

Luopin Wang

✉ wang3712@purdue.edu ☎ 765-714-3469 💬 Luopin Wang 💬 loooooooopi

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

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	West Lafayette, IN
<i>Postdoctoral Researcher, Dr. Ananth Grama & Dr. Nadia Atallah Lanman</i>	<i>06/2024 – Present</i>

- 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	West Lafayette, IN
<i>Graduate Research Assistant, Dr. Majid Kazemian</i>	<i>08/2018 – 05/2024</i>

- 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