

Jingxiao Chen

Contact Information

Address: 1200 Pressler St. RASW912, Houston, TX 77030-3900
Tel: +1 616-920-4055
Email: Jingxiao.chen@uth.tmc.edu
Website: jingxiaochen.com
Google Scholar: <https://bit.ly/2EBdMHI>
Citizenship: China

Education

DOCTOR OF PHILOSOPHY IN BIOSTATISTICS | ANTICIPATED MAY 2023 | THE UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER AT HOUSTON, HOUSTON, TX, US

- Minor: Epidemiology & Breadth: Data Science

MASTER OF SCIENCE IN BIOSTATISTICS | JAN 2018 | CASE WESTERN RESERVE UNIVERSITY, CLEVELAND, OH, US

BACHELOR OF SCIENCE IN MATHEMATICAL STATISTICS | MAY 2016 | PURDUE UNIVERSITY, WEST LAFAYETTE, IN, US

- Discovery Park Undergraduate Research Internship Scholarship, Purdue University 2015-2016

Research Experience

GRADUATE RESEARCH ASSISTANT | THE UNIVERSITY OF TEXAS HEALTH SCIENCE CENTER AT HOUSTON | AUG. 2020 TO PRESENT

Harris County Public Health (HCPH) COVID-19 Project

- Analyzed and monitored the weekly changes of Test Positivity Rate (TPR) for each race/ethnicity group and zip code in Harris County
- Visualized Test Positivity Rate (TPR) and Test Positivity Disparity among race/ethnicity spatial distributions with geographical maps by time series
- Generated reproducible summary reports with new test data using Sweave on a weekly basis

Traumatic Brain Injury (TBI) Prediction Project

- Built machine learning models to predict the prognosis of traumatic brain injury using patient admission demographic data and clinical characteristics.

GRADUATE RESEARCH ASSISTANT | MD ANDERSON CANCER CENTER | AUG. 2018 TO JULY. 2020

Tumor Heterogeneity Project

- Established tumor transcriptome deconvolution pipeline utilizing the computationally efficient DeMixT R-package with OpenMP and additional cancer-specific biological information to understand the tumor microenvironment (TME) using available gene expression cancer consortium such as the Cancer Genome Atlas (TCGA) projects.
- Validated tumor transcriptome deconvolution results using multiple independent validation cancer datasets via survival outcome prediction accuracy improvement (i.e. time-dependent AUC) and clinical characteristics (i.e. tumor subtype & pathological stage)
- Benchmarked multiple deconvolution methods utilize cell-type-specific gene expression from single-cell RNA sequencing (scRNA-seq) data to characterize cell type compositions from bulk RNA-seq data in complex tissues with human retinal tissue single-nuclei RNA sequencing (snRNA-seq) and matching bulk RNA sequencing data.

- Developed scRNA-seq-specific TMS (total mRNA Score) in application of tumor identification

Li-Fraumeni syndrome (LFS) Project

- Built LFSPRO, an R package for TP53 germline mutation carrier estimation, and cancer risk predictions.
- Validated the prediction performance of the penetrance estimates from our competing risk-based statistical model trained with data of 186 pediatric-sarcoma families collected at MD Anderson Cancer Center via two independent cohorts combined.
- Provided the first set of penetrance estimates using a recurrent events survival modeling approach for single primary cancers (SPC) and multiple primary cancers (MPC) for TP53 mutation carriers and demonstrated its accuracy for cancer risk assessment via MD Anderson cohort of TP53 tested individuals.

BIostatistician | CLEVELAND CLINIC | JULY 2017 TO JULY, 2018

- Examined the risk factors, predictive factors, and complications of Postoperative urinary retention (POUR) in patients undergoing elective posterior lumbar decompression with or without fusion for lumbar stenosis
- Evaluated the incidence and risk factors for 90-day readmission and reoperation after elective surgery for lumbar spinal stenosis (LSS).
- Teaching assistant for biostatistics curriculum at Lerner College of Medicine

Publication

- Cao, S., Wang, J. R., Ji, S., Yang, P., **Chen, J.**, Montierth, M. D., ... & Livingstone, J. (2020). Differing total mRNA expression shapes the molecular and clinical phenotype of cancer. *bioRxiv*.
- Shin, S. J., Dodd-Eaton, E. B., Peng, G., Bojadzieva, J., **Chen, J.**, Amos, C. I., ... & Ballinger, M. L. (2020). Penetrance of Different Cancer Types in Families with Li-Fraumeni Syndrome: A Validation Study Using Multicenter Cohorts. *Cancer research*, 80(2), 354-360.
- Shin, S. J., Dodd-Eaton, E. B., Gao, F., Bojadzieva, J., **Chen, J.**, Kong, X., ... & Wang, W. (2020). Penetrance estimates over time to first and second primary cancer diagnosis in families with Li-Fraumeni syndrome: a single institution perspective. *Cancer research*, 80(2), 347-353.
- Shin, S. J., Dodd, E., Peng, G., Bojadzieva, J., **Chen, J.**, Ning, J., ... & Yuan, Y. (2019). Characterizing age-of-onset of multiple primary cancers and specific cancer types in families with Li-Fraumeni syndrome.
- Ilyas, H., Golubovsky, J. L., **Chen, J.**, Winkelman, R. D., Mroz, T. E., & Steinmetz, M. P. (2019). Risk factors for 90-day reoperation and readmission after lumbar surgery for lumbar spinal stenosis. *Journal of Neurosurgery: Spine*, 31(1), 20-26.
- Cao, S., Wang, Z., Gao, F., **Chen, J.**, Zhang, F., Frigo, D. E., ... & Wang, W. (2019). An R Implementation of Tumor-Stroma-Immune Transcriptome Deconvolution Pipeline using DeMixT. *bioRxiv*, 566075.
- Golubovsky, J. L., Ilyas, H., **Chen, J.**, Tanenbaum, J. E., Mroz, T. E., & Steinmetz, M. P. (2018). Risk factors and associated complications for postoperative urinary retention after lumbar surgery for lumbar spinal stenosis. *The Spine Journal*, 18(9), 1533-1539.

Posters & Presentation

- iBright 2019, "Deconvolution reveals cell-type-specific transcriptional effects across cancer types"
- ASHG 2019, "LFSPRO: A risk prediction R package for probabilities of age-of-onset of multiple primary cancers and specific cancer types in families with Li-Fraumeni Syndrome"
- Q-bio 2019, "Deconvolution analysis to understand the tumor-stroma-immune environment in prostate cancer"

Technical Skills

- Programming: R, Python, SAS, JMP, MySQL
- Operating System: Windows, Linux, macOS