

Yumeng (Alan) Zhang

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Education

Monash University 2024/09 – 2028/03 (Expected)
Ph.D. in Computational Biology, Department of Biochemistry and Molecular Biology Melbourne, VIC, Australia
• Supervisors: Jiangning Song & Tony Purcell.

Shanghai Jiao Tong University 2021/09 – 2024/06
M.Sc. in Biology, GPA 3.81/4.0 Shanghai, China
• Courses: Omics Big Data, Structural Bioinformatics, Statistical Methods in Data Science, etc.
• Supervisor: Hong-Yu Ou.

Shanghai Jiao Tong University 2017/09 – 2021/06
B.Sc. in Bioinformatics, GPA 3.58/4.0 (86.90/100) Shanghai, China
• Courses: Data Structures & Algorithms, Bioinformatics, Biostatistical Modeling, Molecular Biology, etc.

Work Experience

Monash University 2023/07 – 2024/04
Research Student Melbourne, VIC, Australia
• Conduct a research project on predicting TCR-antigen recognition using a deep-learning approach.

Shanghai Artificial Intelligence Laboratory 2021/06 – 2021/09
Research Intern Shanghai, China
• Develop a siamese graph attention network to predict variations in protein thermostability upon point mutations.
• Identify potential variants of *Streptomyces mobaraenesis* transglutaminase (smTG) with improved thermostability.

Research Projects

TCR-antigen Recognition Prediction 2023/07 – 2024/09
Biomedicine Discovery Institute, Monash University Melbourne, VIC, Australia
• Predict binding specificity and interactions between T-cell receptors (TCRs) and epitopes presented by MHC-I molecules.
• Interpret spike-specific T-cell responses upon SARS-CoV-2 exposure using predicted TCR specificity and binding ranks.
• Elucidate TCR cross-reactivity in autoimmune disease and cancer immunotherapy via residue-level contacts and simulating peptide library screening.

Bacterial Secreted Protein Prediction 2022/03 – 2023/10
State Key Laboratory of Microbial Metabolism, Shanghai Jiao Tong University Shanghai, China
• Extend the prediction of bacterial secreted proteins to five major types in Gram-negative bacteria.
• Explore the taxonomic distribution of bacterial secretion systems and secreted proteins and provide an analytic platform.

Type IV Secreted Effector Prediction 2020/11 – 2022/01
State Key Laboratory of Microbial Metabolism, Shanghai Jiao Tong University Shanghai, China
• Utilize a pre-trained model for the universal representation of protein sequences to predict type IV secreted effectors.
• Achieve a comparable performance with existing prediction tools and significantly enhance the computation efficiency.

Pan-genome Assembly 2019/12 – 2021/04
Department of Bioinformatics and Biostatistics, Shanghai Jiao Tong University Shanghai, China
• Develop a generic human pan-genome analysis procedure to assemble and analyze the pan-genomes of Tibetans.
• Construct Chinese Tibetan and Han Chinese pan-genomes and extract unique contigs and potential genes.

Cryo-EM Image Denoising 2020/02 – 2020/09
Department of Computer Science and Engineering, Shanghai Jiao Tong University Shanghai, China
• Utilize pre-trained ResNet and siamese neural network to extract features from cryo-EM images effectively.
• Assign pre-labels to the cryo-EM images by clustering and iteratively update model parameters to achieve denoising.

Skills

Programming Languages: Python, R, Bash
Tech Skills: Deep Learning, NGS Data Analysis, PyMOL, SQL, LATEX
Language: TOEFL iBT: 107 (Speaking: 23; Listening: 29; Writing: 25; Reading: 30.)

Awards

Excellent Graduate of Shanghai <i>Shanghai Municipal Education Commission</i>	2024
National Scholarship <i>Ministry of Education, China</i>	2022
The International Genetically Engineered Machine Competition Silver Medal <i>iGEM Foundation</i>	2020
China Undergraduate Mathematical Contest in Modeling (Shanghai) Second Prize <i>CSIAM</i>	2019
Mathematical Contest In Modeling Honorable Mention <i>COMAP</i>	2019

Publications

First author or Co-first author

1. **Y Zhang**, J Guan, C Li, Z Wang, Z Deng, RB Gasser, J Song & HY Ou. (2023) DeepSecE: a deep learning-based framework for multi-class prediction of secreted proteins in Gram-negative bacteria. *Research*, 6, 0258.
2. H Gong[†], **Y Zhang**[†], C Dong, Y Wang, G Chen, B Liang, H Li, L Liu, J Xu & G Li. (2023). Unbiased curriculum learning enhanced global-local graph neural network for protein thermodynamic stability prediction. *Bioinformatics*, 39(10), btad589.
3. **Y Zhang**[†], Y Zhang[†], Y Xiong, H Wang, Z Deng, J Song & HY Ou. (2022) T4SEfinder: a bioinformatics tool for genome-scale prediction of bacterial type IV secreted effectors using pre-trained protein language model. *Briefings in Bioinformatics*, 23(1), bbab420.

Others

1. Y Tang, J Zhang, J Guan, W Liang, MT Petassi, **Y Zhang**, X Jiang, M Wang, W Wu, HY Ou & JE Peters. (2024) Transposition with Tn 3-family elements occurs through interaction with the host β -sliding clamp processivity factor. *Nucleic Acids Research*, 52(17), 10416-10430.
2. Z Yan, F Ge, Y Liu, **Y Zhang**, F Li, J Song & DJ Yu. (2024) TransEFVP: a two-stage approach for the prediction of human pathogenic variants based on protein sequence embedding fusion. *Journal of Chemical Information and Modeling*, 64 (4), 1407–1418.
3. Y Li, B Wu, **Y Zhang**, L Liu, L Bai & T Shi. (2024) Enhanced thermostability of *Streptomyces mobaraensis* transglutaminase via computation-aided site-directed mutations and structural analysis. *New Journal of Chemistry*, 48 (2), 591-602.

Preprints

1. **Y Zhang**, Z Wang, Y Jiang, DR Littler, M Gerstein, AW Purcell, J Rossjohn, HY Ou & J Song. (2024) Epitope-anchored contrastive transfer learning for paired CD8 cell receptor-antigen recognition. *bioRxiv*, 2024.04.05.588255.
2. Z Wang, **Y Zhang**, Y Xu, S Imoto, H Chen & J Song (2024) Histo-Genomic Knowledge Distillation For Cancer Prognosis From Histopathology Whole Slide Images. *arXiv*, 2403.10040.
3. LC Shen, L Yan, Z Liu, **Y Zhang**, Z Wang, Y Guo, J Rossjohn, J Song & DJ Yu. (2023) ConBoTNet: supervised contrastive learning enhances MHC-II peptide binding affinity prediction. *bioRxiv*, 2023.12.21.572942.