

Tzu-Tang Lin

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PROFESSIONAL SUMMARY

AI × Bioinformatics Researcher & Developer with 7+ years of cross-disciplinary R&D experience spanning drug discovery, genomics, and biomedical AI. Proven expertise in AI-driven RNA–small molecule drug modeling, antimicrobial peptide and functional protein design, large-scale whole-genome sequencing (WGS) and genome-wide association studies (GWAS), and electronic health records (EHR)-based medical applications. Experienced in independent research, publishing peer-reviewed articles, serving as a reviewer, and mentoring others. Skilled in leading end-to-end research pipelines—from dataset curation to deep learning model development—and collaborating with academia, hospitals, and industry partners.

PROFESSIONAL EXPERIENCE

Research Assistant — University of Florida, College of Pharmacy | May 2024 – Aug 2025

- Developed a cross-domain multimodal contrastive learning framework for RNA–ligand binding affinity prediction, integrating RNA sequences and ligand SMILES embeddings from large language models (LLMs; RiNALMo, SMI-TED) with 3D structural information into a CLIP-based foundation model; achieved Test RMSE 1.68, outperforming the fine-tuned/retrained benchmark model (1.85).
- Conducted fine-tuning and transfer learning leveraging Graph Neural Networks (GNNs) - including the Geometric Interaction Graph Neural Network (GIGN) - alongside 3D-CNN models and a self-developed representation learning module.
- Curated and processed RNA-small molecule structure datasets from biomolecular databases (PDB, PDBbind, HARIBOSS). Designed and implemented automated pipelines for ligand-binding pocket identification, structure-based clustering using both RNA3DB and RMAAlign, and multi-level feature extraction with RDKit, Biopython, and PyMOL.
- Applied in silico drug discovery and design tools - including RNAmigos for virtual screening (10,000,000 molecules across 3 targeted RNAs), AutoDock Vina for docking score evaluation, and DeepCoy for decoy molecule generation.
- Explored AI-based protein design by leveraging generative AI models such as RFdiffusion to generate novel protein structures, using AlphaFold for structural prediction, and ProteinMPNN for sequence design.

Research Assistant — Virginia Tech, Dept. of Computer Science | Aug 2023 – Apr 2024

- Performed metagenomic analysis of aquatic plants to identify antimicrobial resistance genes (ARGs) and antimicrobial peptides (AMPs) using bioinformatics tools, including alignment (Diamond BLAST, Minimap), assembly (MEGAHIT, MetaSPAdes), taxonomic classification (Kraken), and genomic analysis (Fastp, Vsearch, Bedtools).
- Developed PathoVF, a dual-approach ML-based bioinformatics tool for predicting pathogenic and virulence factors, applying multi-modal DNA encoding methods for pathogenic detection and leveraging protein sequence descriptors with protein LLMs (ProtBERT, ESM-1b) for virulence factor classification.

Data Scientist — Cathay Financial Holdings, Data Science R&D Lab | Dec 2022 – May 2023

- Enhanced Sepsis early-warning systems and supported drug recommendations by implementing Feature Tokenizer Transformer models using Electronic Health Records (EHR) tabular data for the Cathay General Hospital ICU, achieving accuracy 0.915.
- Collaborated on multiple Financial Technology (FinTech) Agile projects, including developing a handwritten signature recognition system, generating synthetic banking data using generative AI, and implementing a financial AI agent application with federated learning technology.
- Leveraged AWS cloud services for project workflows, including EC2 for scalable compute, SageMaker for model training and deployment, and S3 for secure data storage and retrieval.
- Achieved a bronze medal (top 9% worldwide) in Kaggle's Novozymes Enzyme Stability Prediction Challenge as a solo participant, implementing an ensemble model that incorporated several protein engineering features.
- Served as an instructor for the Cathay General Hospital Data Science Workshop, providing hospital staff with Python programming and data processing training materials.

Research Assistant / Bioinformatics Engineer — Academia Sinica, Institute of Information Science | Jun 2019 – Dec 2022

- Proposed and developed an AI-driven antimicrobial peptide development platform to generate and evaluate new peptide drug candidates. Performed functional peptide sequential dataset curation and analysis, and implemented deep learning models—including Convolutional Neural Networks (CNNs), Long Short-Term Memory (LSTM) networks, Doc2Vec embeddings, ensemble modeling for predictor development, and Wasserstein Generative Adversarial Network with gradient penalty (WGAN-gp) for data augmentation and peptide generation.
 - Designed two out of eight peptides that demonstrated activity against cancer and antibiotic-resistant bacteria via in vitro experiments; MIC 2–45 µg/mL across species.
 - Packaged the prediction models into AI4AXP, a user-friendly web platform for predicting peptide activities (antibacterial, antifungal, anticancer, antiviral, anti-coronavirus, hemolysis).
 - Invited to showcase at the 2021 and 2022 Healthcare+ Expo Taiwan, and awarded the Taiwan 20th National Innovation Award (2023) for the "AI Fleming" project.
- Analyzed the Taiwan Biobank human genome database and developed deep learning models for predicting disease-related phenotypes (e.g., obesity, hearing loss) using single-nucleotide polymorphisms (SNPs) for precision medicine applications.
- Conducted genome-wide association studies (GWAS) on aquatic species (grouper, tilapia) using bioinformatics tools such as PLINK (Whole Genome Association Analysis Toolset), GATK (Genome Analysis Toolkit), and DeepVariant to identify and analyze high-quality SNPs, leading to patented know-how transferred to Opportunity Biotech Co., Ltd. for aquaculture SNP microarray probe design.

