JUSTIN Z. TAM

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SUMMARY

Ph.D. candidate in Computer Science applying deep learning, graph neural networks, and AI systems engineering to problems in bioinformatics and structural biology. Dissertation research centers on explainable GNN models and 3D visualization for protein-protein interaction analysis.

Developed modular, multi-agent workflows for terabyte-scale data analysis at Los Alamos National Lab, and enhanced structure-aware mRNA modeling at Moderna using graph-based and transformer models. Bridging research innovation with scalable real-world applications across industry and labs.

EDUCATION

Ph.D. Candidate in Computer Science/Bioinformatics Aug 2020 - Dec 2025
Lehigh University, P.C. Rossin College of Engineering, Bethlehem, PA
Advisor: Brian Y. Chen

B.A. in Mathematics, Minor in Computer Science and Chemistry Aug 2015 - May 2019
Skidmore College, Saratoga Springs, NY

TECHNICAL SKILLS

Programming: Python, C, C++, Matlab, JavaScript
AI/ML Frameworks: PyTorch, Tensorflow, LangChain , LangGraph, Sklearn, NodeJS, MongoDB, Git, Docker
Specialized Domains: Protein-Protein Structure Analysis, mRNA Prediction, Transformer models (Seq2Seq, BERT), Agentic Workflows, Graph-based deep learning

EXPERIENCE

Los Alamos National Lab, Los Alamos, NM: AI Systems Research Intern May 2025 - August 2025

- Built a modular multi-agent AI workflow to automate terabyte-scale simulation data analysis, in collaboration with Argonne National Lab.
- Integrated LangChain and LangGraph for schema-aware database querying and intelligent task delegation to support plug-and-play scientific pipelines.
- Evaluated modularity, scalability, and interpretability in agentic system design to inform future scientific AI infrastructure at LANL.

Moderna Therapeutics, Cambridge, MA: Bioinformatics Research Co-op Jan 2024 - June 2024

- Developed deep learning models (GNNs and transformers) in PyTorch to analyze structural properties of human-like mRNA.
- Discovered a novel method to modify normally inflexible mRNA properties in mRNA prediction using graph-based features, drawing attention from executive leadership including the VP and directors of digital research.
- Contributed production-level improvements to Moderna's mRNA analysis pipeline and advanced structure-aware prediction tools.

Lehigh University, Bethlehem, PA: Graduate Researcher Aug 2020 - Dec 2025

- Leading development of explainable GNNs for protein-protein interaction modeling, mutation impact prediction, and structural representation learning.
- Published six peer-reviewed papers (five first-author) in venues such as ACM-BCB, MDPI, and IEEE BIBM.
- Deployed a containerization framework for bioinformatics tools, recognized as a Best Paper Finalist, CSBW 2023.

New York City College of Technology, Brooklyn, NY: Adjunct Professor in Mathematics Aug 2019 - June 2020

- Taught pre-calculus, calculus I, and calculus II, integrating new instructional infrastructure.
- Aided in development of a web-based interactive homework and grading system, adopted department-wide to improve consistency.

PUBLICATIONS

Tam, J.Z. et al. Automatic Explanation of Protein-Protein Binding Mechanism: A Preliminary Study.
Computational Structural Bioinformatics Workshop (pp. 84-97). Cham: Springer Nature Switzerland, Mar 26, 2025

Tam, J.Z. et al. A Containerization Framework for Bioinformatics Software to Advance Scalability, Portability, and Maintainability
Proceedings of the 14th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics, Sept 3–6, 2023

- Independent full-stack development project to build a container framework with reusable templates, streamlining the dissemination and deployment of Bioinformatics software.
- Awarded best paper finalist of CSBW at ACM-BCB 2023

Liu, Y., Armstrong, G., **Tam, J.Z.**, & Chen, B. Y. **MechPPI: Binding Mechanism-based Machine-Learning tool for Predicting Protein-Protein Binding Affinity Changes Upon Mutations**
bioRxiv, Oct 31, 2023

- Presented a state-of-the-art ML method leveraging gradient boosted trees and shapley values to curated mechanistic features for analyzing protein-protein binding affinity changes.

Tam, J. Z. et al. HBcompare: Classifying Ligand Binding Preferences with Hydrogen Bond Topology
Biomolecules, MDPI, Oct 28, 2022

- Presented a graph neural network pipeline for analyzing hydrogen bond topology in proteins
- Performed a benchmark study using various machine learning methods like graph neighborhood aggregation strategies, graph kernels, principal component analysis, and convolutional neural networks.

Tam, J. Z., Palumbo, T., Miwa, J. M., & Chen, B. Y. **Analysis of Protein-Protein Interactions for Intermolecular Bond Prediction**
Molecules, MDPI, Sep 21, 2022

- Designed a novel graph network representation of protein-protein interactions, accurately representing intermolecular bonds with efficient representations using networkx.

Tam, J. Z., Palumbo, T., Miwa, J. M., & Chen, B. Y. **DiffBond: A Method for Predicting Intermolecular Bond Formation**
2021 IEEE International Conference on Bioinformatics and Biomedicine (BIBM), IEEE, Dec 9, 2021

LANGUAGES

English (Native)
Mandarin (Fluent)