

Education

- 2021–2024 **Fudan University, M.S.**
- Major: Applied Mathematics
 - Research Interests: Protein Language Model, Homologous Protein Search, Protein Function Prediction
 - English: TOFEL 102 (28+27+21+26)
- 2017–2021 **Southeast University, B.S.**
- Major: Automation (Pattern Recognition)
 - Grades: 88.4/100, 3.8/4.0, 9/114
 - Scholarship: Haila Scholarship (2/114)

Competition awards

- 2023 **Kaggle — CAFA 5 Protein Function Prediction, Rank 1 in the Leaderboard**
- 2021 **China Computer Federation Bioinformatics Conference Challenge 2, Rank 3**
- 2018 **ACM-ICPC Asian Regional Competition Nanjing Station, Bronze Medal**

Research experiences

- 2021–2024 **Graduate Student Researcher, Fudan University (Shanghai, China), Advisor:** Shanfeng Zhu

Research topics

- 2022–2023 **PLMSearch, Under the second round of peer review at Nature Communications**, Invited to present on **WAIC 2023 (World Artificial Intelligence Conference)**
Wei Liu, Ziyi Wang, Ronghui You, Chenghan Xie, Hong Wei, Yi Xiong, Jianyi Yang and Shanfeng Zhu**
- We propose PLMSearch (**P**rotein **L**anguage **M**odel), a homologous protein search method with only sequences as input. With deep representations from a pre-trained protein language model to predict similarity, PLMSearch can capture the remote homology information hidden behind the sequences.
 - PLMSearch can search millions of query-target protein pairs in seconds like MMseqs2 while increasing the sensitivity by more than threefold, and is comparable to state-of-the-art structure search methods.
 - Webserver: <https://dmiip.sjtu.edu.cn/PLMSearch>
 - Github: <https://github.com/maovshao/PLMSearch>
 - BioRxiv: <https://doi.org/10.1101/2023.04.03.535375>

Research funding application

2023- **Photosynthetic Fund Phase III, *Large-scale Protein Function Prediction***

- Parallel optimization of the existing NetGO framework to power large-scale function prediction.

2022-2023 **Wudao Research Funding of Beijing Academy of Artificial Intelligence, *Protein Language Model Pre-training***

- We offer a unified contrastive learning paradigm as well as a prompt-guided multi-task pre-training framework to assist SimPLM in learning from multi-modal protein similarity at the same time.
- We also employ a prompt fine-tuning module to provide downstream tasks the on-demand flexibility of utilizing respective protein similarity.
- SimPLM outperforms state-of-the-art general protein language models in rich functional prediction and remote homology prediction tests.

Internship experience

2020–2021 **ByteDance (TikTok), Shanghai, Real-Time Communications Client Department**

- Research and development engineer, responsible for the development of the basic components (2020.10-2021.03)
 - Reconstruction of log report module
 - Task scheduling and execution status reporting
 - Thread deadlock detection