics**
Zhang, W., Plevritis, S.
AMER ASSOC CANCER RESEARCH.2018
- **GFPT2-Expressing Cancer-Associated Fibroblasts Mediate Metabolic Reprogramming in Human Lung Adenocarcinoma** *CANCER RESEARCH*
Zhang, W., Bouchard, G., Yu, A., Shafiq, M., Jamali, M., Shrager, J. B., Ayers, K., Bakr, S., Gentles, A. J., Diehn, M., Quon, A., West, R. B., Nair, et al
2018; 78 (13): 3445–57
- **GFPT2-expressing cancer-associated fibroblasts mediate metabolic reprogramming in human lung adenocarcinoma.** *Cancer research*
Zhang, W., Bouchard, G., Yu, A., Shafiq, M., Jamali, M., Shrager, J. B., Ayers, K., Bakr, S., Gentles, A. J., Diehn, M., Quon, A., West, R. B., Nair, et al

2018

- **Towards in vivo estimation of reaction kinetics using high-throughput metabolomics data: a maximum likelihood approach** *BMC SYSTEMS BIOLOGY*
Zhang, W., Kolte, R., Dill, D. L.
2015; 9
- **Liquid chromatography/mass spectrometry methods for measuring dipeptide abundance in non-small-cell lung cancer.** *Rapid communications in mass spectrometry : RCM*
Wu, M., Xu, Y., Fitch, W. L., Zheng, M., Merritt, R. E., Shrager, J. B., Zhang, W., Dill, D. L., Peltz, G., Hoang, C. D.
2013; 27 (18): 2091-2098
- **Identification of drug targets by chemogenomic and metabolomic profiling in yeast** *PHARMACOGENETICS AND GENOMICS*
Wu, M., Zheng, M., Zhang, W., Suresh, S., Schlecht, U., Fitch, W. L., Aronova, S., Baumann, S., Davis, R., St Onge, R., Dill, D. L., Peltz, G.
2012; 22 (12): 877-886