Wei Zhang

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Research Interests

Multi-omics Integration, Machine Learning, Deep Learning, Random Forests, Variable Selection, Meta-analysis, Biomarker Detection, Subtype Clustering, Statistical Genomics, Epigenetics, Neurodegenerative Disease and Cancers

Research Experience

University of Miami	Miami, FL
Postdoctoral Associate	Sep 2024 - Present
• Develop and implement advanced computational and machine learning methods for the analysis of	large-scale omics data
• Conduct computational analyses to identify biomarkers and therapeutic targets using multi-omics d	lata integration
 Develop and apply machine learning models for predictive analytics in biomedical research 	
• Maintain and optimize computational clusters and cloud computing environments to support large	-scale data analysis
Graduate Research Assistant	May 2022 - Aug 2024
 Collaborated with a diverse team to research and analyze genomic data for association studies, bion predictions in late-onset Alzheimer's Disease, triple-negative breast cancer, and colorectal cancer 	narker discoveries, and disease
• Published multiple research papers contributing to the field of biomarker detection and disease pred	liction
\circ Supported in drafting and editing grant proposals, ensuring clarity and alignment with project object	ctives
EDUCATION	
University of Miami	Miami, FL
Ph.D. in Biostatistics Advisor: Chen, X. Steven, Ph.D.	Aug 2024
 Dissertation: Integrative Multi-Omics Analysis Using Multivariate Random Forest 	
The George Washington University	Washington, DC
M.S. in Statistics	May 2019
State University of New York at Binghamton	Binghamton, NY

B.S. in Economics Analysis & Actuarial Math

PROJECTS

Multivariate Random Forest Framework for Multi-omics Data Integration

Tools: R, Random Forest, method development

- Developed a random forestbased method integrating multi-omics datasets to improve predictive accuracy compared to single-omics analyses significantly.
- Implemented simulation and real data validation compared with benchmarking methods, achieving enhanced biomarker detection accuracy.
- Created comprehensive documentation and methodology pipelines, ensuring replicability of translational research applications.
- Ongoing work in developing multi-omics integration for disease subtyping and data imputation.
- Github Repositories:
 - * 🖓 An Integrative Multi-Omics Random Forest Framework for Robust Biomarker Discovery
- Tumor and CellLine Transcriptomes Alignment with Deep Neural Networks

Tools: Python, Pytorch, Variational Autoencoder (VAE)

- Develop a deep learning framework integrating Variational Autoencoders and domain-adversarial training to align tumor and cell-line transcriptional profiles.
- Enable generalization to new transcriptomic datasets by projecting them into a shared latent space and mitigating systematic domain-specific biases.

Epigenetic Biomarkers for Alzheimers and Cognitive Health

Tools: R, statistical modeling, longitudinal cohort analysis

- Identified and validated blood-based DNA methylation signatures predictive of incident dementia in longitudinal cohorts.
- Evaluated reliability of the Illumina MethylationEPIC v1.0 platform for robust epigenomic measurements.
- Discovered distinct cerebrospinal fluid biomarker-associated methylation profiles from Alzheimers patients and cognitively normal subjects.

Ongoing

May 2017

Ongoing

2023 - 2025

- Collaborated on statistical methodology development and comprehensive data analyses to advance cognitive resilience research.
- Github Repositories:
 - * **O** Blood DNA Methylation Signature for Incident Dementia: Evidence from Longitudinal Cohorts
 - * 🗘 DNA Methylation Signature of a Lifestyle-based Resilience Index for Cognitive Health
 - * 🗘 Critical Evaluation of the Reliability of DNA Methylation Probes on the Illumina MethylationEPIC v1.0 BeadChip Microarrays
 - * C Distinct CSF biomarker-associated DNA methylation in Alzheimer's disease and cognitively normal subjects

• Prediction Models for Cancer Biomarkers

Tools: R, WGCNA, meta-analysis

- Developed transcriptome-based prediction models for chemotherapy response using matched colorectal tumor-organoid gene expression data.
- Implemented network-based biomarker selection methods to enhance prediction accuracy in oncology studies.
- Performed a meta-analysis on triple-negative breast cancer datasets to identify robust gene signatures linked to neoadjuvant chemotherapy outcomes.
- Contributed to interdisciplinary research initiatives, informing personalized treatment strategies in cancer care.
- Github Repositories:
 - * 🗘 Enhancing Chemotherapy Response Prediction via Matched Colorectal Tumor-Organoid Gene Expression Analysis and Network-Based Biomarker Selection
 - * 🗘 Transcriptome Meta-Analysis of Triple-Negative Breast Cancer Response to Neoadjuvant Chemotherapy

