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) such as RiNALMo and SMI-TED, alongside 3D structural information, into a CLIP-based foundation model.
- 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 RNA3DB and RMalign, and multi-level feature extraction with RDKit, Biopython, and PyMOL.
- Applied in silico drug discovery and design tools - including RNAmigos for virtual screening, 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.
- 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.
- 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.
  - Packaged the prediction models into AI4AXP, a user-friendly web platform for predicting peptide activities (antibacterial, antifungal, anticancer, antivirus, 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 BiostatisticsAwarded
Undergraduate Research Fellowship, Ministry of Science and Technology (MOST), Taiwan

PUBLICATIONS

1. **Lin T-T**. et al. (2023) Intelligent De Novo Design of Novel Antimicrobial Peptides, International Journal of Molecular Sciences, 24(7), 6788.
2. **Lin T-T**. et al. (2023) Identifying Antifungal Peptides via Embedding and DL Models, (Submitted)
3. **Lin T-T**. et al. (2022) AI4AVP: GAN-Augmented Antiviral Peptide Predictor, Bioinformatics Advances, 2(1).
4. Sun Y-Y[†], **Lin T-T**[†] et al. (2022) Peptide-based Drug Predictions for Cancer Therapy, Pharmaceuticals, 15(4), 422.
5. Chen C-C. et al. (2022) Microsatellite DNA Markers for Selective Breeding of Tilapia, Genes, 13(1), 99.
6. **Lin T-T**. et al. (2021) AI4AMP: AMP Predictor using Physicochemical Encoding, mSystems, 6:e00299-21.

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

- Peer-reviewed a paper for Briefings in Bioinformatics (2022)
- Presented 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
- Co-recipient of the 20th National Innovation Award (Academic Research Category), awarded by the Research Center for Biotechnology and Medicine Policy, for the project "AI Fleming:

AI-powered platform for advanced generation, selection, and validation of functional and therapeutic peptides" (2023)

TECHNICAL SKILLS