

Luopin Wang

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PROFESSIONAL SUMMARY

PhD in Computer Science with 7+ years of experience in computational biology and bioinformatics, spanning both academic research and industry. Proven expertise in applying deep learning to cancer and immune-related multi-omics data, including bulk and single-cell sequencing. Demonstrated success in translational research, tool development, and collaborative publications in high-impact journals.

EDUCATION

Purdue University, Department of Computer Science <i>PhD in Computer Science</i>	West Lafayette, IN 08/2018-05/2024
Wuhan University, International School of Software <i>Bachelor of Engineering, Software Engineering</i>	Wuhan, China 09/2014-06/2018

TECHNICAL SKILLS

- **Programming:** Proficient in Python, R, and Java; working knowledge of C++, C, Julia, and MATLAB.
- **Deep Learning:** Extensive experience with PyTorch for developing deep learning and graph-based models.
- **NGS & Multi-Omics Analysis:** Skilled in processing and integrating RNA-seq, scRNA-seq, ATAC-seq, ChIP-seq, eCLIP-seq, CUT&RUN, CUT&Tag, Hi-C, HiChIP, 4C, and long-read sequencing data.
- **High-Performance Computing:** Proficient with SLURM and PBS-based clusters for scalable data processing and model training.
- **Data Visualization:** Experienced with Matplotlib, Seaborn, ggplot2, GraphPad Prism, and DataGraph for scientific visualization and exploratory analysis.

SELECTED RESEARCH PROJECTS

Purdue University <i>Postdoctoral Researcher, Dr. Ananth Grama & Dr. Nadia Atallah Lanman</i>	West Lafayette, IN 06/2024 – Present
<ul style="list-style-type: none">• Developing scMeta-TME, a transformer-based model that integrates tumor microenvironment context to predict metastatic potential from single-cell primary tumor transcriptomes.• Designed scMeta, a graph transformer framework for predicting metastasis risk at single-cell resolution and identifying high-risk subpopulations, with integrated gradient-based gene prioritization. (under review)• Developed PreMet, a deep learning model combining variational autoencoders with supervised latent space learning to accurately predict metastasis sites from bulk tumor transcriptomic profiles.	
Purdue University <i>Graduate Research Assistant, Dr. Majid Kazemian</i>	West Lafayette, IN 08/2018 – 05/2024
<ul style="list-style-type: none">• Designed a GNN-based framework to predict drug-induced transcriptomic responses across cell types, supporting personalized drug repurposing.• Built PET (Pathway Ensemble Tool) and the first experimental benchmark for pathway analysis methods, improving accuracy, reproducibility, and reducing false positives (Nature Communications 2024).• Identified prognostic biomarkers from TCGA data and proposed candidate drugs to normalize gene dysregulation in bladder cancer.• Developed a convolutional neural network-based tool integrating eCLIP-seq and RNA structures to predict RBP binding sites with state-of-the-art performance.• Led and maintained bioinformatics pipelines and NGS analysis for collaborative projects with NIH, Dundee, and internal labs.	

- Developed predictive models for ethnicity and sex classification using variant calls from TCGA, demonstrating population-level insights from germline genomic data.

Wuhan University

Wuhan, China

Undergraduate Research Intern, supervised by Dr. Xing Chen

10/2016 - 04/2017

- Developed a novel computational framework, using single low-rank embedding, to predict miRNA-disease associations using a personalized recommendation-based algorithm, achieving superior performance over existing models.

INDUSTRY EXPERIENCE

BioMarin Pharmaceutical Inc.

San Rafael, CA

NGS Intern, supervised by Dr. Marissa Holmbeck

05/2022-08/2022

- Built and deployed pipelines for Nanopore long-read sequencing analysis of gene therapy constructs, improving data interpretation efficiency.
- Presented results across functional teams, informing downstream therapeutic development decisions.

SELECTED AWARDS

- Purdue Institute for Cancer Research (PICR) Outstanding Doctoral Student Award. 2024
- Purdue University Department of Biochemistry's Dr. Beach Travel award 2022
- Purdue University Department of Biochemistry's Dr. Henry A. Moses Award 2021
- Excellent student and Outstanding student of Wuhan University 2014-2016

SELECTED PUBLICATIONS

- **Luopin Wang***, Aryamav Pattnaik*, et al., "Unbiased discovery of cancer pathways, biomarkers and therapeutics using a new Pathway Ensemble Tool and Benchmark", *Nature Communications* 15, 7288 (2024).
- **Luopin Wang**, Jun Liang, et al, "Epstein-Barr Virus episome physically interacts with active regions of the host genome in lymphoblastoid cells", *Journal of Virology*. 94 (24), e01390-20.
- ZhuHong You*, **Luopin Wang***, et al, "PRMDA: personalized recommendation-based MiRNA-disease association prediction", *Oncotarget*. 8(49): 85568-85583.
- Yan B.*, Freiwald T. *, Chauss D. *, **Luopin Wang***, et al, "SARS-CoV-2 drives JAK1/2-dependent local complement hyperactivation", *Science Immunology*. 6(58):eabg0833.
- McGregor R. *, Chauss D. *, Freiwald T. *, Yan B. *, **Luopin Wang***, et al, "Autocrine vitamin D signaling switches off pro-inflammatory programs of TH1 cells", *Nature Immunology*. 1-13.

* denotes joint first author

SELECTED PRESENTATIONS

- "Evaluate pathway analysis methods: from benchmark to best practices", **oral presentation** at 4th annual RECOMB/ISCB Conference on Regulatory & Systems Genomics with DREAM Challenges RSGDREAM 2022, Las Vegas, NV. 11/2022
- "Evaluate pathway analysis methods: from benchmark to best practices", poster presentation at 25th International Conference on Research in Computational Molecular Biology (RECOMB), virtual. 08/2021