

Tairan Song

Email: tairan.song@outlook.com Tel: (+1) 734-819-0577

Education

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- Michigan State University**, East Lansing, MI, USA Aug 2023 – Present
Ph.D. Student in Computational Mathematics, Science and Engineering
Advisor: Dr. Adam Alessio
- King's College London**, London, United Kingdom Sep 2021 – Sep 2022
M.Sc. in Applied Statistical Modelling & Health Informatics
Advisors: Dr. Ioannis Bakolis, Dr. Amy Ronaldson; **Graduated with Distinction**
- University of Liverpool**, Liverpool, United Kingdom Sep 2018 – Jun 2021
B.Sc. in Mathematics and Statistics; **Second Class Honours (Upper Division)**

Publications

Zhang, T., Jia, H., **Song, T.**, Lv, L., Gulhan, D. C., Wang, H., ... & Shen, N. (2023). De novo identification of expressed cancer somatic mutations from single-cell RNA sequencing data. *Genome Medicine*, 15(1), 115.

Conference Submissions

Song, T., Noyes, S. L., Muterspaugh, R., Munavar Ali, M. A., Zhou, S., Tobert, C., Lane, B. R., Lim, E., Alessio, A. *Predicting Kidney Cancer Grade from Highly Variable Contrast Timing CT*. Submitted to SIIM 2026, under review.

Research Experience

Kidney Cancer Grade from Highly Variable Contrast Timing CT

Advisor: Dr. Adam Alessio Michigan State University Jan 2025 – Dec 2025

- Developed a radiomics-based modeling framework for renal mass grading from heterogeneous abdominal CT with highly variable contrast timing, addressing protocol-induced intensity shifts beyond phase-specific imaging pipelines.
- Designed a reference-region-aware feature representation that augments tumor radiomics with quantitative descriptors from surrounding anatomical regions (normal kidney, aorta, inferior vena cava), enabling contrast-timing-robust classification without explicit phase normalization or labeling.
- Implemented and evaluated an end-to-end pipeline including automatic multi-organ segmentation (nnU-Net, TotalSegmentator), high-dimensional radiomics extraction, supervised feature reduction, and cross-validated classification, demonstrating consistent performance gains over tumor-only models for multi-class and binary grading tasks.

De Novo Identification of Expressed Cancer Somatic Mutations from scRNA Sequencing Data

Advisor: Dr. Ning Shen Zhejiang University Sep 2022 – Mar 2023

- Contributed to the development and evaluation of the RESA (Recurrently Expressed SNV Analysis) computational framework for high-precision de novo identification of expressed somatic mutations from scRNA-seq data, which consistently outperforms existing methods across multiple benchmark

datasets.

- Implemented and validated the joint logistic regression component (RESA-jLR) within the RESA pipeline to expand the pool of detectable somatic variants and improve mutation calling performance.
- Performed extensive data preprocessing, mutation calling workflows, and empirical performance evaluation, and generated publication-ready figures supporting sensitivity and precision benchmarking against other methods reported in the study.

Teaching Experience

Teaching Assistant	Michigan State University	Jan 2025 – May 2025
<ul style="list-style-type: none">• CMSE 202: Computational Modeling and Data Analysis II		

Professional Experience

Research Assistant	Zhejiang University	Sep 2022 – Mar 2023
<ul style="list-style-type: none">• Contributed to the RESA project for de novo identification of expressed somatic mutations from single-cell RNA sequencing data, supporting sequencing data analysis and model validation efforts.• Provided sequencing data analysis support for collaborative mouse studies, including single-cell RNA sequencing and bulk RNA-seq experiments.		

Awards

NSF NRT-IMPACTS Fellowship	Michigan State University	Awarded Sep 2023
One-semester fellowship funded by the National Science Foundation Research Traineeship Program (NSF DGE-1828149).		

Skills

Programming: Python, R, SQL

ML & AI: Scikit-learn, PyTorch, TensorFlow, NLP, Transformers

MLOps & Systems: SLURM, Git, High Performance Computing, CI/CD

Research: Statistical Analysis, Translational Science, Interdisciplinary Research, Biomedical Image Analysis