

LINFENG WANG

wanglinfeng1115@gmail.com ♦ +44 7599610897 ♦ linkedin.com/in/w15 ♦ linfeng-wang.github.io/

TECHNICAL STRENGTH

Language & Frameworks:	Python, PyTorch, PyG, R, Bash, MySQL, HTML/CSS, C++
Machine learning:	Scikit-learn, Transformers, LLMs, CNNs, RNNs, GNNs, VAEs, XGBoost
Development Tool:	Pandas, NumPy, Docker, Git, Nextflow, Google Cloud, Jupyter, Huggingface, Chroma
Visualization:	OpenCV, Unity, Matplotlib, Plotly, ggplot2

EDUCATION

London School of Hygiene and Tropical Medicine, DPhil Computational Genomics	Oct 2021 – Oct 2025 (expected)
Dissertation: <i>Machine Learning-Enhanced Drug Resistance and Bioinformatics Transmission Profiling of Tuberculosis Using Genome Sequencing</i>	
Imperial College London, MRes Bioengineering (Hons), Merit	Oct 2019 – Oct 2020
Modules: Computational & Statistical Methods for Research, Frontiers in Bioengineering, Biomaterials Dissertation: <i>Design of an Artificial Bruch's Membrane from Synthetic Polyesters.</i>	
King's College London, BSc Biochemistry (Hons), 1st	Sep 2016 – Jul 2019
Module selected: Bioinformatics, Protein structure and design, Human genomics. Dissertation: <i>Investigation of Concordance Between Molecular Dynamics Simulation and FRET Biosensor using Designed Protein Linker System.</i>	

EXPERIENCE

PhD researcher - LSHTM (Clark Campino Phelan lab), London UK	Jul 2022 – Sept 2025
Project: Deep Learning and Statistical Modelling for Tuberculosis Drug Resistance and Transmission	
<ul style="list-style-type: none">- Developed interpretable deep learning models (CNN, RNN, GNN, Transformer) in PyTorch and JAX to predict TB drug resistance from genomic data- Built statistical pipelines in Python for GWAS, PCA, logistic regression, and odds ratio analysis on Philippine TB datasets- Created a genetic algorithm-based tool for gene amplicon design using Python and Nextflow- Reduced model complexity and compute time by transitioning from raw sequence to SNP frequency input	
Machine learning consultant - Deep Science Venture, London UK	Mar 2025 -
Project: Sequence-Based Drug Discovery using Deep Generative Models	
<ul style="list-style-type: none">- Trained CNN, RNN, and VAE models on biological sequences with data augmentation and hyperparameter optimization- Applied SHAP, LIME, and DeepLIFT to extract interpretable biological insights from deep models- Supported strategic model design for generative sequence discovery tasks	
Data study group hackathon participant – The Alan Turing Institute, London UK.	Jan 2024
Project: Shallow Gas Hazard Detection in Offshore Seismic Data	
<ul style="list-style-type: none">- Led deep learning model development for detection and segmentation on geophysical imagery using CNNs with contrastive learning- Delivered 90% classification accuracy on legacy seismic datasets under 2-week sprint- Collaborated across domain boundaries to translate geoscience challenges into ML solutions	
Machine learning Intern - Linkevity, London UK	Aug 2024 – Oct 2024
Project: Graph-Based Drug-Drug Interaction Prediction	
<ul style="list-style-type: none">- Built and optimized MLP and GNN models in Python for predicting compound interactions- Conducted benchmarking studies across model architectures to improve predictive performance- Scaled ML training workflows using Google Cloud Platform for high-throughput experimentation	
Data Science intern - ByteDance, London UK	Aug 2022 – Feb 2023
Project: Neoantigen Insight Platform and Market Landscape Scouting	
<ul style="list-style-type: none">- Built SQL-integrated chemical database and applied autoencoders to reveal neoantigen patterns across biological datasets- Coordinated interdisciplinary market research on biologics and small molecules- Authored bi-weekly research briefings and developed end-to-end ML pipelines for discovery support	

PUBLICATIONS (6 First authored, 9 in total)

- Wang, L., Thawong, N., Thorpe, J., Higgins, M., Tan, M., Sawaengdee, W., Mahasirimongkol, S., Perdigao, J., Campino, S., Clark, T. G. & Phelan, J. E. A novel tool for designing targeted gene amplicons and an optimised set of primers for high-throughput sequencing in tuberculosis genomic studies. *bioRxiv*, (Submitted to *BMC genomics*). doi: <https://doi.org/10.1101/2025.01.13.632698> (**presented at ESM2024-poster and ASMicrobe-talk**) - Website: <https://genomics.lshtm.ac.uk/webtoast/#/> **software package**: <https://pypi.org/project/toast-amplicon/>
- Wang, L., Campino, S., Phelan, J. & Clark, T. G. Mixed infections in genotypic drug-resistant Mycobacterium tuberculosis. *Scientific Reports* **13**, 1–8 (2023). doi: <https://doi.org/10.1038/s41598-023-44341-x>
- LSTM-Based Transfer Learning Models for Tuberculosis-Targeted Antimicrobial Peptide Classification and Generation. (submitted for publication)
- Decoding Positive Selection in Mycobacterium tuberculosis with Phylogeny-Guided Graph Attention Models. (forth coming).
- Data Study Group Final Report: British Geological Survey - Detecting Shallow Gas from Marine Seismic Images". The Alan Turing Institute (2025)
- Phelan, J., Niazi, F., Wang, L., Ngwana-Joseph, G. C., Sobkowiak, B., Cohen, T., Campino, S. & Clark, T. G. TGV: suite of tools to visualize transmission graphs. *NAR Genomics and Bioinformatics* **6**(4) (2024). doi: <https://doi.org/10.1093/nargab/lqae158>

