## Ziyang Xu

Ph.D. Student in Mathematics, The Chinese University of Hong Kong

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Aug. 2024 -

Lanzhou, China

Nanjing, China

Hong Kong SAR, China

Sept. 2020 - Jun. 2024

Sept. 2017 - Jul. 2020

Oct. 2024 - Oct. 2025 Hong Kong SAR, China

Jul. 2024 - Aug. 2024

Jan. 2023 - Oct. 2023 London, Canada

Beijing, China

#### EDUCATION BACKGROUND

•The Chinese University of Hong Kong

Ph.D. in Mathematics

Supervisor: Tieyong Zeng, Liu Liu

Lanzhou University

B.S. in Statistics | GPA: 92.69/100 | Ranking: 1/52

Supervisor: Zhouping Li, Xingxing Jia

•High School Affiliated To Nanjing Normal University

ACADEMIC EXPERIENCES

Research Intern, Theory Lab of Huawei in Hong Kong Research Institute

Project: Mathematical-Model-Based Image Algorithm Research, PI: Tieyong Zeng

•Peking University

•Western University

•Huawei

AI for Mathematics Formalization and Theorem Proving Seminar, BICMR

Mitacs Globalink Research Intern, The Schulich School of Medicine & Dentistry,

Project: Deep Learning for Integrating Multimodal Data for Precision Medicine, Supervisor: Pingzhao Hu

### Interests and Skills

- Research Interests: Large Language Model, Image Processing
- Programming: LLM Fine-tuning and Deployment, Module Optimization, Android/Windows App Development.

#### SELECTED PUBLICATIONS

# REACT: Representation Extraction And Controllable Tuning to Overcome Overfitting in LLM Knowledge Editing

Haitian Zhong, Yuhuan Liu, Ziyang Xu, Guofan Liu, Qiang Liu, Shu Wu, Zhe Zhao, Liang Wang, Tieniu Tan. EMNLP main 2025 We introduce REACT (Representation Extraction And Controllable Tuning), a unified two-phase framework designed for precise and controllable knowledge editing. Relevant experiments on EVOKE benchmarks demonstrate that REACT significantly reduces overfitting across nearly all evaluation metrics, and experiments on COUNTERFACT and MQuAKE shows that our method preserves balanced basic editing performance (reliability, locality, and generality) under diverse editing scenarios.

## Biology Instructions: A Dataset and Benchmark for Multi-Omics Sequence Understanding Capability of Large Language Models [PDF]

Haonan He, Yuchen Ren, Yining Tang, Ziyang Xu, Junxian Li, Minghao Yang, Di Zhang, Dong Yuan, Tao Chen, Shufei Zhang, Yuqiang Li, Nanqing Dong, Wanli Ouyang, Dongzhan Zhou, Peng Ye. EMNLP findings 2025

We introduce Biology-Instructions, the first large-scale multi-omics biological sequences-related instruction-tuning dataset including DNA, RNA, proteins, and multi-molecules, designed to bridge the gap between large language models (LLMs) and complex biological sequences-related tasks.

## PTransIPs: Identification of phosphorylation sites enhanced by protein PLM embeddings [PDF] [Code]

Ziyang Xu, Haitian Zhong, Bingrui He, Xueying Wang, Tianchi Lu. IEEE Journal of Biomedical and Health Informatics

PTransIPs, a new deep learning framework for the identification of phosphorylation sites. PTransIPs utilizes protein pre-trained language model (PLM) embeddings to achieve SOTA performance, with AUCs of 0.9232 and 0.9660 for S/T and Y sites, respectively. PTransIPs is also a universal framework for all peptide bioactivity tasks.

## SELECTED HONORS AND AWARDS

•Brilliant Graduate of Lanzhou University - Academic Type, (Top 5 from university)	[News]	Jun. 2024
•CUHK Vice-Chancellors PhD Scholarship,		Mar. 2024
•Outstanding Graduate of Gansu Province, [News]		Mar. 2024
•Chun-Tsung Scholar, (The 25th Annual) [News]		May. 2023
•Mitacs Globalink Research Intern Scholarship, (2023) [News]		April. 2023
•National Scholarship, $(Rank 1/117)$ [News]		Dec. 2022
•Merit Student of Gansu Province, (0.6%) [News]		Jun. 2022
•National Scholarship, $(Rank 1/157)$ [News]		Dec. 2021