YUANYUAN ZHANG

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EDUCATION

Purdue University , West Lafayette, IN, US <i>Ph.D student</i> in Computer Science, GPA: 3.8/4.0	2021.9 – 2026.5(expect)
University of Chinese Academy of Sciences , Beijing, China <i>Master</i> in Computer Science	2018.8 - 2021.6
Sichuan University, Sichuan, China Bachelor in Computer Science and Technology	2014.9 - 2018.6
Experience	
 Noble Lab and Wang Lab, University of Washington Seattle, WA, US Summer intern Advisor: Prof. William Stafford Noble and Sheng Wang Self-supervised foundation model on Hi-C image data developed a contrastive based masked autoencoder for Hi-C data. integrated vision transformer as network architecture. Neural radiance field(NeRF) on cryo-EM 3D image reconstruction worked on NeRF application on cryo-EM 3D image designed heterogenity-aware encoder for cryo-EM heterogeneity problem utilized hash encoding to effectively encode the query coordinates. 	2024.6 – 2024.8
KiharaLab, Purdue University West Lafayette, IN, US	2022.5 - Present
Research assistant	
 Flow-matching on cryo-EM map segmentation developed a conditioned rectified flow matching algorithm for cryo-EM 3D det used Unet based transformer architecture to effectly extract features 	nsity image segmentation
3D detection on Cryo-EM map	
 proposed a 3D-MUNet to accurately detect structural class from 3D density in <i>Protein structure prediction based on AlphaFold2</i> proposed a fine-tuning pipeline to optimize structure module in AF2 under correst designed multi-task loss to optimize structure prediction 	put. nstraints.
Key Laboratory of Nerwork Data Science and Technology, CAS Beijing	g, China 2019.8 – 2021.6
Research assistant	
Sentiment analysis and knowledge graph network by deep learning	
Xiaomi Co., Ltd. Beijing, China Machine Learning Algorithm Intern Optimize recommendation algorithm based on feeds information	2019.3 – 2019.7
Selected Publications	

• Wang, X.*, **Zhang, Y.***, Ray, S., Jha, A., Doulatov, S., Wang S. & Noble, W. (2024). A generalizable Hi-C foundation model for chromatin architecture, single-cell and multi-omics analysis across species. Hi-C and Multi-omics Analysis. *Science* (Under 1st review). https://www.biorxiv.org/content/10.1101/2024.12.16.628821v1.abstract

- Zhang, Y., Zhang, Z., Kagaya, Y., Terashi, G., Zhao, B., Xiong, Y., & Kihara, D. (2023). Distance-AF: Modifying Predicted Protein Structure Models by Alphafold2 with User-Specified Distance Constraints. *Science Advances*. (Under 1st review) https://www.biorxiv.org/content/10.1101/2023.12.01. 569498v1
- Qu, H., Wang, X., **Zhang, Y.**, Wang, S., Noble, W. S., & Chen, T. (2025). CryoNeRF: reconstruction of homogeneous and heterogeneous cryo-EM structures using neural radiance field. *Nature Communications*. (Under 1st review) https://www.biorxiv.org/content/10.1101/2025.01.10.632460v1
- Zhang, Y., Wang, X., Li, S., Terashi, G., Nakamura, T. & Kihara, D. (2024). DAQ-ATOM score for protein models evaluation from high-resolution Cryo-EM maps.(In submission)
- Zhang, Y., Wang, X., Zhang, Z., Huang, Y., & Kihara, D. (2024). Assessment of Protein–Protein Docking Models Using Deep Learning. Protein-Protein Docking: Methods and Protocols, 149-162.
- Wang, X., **Zhang, Y.**, Yu, S., Liu, X., & Wang, F. Y. (2018). Computerized adaptive English ability assessment based on deep learning. In Image and Video Technology: PSIVT 2017 International Workshops, Wuhan, China, November 20-24, 2017, Revised Selected Papers 8 (pp. 158-171). Springer International Publishing.
- Wang, X., **Zhang, Y.**, Yu, S., Liu, X., Yuan, Y., & Wang, F. Y. (2017, October). E-learning recommendation framework based on deep learning. In 2017 IEEE international conference on systems, man, and cybernetics (SMC) (pp. 455-460). IEEE.
- Farheen, F., Broyles, B. K., **Zhang, Y.**, Ibtehaz, N., Erkine, A. M., & Kihara, D. (2024). Predicting transcriptional activation domain function using Graph Neural Networks. bioRxiv, 2024-05.
- Bou Abdallah, F., Fish, J., Terashi, G., **Zhang, Y.**, Kihara, D., & Arosio, P. (2024). Unveiling the stochastic nature of human heteropolymer ferritin self assembly mechanism. Protein Science, 33(8), e5104.
- Gagliardi, L., Raffo, A., Fugacci, U., Biasotti, S., Rocchia, W., Huang, H., Amor, B.B., Fang, Y., Zhang, Y., Wang, X. and Christoffer, C., 2022. SHREC 2022: Protein–ligand binding site recognition. Computers & Graphics, 107, pp.20-31.
- Lensink, M. F., Brysbaert, G., Raouraoua, N., Bates, P. A., Giulini, M., Honorato, R. V., ..., **Zhang,** Y., ...& Wodak, S. J. (2023). Impact of AlphaFold on structure prediction of protein complexes: The CASP15 CAPRI experiment. Proteins: Structure, Function, and Bioinformatics, 91(12), 1658-1683.

$oldsymbol{\Psi}$ Honors and Awards

D.E. Shaw DESRES Doctoral Fellowship, New York, US	2024.3
Graduate Student Scholarship of ICT CAS (Top 1%), Beijing, China	2018.9-2021.6
Outstanding Graduate of Sichuan University (Top 1%) Chengdu, China	2018.6
Outstanding Student of Sichuan University (Top 3%), Chengdu, China	2015.9-2018.6
National Endeavor Fellowship (Top 1%), Sichuan Universiy, Chengdu, China	2016.9-2017.6

SKILLS

- Expertise: Python, Deep Learning, Machine Leanring, Pytorch, TensorFlow
- Capable: Hadoop, Spark, C, C++, Java, Matlab