Tairan Song

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Education

Michigan State University, East Lansing, 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
Academic Advisor: Dr. Jinlai Li; **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. (2025). *Predicting Kidney Cancer Grade from Highly Variable Contrast Timing CT*. Submitted to SIIM 2026, under review.

Research Experience

Spatially Aware Modeling of Renal Tumor Heterogeneity from Abdominal CT

Advisor: Dr. Adam Alessio Michigan State University Jan 2026 – Present

- Extending contrast-timing–robust radiomics frameworks toward spatially aware modeling of renal tumors in abdominal CT, with a focus on intra-tumoral and peri-tumoral heterogeneity.
- Investigating sub-regional representations of renal parenchyma and tumor compartments (core vs. margin) and exploring multimodal fusion of image-derived features with clinical variables to improve robustness, interpretability, and cross-cohort generalization.

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, explicitly addressing variability introduced by inconsistent contrast timing across real-world imaging protocols, and implemented an end-to-end pipeline with automatic multi-organ segmentation (nnU-Net for renal regions and TotalSegmentator for vascular structures), high-dimensional radiomics extraction, and supervised feature reduction.
- Proposed a reference-region–aware feature representation that augments tumor radiomics with quantitative descriptors from surrounding anatomical regions (normal kidney, aorta, inferior vena cava), improving robustness to contrast-timing variation without explicit phase normalization.

- Systematically evaluated multiple feature reduction strategies and classifiers under cross-validation, demonstrating consistent performance gains over tumor-only models for both 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

- CMSE 202: Computational Modeling and Data Analysis II Jan 2025 – May 2025

Professional Experience

Research Assistant Zhejiang University Sep 2022 – Mar 2023

- Contributed to the RESA framework for detecting expressed somatic mutations from scRNA-seq data, focusing on sequencing data analysis, model validation, and figure generation.
- Supported multi-omics sequencing data analysis for collaborative mouse studies, including scRNA-seq, bulk RNA-seq, and ChIP-seq.

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: PyTorch, scikit-learn; deep learning for medical imaging (CNN-based architectures, e.g., U-Net); NLP and Transformer-based models

MLOps & Systems: SLURM, Git, High Performance Computing

Research: Medical Imaging Analysis, Biological sequence Analysis, Statistical Analysis, Interdisciplinary Research