Tairan Song

EDUCATION

Michigan State University, East Lansing, Michigan, USA

Ph.D. student in Computational Mathematics, Science and Engineering

Aug 2023 – Present

Advisor: Dr. Adam Alessio

King's College London, London, Greater London, United Kingdom

Master of Science (M.Sc.) in Applied Statistical Modelling & Health Informatics

Sep 2021 – Sep 2022

Advisor: Dr. Ioannis Bakolis & Dr. Amy Ronaldson; Graduation with distinction degree

University of Liverpool, Liverpool, Merseyside, United Kingdom

Bachelor of Science (B.Sc.) in Mathematics and Statistics

Graduation with Second class honours, upper division

Sep 2018 – Jun 2021

Publication

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.

RESEARCH EXPERIENCE

Kidney Cancer 3D CT Image Segmentation Project

Advisor: Dr. Adam Alessio

Michigan State University (Jan 2025 – Present)

- Developed algorithms for precise segmentation of kidney cancer in 3D CT scans, improving diagnostic and treatment planning accuracy using advanced deep learning techniques.
- Implemented Swin UNET, enhancing traditional models with a hierarchical Transformer structure for better image analysis in high-resolution medical imaging.

Enhancing Transcription Factor Binding Site Prediction with Epigenetic Data: A BERT-Based ML Innovation Michigan State University (Oct 2023 –Apr 2024)

- Developed a machine learning framework utilizing the BERT model to predict transcription factor binding sites by integrating DNA sequences with epigenetic markers and chromatin accessibility data.
- Applied the model to non-coding regions to explore the impact of genetic variations on gene regulation. Improved prediction accuracy, revealing new insights into the regulatory roles of non-coding DNA in disease.

Multi-Omics Analysis of Chromatin Interactions and Transcriptional Regulation in Mutant and Wild-Type Samples Michigan State University (Mar 2024 – Aug 2024)

- ChIP-seq Analysis: Performed genome-wide analysis to identify chromatin binding sites, removing PCR duplicates and low-quality reads, and called peaks at specific loci.
- Pro-seq Analysis: Conducted gene expression profiling, focusing on key regulatory genes, and quantified reads within specific genomic regions.
- 3C-seq Analysis: Quantified chromatin interactions at target loci and generated cumulative interaction plots, excluding bait points for accuracy.

De Novo Identification of Expressed Cancer Somatic Mutations from Single-Cell RNA Sequencing Data Advisor: Dr. Ning Shen Zhejiang University Medical Centre (Sep 2022 – Mar 2023)

- Contributed to the RESA (Recurrently Expressed SNV Analysis) project, which developed a framework to detect expressed somatic mutations from scRNA-seq data.
- Performed data analysis and preprocessing for single-cell RNA-seq data; developed and optimized the joint logistic regression model (RESA-jLR) for mutation detection.

Association between Air Pollution Exposure and Mental Health Service Use for Dementia Individuals in South London Master's Dissertation (Supervisors: Dr. Ioannis Bakolis & Dr. Amy Ronaldson). KCL (Nov 2021 – Sep 2022)

- Extracted research sample via SQL from CRIS database and performed data processing and statistical modelling in STATA.
- Built statistical models using negative binomial regression and logistical regression to analyse the association between air pollution exposure and mental health functioning and explored the application of epidemiological design.
- This study ultimately concluded that residential air pollution exposure was associated with increased use of mental health services for dementia treatments. Interventions to reduce air pollution exposure could potentially improve treatment outcomes and reduce healthcare costs in dementia patients.

PROFESSIONAL/CAREER EXPERIENCE

Sep 2022 – Mar 2023

Research Assistant (Advisor: Dr. Ning Shen).

• Participate in a project of the research group, the project is about trying to detect somatic mutations in single cell RNA sequencing data (10X). Responsible for all kinds of sequencing analysis, including single-cell RNA sequencing and bulk-RNA sequencing in the research group.

AWARD

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

SKILLS & ACHIEVEMENT

Programming: Python, R, MATLAB, Microsoft Office Suite (Word, Excel, PowerPoint)