Feng Jiang

+1 (682) 208 3748 - alanfengjiang@gmail.com - UTA 4th Year PhD - Arlington, TX, USA

EDUCATION

The University of Texas at Arlington — Ph.D. in Computer Science
GPA: 4.0/4.0 — *Fall 2022 - Present, Arlington, TX*

RECENT HONORS

Best Ph.D — The University of Texas at Arlington
John S. Schuchman Outstanding Doctoral Student — *Apr 2023*

RESEARCH INTERESTS

- Multimodal Foundation Models for Computational Biology
- AI-driven Drug Discovery: molecular representation learning, drug-target interaction prediction
- Immunoinformatics: TCR/BCR-antigen binding prediction, epitope identification
- Graph Neural Networks and Deep AUC Maximization

SELECTED PUBLICATIONS

4 selected from 15+ publications including NeurIPS (Spotlight), ICCV, ECCV, AAAI, and top journals.

- **Feng Jiang**, Mangal Prakash, Hehuan Ma, Jianyuan Deng, Yuzhi Guo, Amina Mollaysa, Tommaso Mansi, Rui Liao and Junzhou Huang, "TRIDENT: Tri-Modal Molecular Representation Learning with Taxonomic Annotations and Local Correspondence", In Proc. of the 39th Annual Conference on Neural Information Processing Systems, NeurIPS'25, San Diego, CA, USA, December 2025. (***NeurIPS Spotlight, 3% acceptance rate***)
- **Feng Jiang**, Amina Mollaysa, Hehuan Ma, Tommaso Mansi, Junzhou Huang, Mangal Prakash and Rui Liao, "GRAM-DTI: Adaptive Multimodal Representation Learning for Drug–Target Interaction Prediction", NeurIPS 2025 2nd Workshop on Multi-modal Foundation Models and Large Language Models for Life Sciences.
- **Feng Jiang**, Yuzhi Guo, Hehuan Ma, Saiyang Na, Weizhi An, Bing Song, Yi Han, Jean Gao, Tao Wang and Junzhou Huang, "AlphaEpi: Enhancing B Cell Epitope Prediction with AlphaFold 3", In Proc. of the 15th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, ACM BCB'24, Shenzhen, China, November 2024.
- **Feng Jiang**, Yuzhi Guo, Hehuan Ma, Saiyang Na, Wenliang Zhong, Yi Han, Tao Wang and Junzhou Huang, "GTE: A Graph Learning Framework for Prediction of T-Cell Receptors and Epitopes Binding Specificity", Briefings in Bioinformatics, Volume 25, Issue 4, July 2024.
- *Full publication list: Google Scholar* *Personal website: fengjiang02.github.io*

INDUSTRY EXPERIENCE

Johnson & Johnson Research & Development — **NJ, USA**
R&D Data Science & Digital Health DSAI Intern — *May 2025 - Aug 2025*

- Developed multimodal large language models for molecule property prediction and drug-target binding affinity prediction, integrating molecular, protein, and textual descriptions to enhance prediction accuracy.
- Built and curated large-scale molecular datasets from PubChem for pre-training foundation models, achieving state-of-the-art performance on property prediction benchmarks.
- **Recognition:** Work selected as team highlight showcase for exceptional research impact and innovation.
- **Publications:** 1 NeurIPS workshop poster, 1 ICML workshop paper, and 1 manuscript submitted to ICLR'26.

RESEARCH EXPERIENCE

- **Advanced Multimodal Alignment for Molecular Representation Learning (2024.12-Now)**. Proposed TRIDENT with volume-based alignment via Gramian matrices for superior cross-modal correspondence learning (NeurIPS'25 Spotlight). Developed novel techniques for DTI prediction (ICLR'26 submission) and disentangled frameworks for enhanced interpretability.
- **Multimodal Learning for Protein Function and Epitope Prediction (2024.2-12)**. LLaPA: Integrated protein sequences with UniProt descriptions for function prediction. AlphaEpi: Combined ESM-2 and AlphaFold 3 for B-cell epitope prediction (ACM BCB'24).
- **Graph Framework for TCR-Epitope Binding (2023.7-2024.3)**. Developed graph-based framework modeling binding as topology learning with deep AUC maximization, achieving SOTA performance (Briefings in Bioinformatics).