Research Intern — Academia Sinica, Institute of Information Science | Jul 2018 – Jun 2019

- Proposed and implemented a physicochemical-based protein encoding method (PC6) for machine learning modeling of protein representations, integrating it into antimicrobial peptide (AMP) prediction workflows and culminating in the AI4AMP deep learning-based predictor, which surpassed prior state-of-the-art performance.

EDUCATION

University of Florida | May 2024 – Aug 2025

PhD Program in Pharmaceutical Sciences — Withdrawn

Focus: AI Drug Discovery (AIDD)

National Taiwan University | Sep 2015 – Jun 2019

B.S. in Agronomy

Specialization in Experimental Design and Biostatistics

Awarded Undergraduate Research Fellowship, Ministry of Science and Technology (MOST), Taiwan

PUBLICATIONS

Tzu-Tang Lin, Li-Yen Yang, Chung-Yen Lin, Ching-Tien Wang, Chia-Wen Lai, Chi-Fong Ko, Yang-Hsin Shih, Shu-Hwa Chen, 2023. Intelligent De Novo Design of Novel Antimicrobial Peptides against Antibiotic-Resistant Bacteria Strains. *International Journal of Molecular Sciences*, 24(7), 6788. <https://doi.org/10.3390/ijms24076788>

Tzu-Tang Lin, Wen-Chih Cheng, I-Hsuan Lu, Chung-Yen Lin, Shu-Hwa Chen, 2023. Identify Antifungal Peptides using Document Embedding and Physicochemical Property Encoding Deep Learning Models (Submitted).

Tzu-Tang Lin, Yi-Yun Sun, Wen-Chih Cheng, I-Hsuan Lu, Shu-Hwa Chen, Chung-Yen Lin, 2022. AI4AVP: An Antiviral Peptides Predictor in Deep Learning Approach with Generative Adversarial Network Data Augmentation. *Bioinformatics Advances*, 2(1), vbac080. <https://doi.org/10.1093/bioadv/vbac080>

Yih-Yun Sun[†], **Tzu-Tang Lin**[†], Wen-Chih Cheng, I-Hsuan Lub, Shu-Hwa Chen, Chung-Yen Lin, 2022. Peptide-Based Drug Predictions for Cancer Therapy by Using Deep Learning. *Pharmaceuticals*, 15(4), 422. <https://doi.org/10.3390/ph15040422>

Che-Chun Chen, Chang-Wen Huang, Chung-Yen Lin, Chia-Hui Ho, Hong N. Pham, Te-Hua Hsu, **Tzu-Tang Lin**, Rong-Hwa Chen, Shuenn-Der Yang, Chin-I. Chang, Hong-Yi Gong, 2022. Development of Disease-Resistance-Associated Microsatellite DNA Markers for Selective Breeding of Tilapia (*Oreochromis* spp.) Farmed in Taiwan. *Genes*, 13(1), 99. <https://doi.org/10.3390/genes13010099>

Tzu-Tang Lin, Li-Yen Yang, I-Hsuan Lu, Wen-Chih Cheng, Zhe-Ren Hsu, Shu-Hwa Chen, Chung-Yen Lin, 2021. AI4AMP: An Antimicrobial Peptide Predictor Using Physicochemical Property-Based Encoding Method and Deep Learning. *mSystems*, 6(3), e00299-21. <https://doi.org/10.1128/mSystems.00299-21>

PATENTS

Chung-Yen Lin, Shu-Hwa Chen, I-Hsuan Lu, **Tzu-Tang Lin**, Ping-Heng Hsieh, Hsueh-Chien Cheng, 'Optimizing the SNP (Single-Nucleotide Polymorphism) microarray probes design and construction of the analytic pipeline for SNP calling and Genotyping based on the Whole Genome Assembly', 2020, 05T-1091014

LEADERSHIP

- Co-recipient of the 20th National Innovation Award (Academic Research Category, 2023) for the project AI Fleming: AI-powered platform for advanced generation, selection, and validation of functional and therapeutic peptides, awarded by the Research Center for Biotechnology and Medicine Policy.
- Served as instructor for the Cathay General Hospital Data Science Workshop (2023), delivering Python programming and data processing training for hospital staff.
- Supervised four summer interns at Academia Sinica, Institute of Information Science (2019-2022), guiding them to successfully complete their research projects.
- Delivered the invited talk "Hunt for Novel Antibiotics: Discovering New Antimicrobial Peptides in AI" at the 2022 Kiss Science event, hosted by the National Science and Technology Council, Taiwan.
- Peer-reviewed a paper for Briefings in Bioinformatics (2022, Impact Factor: 13.994).