Jingran Wang

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Education

Medical College of Soochow University *Sept 2022 – July 2026*
- Major: BS in Bioinformatics
- Cumulative GPA: 3.9/4.0 — Major GPA: 4.0/4.0 — Rank in class: 1/35
- Awards: First Class Scholarship for Studying (2024), Second Class Scholarship for Innovation (2024), Award for Social Contribution (2024), Comprehensive Scholarship (2024)

University of California, Berkeley *Jan 2025 – May 2025*
- Program: Berkeley Global Access
- Enrolled Courses: Artificial Intelligence (CS 188), Machine Learning (CHEM 277B), Biophysical Chemistry (CHEM C130), Quantitative Biology (CMPBIO C210)

Publications

1. **Wang, J.**, Yang, M., Zong, C., Gennady, V., Xiao, F., Hu, G. (2025) *protPheMut: An Interpretable Machine Learning Tool for Classification of Cancer and Neurodevelopmental Disorders in Human Missense Variants. bioRχiv* (under review at *Bioinformatics*, first author) doi.org/10.1101/2025.01.06.631365 ↗

2. Yang, M.[†], **Wang, J.**[†], Zhou, Z., Li, W., Gennady, V., Xiao, F., Hu, G. (2025) *Decoding Mechanisms of PTEN Missense Mutations in Cancer and Autism Spectrum Disorder using Interpretable Machine Learning Approaches. bioRχiv* (under review at *JCIM*, co-first author) doi.org/10.1101/2025.01.16.633473 ↗

3. **Wang, J.**, Hao, Z., Lin, L., Liu, J., Wang, J., Tang, Z., Geng, D., Ni, C., Yang, H., Li, K., Du, J. (2025) *CT-based Osteoporosis Classification and Bone-Muscle Interaction Mapping Using Multiple Interpretable Machine Learning Models with the BMINet Framework. medRχiv* (first author) doi.org/10.1101/2025.02.12.25321163 ↗

4. **Wang, J.** (2023) *Blood Lipids and Cardiovascular Disease: A Mendelian Randomization Study. Transactions on Materials, Biotechnology and Life Sciences* (FBB 2023, first author) doi.org/10.62051/qamtcg89 ↗

Research Experience & Projects

Ministry of Education Key Laboratory of Geriatric Diseases and Immunology (Prof. Guang Hu) & Chapman University Schmid College of Science and Technology (Prof. Gennady Verkhivker)

1. Development of protPheMut Tool Tool Website ↗ Project Homepage ↗
Provincial Sponsored Project, Project Leader *Feb. 2024 – Present*
- Developed **protPheMut**, an online server tool that automatically calculates multi-perspective mutation characteristics with advanced interpretability
- Designed a comprehensive machine learning framework providing visual results including biological indicator analysis, mutation significance scoring, inter-molecular network impact assessment, and protein dynamics visualization
- Implemented the model to classify multiphenotypic effects (Neural Development Disorders and cancer) caused by onco-protein missense mutations, emphasizing their impact on inter-molecular networks and protein dynamics
- Achieved state-of-the-art performance in predicting phenotypic effects, with AUROC of 0.8501 for PI3Ka and 0.9349 for multi-phenotype PTEN mutations, offering insights into phenotype formation mechanisms through model interpretability

2. Molecular Mechanism of PTEN Missense Mutations Project Homepage ↗
Project Co-leader *Nov. 2023 – Present*
- Led integrated computational research investigating molecular mechanisms of PTEN missense mutations shared between autism spectrum disorder (ASD) and cancer
- Developed interpretable machine learning models to predict mutations with shared phenotypic effects
- Conducted comprehensive computational studies using molecular dynamic simulations, inter-molecular pathway analysis, and advanced machine learning screening techniques
- Revealed local conformational changes in PTEN protein structure and long-term allosteric pathway alterations critical to mutation impacts

3. Deep Learning in Complex Biological Interaction System   Project Homepage 🔗
Project Co-leader   *Sept. 2024 – Present*

- Utilized protein language model ESM-2 to generate advanced protein sequence embeddings as network node features
- Constructed inter-molecular dynamic network using Elastic Network Model (ENM) to characterize residue vibration covariance
- Applied Graph Attention Model to embed and pool large dynamic networks into vector representations, mapping protein dynamic structures to protein-protein interaction network topology
- Developed conceptual framework for future disease and drug target detection using advanced deep learning techniques like Graph Convolutional Networks and Graph Transformers

Department of Orthopedic Surgery (by Dr. Jun Du), the First Affiliated Hospital of Soochow University

1. Development of BMINet and Insight into Osteoporosis   Package Website 🔗 Project Homepage 🔗
Project Leader   *Feb. 2024 - Present*

- Collected and processed retrospective medical data from 444 patients, including DXA, CT, and MRI scans
- Measured CT values for 6 vertebrae and 30 adjacent muscle groups to assess bone and muscle density
- Developed multiple interpretable machine learning models to classify osteoporosis and construct bone-muscle interaction networks
- Uncovered complex bone-muscle interaction patterns showing vertebrae-dominated early interactions shifting to muscle-clustered modules in advanced stages
- Developed and open-sourced BMINet, a Python package for researchers to analyze interaction networks

BioDesign Center (by Prof. Hongwu Ma), Tianjin Institute of Industrial Biotechnology, Chinese Academy of Sciences

Research Assistant   *July 2023 - Aug. 2023*

- Contributed to the design of a Graph Neural Network model for enzymatic dataset mining
- Developed advanced machine learning techniques to predict catalytic efficiency of enzymes
- Analyzed complex biochemical data to identify potential catalytic enzymes, providing valuable insights into potential biotechnology applications
- Explored innovative methods for discovering new catalytic properties, utilized deep learning approaches to enhance understanding of enzyme function and activity

Yale School of Public Health, Yale University (by Prof. Shuangge Ma)

Research Training   *Jan. 2023- Nov. 2023*

- Conducted a two-sample Mendelian randomization study investigating causal relationships between blood lipids and cardiovascular disease (CVD)
- Investigated causal associations of HDL-C, LDL-C, and triglycerides with cardiovascular disease with genetic data from over 400,000 individuals in the UK Biobank and outcome data from the FinnGen consortium to examine lipid-related CVD risks
- Discovered significant causal links between elevated lipid levels and increased CVD risk, providing critical insights into lipid management and CVD prevention strategies

Skills & Stuff

Technical Skills: Python, R, PHP, JavaScript, HTML5, C, PostgreSQL, Linux

ML & DL: GNN, CNN, Transformer, PyTorch, PyG, Scikit-Learn

Biology & Bioinformatics: Molecular Biology, Biochemistry, Biophysics, Cellular Biology, SDS-Page, PCR, Western Blot, Genomic Informatics, Proteomic Informatics, Metabolomics Informatics, Bioinformatics Algorithms, GROMACS, Augustus, Clustal, Prody, FoldX, MetaboAnalyst, IGV, Cytoscape etc.

Interests: Badminton, Long-distance running, Swimming, Traveling

Internships & Voluntary work

Suzhou Heart Bar Artificial Intelligence Company: Volunteered to deploy LLMs (Large Language Models) to offer psychological tests among primary school and high school students in order to guard against mental illness of teenagers

Suzhou BenQ Hospital: Volunteered to keep patients' safety and handle emergency issues