PUBLICATIONS AND PREPRINTS

J=JOURNAL, S=IN SUBMISSION, T=THESIS

2023 - 2024

- [J.1] Zhang W, Young JI, Gomez L, Schmidt MA, Lukacsovich D, Kunkle B, Chen XS, Martin ER, Wang L. (2025). Blood DNA methylation signature for incident dementia: Evidence from longitudinal cohorts. *Alzheimer's & Dementia*, 21:e14496.
- [J.2] Zhang W, Wu C, Huang H, Bleu P, Zambare W, Alvarez J, Wang L, Paty PB, Romesser PB, Smith JJ, Chen XS. (2025). Enhancing chemotherapy response prediction via matched colorectal tumor-organoid gene expression analysis and network-based biomarker selection. *Translational Oncology*, 52:102238.
- [S.1] Zhang W, Huang H, Wang L, Lehmann BD, Chen XS. (2025). An Integrative Multi-Omics Random Forest Framework for Robust Biomarker Discovery. Manuscript submitted for publication in *GigaScience*. Preprint available at bioRxiv.
- [S.2] Chen XS, Lukacsovich D, Zambare W, Wu C, Huang H, Zhang W, Kim MJ, et al. (2025). Integrating Tumor and Organoid DNA Methylation Profiles Reveals Robust Predictors of Chemotherapy Response in Rectal Cancer. Preprint available at medRxiv.
- [S.3] Zhang W, Lukacsovich D, Young JI, Gomez L, Schmidt MA, Martin ER, Kunkle BW, Chen X, OShea DM, Galvin JE, Wang L. (2024). DNA Methylation Signature of a Lifestyle-based Resilience Index for Cognitive Health. Alzheimer's Research & Therapy. In press.
- [T.1] Zhang W. (2024). Integrative Multi-Omics Analysis using Multivariate Random Forest. PhD Thesis, University of Miami.
- [J.3] Zhang W, Young JI, Gomez L, Schmidt MA, Lukacsovich D, Varma A, Chen XS, Kunkle B, Martin ER, Wang L. (2024). Critical evaluation of the reliability of DNA methylation probes on the Illumina MethylationEPIC v1.0 BeadChip microarrays. *Epigenetics*, 19(1):2333660.
- [J.4] Lukacsovich D, O'Shea D, Huang H, Zhang W, Young JI, Chen XS, et al. (2024). MIAMI-AD: An integrative knowledgebase facilitating exploration of DNA methylation across sex, aging, and Alzheimers disease. *Database*, 2024, baae061.
- [J.5] Zhang W, Young JI, Gomez L, Schmidt MA, Lukacsovich D, Varma A, Chen XS, Martin ER, Wang L. (2023). Distinct CSF biomarker-associated DNA methylation in Alzheimer's disease and cognitively normal subjects. Alzheimer's Research & Therapy, 15:78.
- [J.6] Zhang W, Li E, Wang L, Lehmann BD, Chen XS. (2023). Transcriptome meta-analysis of triple-negative breast cancer response to neoadjuvant chemotherapy. *Cancers*, 15(8):2194.
- [J.7] Silva TC, Zhang W, Young JI, Gomez L, Schmidt MA, Varma A, Chen XS, Wang L. (2022). Distinct sex-specific DNA methylation differences in Alzheimers disease. *Alzheimer's Research & Therapy*, 14(1), 121.

PRESENTATIONS

O=CONTRIBUTED TALK, P=POSTER

- [0.1] An Integrative Multi-Omics Random Forest Framework for Robust Biomarker Discovery, STATGEN: Conference on Statistics in Genomics and Genetics. May 2025. Minneapolis, MN, USA.
- **[P.1]** An X chromosome-wide DNA methylation study of Alzheimers disease, *Alzheimer's Association International Conference (AAIC)*. Jul 2024. Virtual Poster.
- [O.2] Unlocking the potential of multi-omics data integration using multivariate random forest approach, International Biometric Society Eastern North American Region (ENAR) Annual Meeting. Mar 2024. Baltimore, MD, USA.
- [P.2] Distinct CSF biomarker-associated DNA methylation in Alzheimer's disease and cognitively normal subjects, *Alzheimer's Association International Conference (AAIC)*. Jul 2023. Virtual Poster.
- **[P.3]** Iterative Multivariate Random Forest for Feature Selection in Integrating Multi-Omics Datasets, Annual American Statistical Association (ASA) Florida Chapter Meeting. Mar 2023. Gainesville, FL, USA.

TEACHING EXPERIENCE

TEACHING ASSISTANT	
• EPH705 Advanced Statistical Methods Professor: Wang, Lily University of Miami	2022 - 2024
• STAT6201 Applied Linear Models Professor: Barut, Emre The George Washington University	2018
PROFESSIONAL DEVELOPMENT	
WORKSHOPS	
• Duke Electronic Health Records Study Design Workshop Duke University	Dec 2024
Code Rigor and Reproducibility with R Boot Camp Columbia University	July 2023
Skills	
 Proficient in R/Rstudio and Python for package building, data analysis, and visualization Comprehensive skills in SAS for various statistical applications Familiar with Linux in system and command 	
HONORS AND AWARDS	
Award of Academic Merit University of Miami	Aug 2024
Student Competition Award ASA Florida Chapter Meeting • Best student poster	March 2023 [\$]
Travel Award University of Miami	<i>Mar</i> 2023

PROFESSIONAL SERVICES AND ACTIVITIES

Manuscript Peer Review

Manuscript Reviewer

• Nature Communication; Scientific Reports; Discover Applied Sciences; Biology Direct; Discover Oncology; Medicine in Omics

Membership

Member

• International Biometric Society (ENAR)

• American Statistical Association (ASA)

• International Society to Advance Alzheimer's Research and Treatment (ISTAART)

ADDITIONAL INFORMATION

Languages: English (Proficiency level), Mandarin (Native Speaker), Cantonese (Proficiency level) Interests: Tennis