

Jingxiao Chen

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Summary

Ph.D. student trained in biostatistics, with strong programming, statistics and communication skills developed from extensive research experience and ability independently or as part of a team. Special expertise in the following areas:

- Statistics
- Machine Learning
- Deep Learning
- Statistical Modeling
- Data Visualization
- Data Cleaning and Wrangling
- Data Mining
- Data Analytics

Education

University of Texas Health Science Center at Houston

Ph.D., Biostatistics

Houston, TX
Anticipated in May 2023

Case Western Reserve University

M.S., Biostatistics

Cleveland, OH

January 2018

Purdue University

B.S., Mathematical Statistics

West Lafayette, IN

May 2016

Professional Experience

Graduate Research Assistant

August 2020 – Present

The University of Texas Health Science Center at Houston

Houston, TX

- Developing machine learning models that improve the prediction accuracy of the prognosis of traumatic brain injury using patient admission demographic data and clinical characteristics with supervised learning algorithms
- Performing statistical analysis with the unstructured data monitor the trend of daily and weekly SARS-CoV-2 infections in Greater Houston to inform public health policy
- Visualizing spatial distribution data with geographical maps by time series
- Generating reproducible summary reports with new data using Sweave on a weekly basis

Graduate Research Assistant

August 2018 – July 2020

MD Anderson Cancer Center

Houston, TX

- Conducted methodological research on unsupervised clustering and classification on high dimensional single-cell RNA sequencing (scRNA-seq) data

- Deployed survival analysis and time-dependent AUC (Receiver Operator Characteristics analysis) using clinical characteristics (i.e. tumor subtype & pathological stage) to validated tumor transcriptome decomposition results
- Established tumor transcriptome deconvolution analysis pipeline to understand the tumor microenvironment (TME) using available gene expression cancer consortium such as the Cancer Genome Atlas (TCGA) projects
- Built LFSPRO, an R package for TP53 germline mutation carrier estimation, and cancer risk predictions which outperformed typical clinical diagnostic criteria
- Benchmarked deconvolution methods utilize cell-type-specific gene expression from scRNA-seq data to characterize cell type compositions from bulk RNA-seq data in complex tissues
- Prepared manuscripts for grants and publication in peer-reviewed journals

Biostatistician

Cleveland Clinic

July 2017 – July 2018

Cleveland, OH

- Performed feature selection, multiple regression, tree-based methods and regularization regression to examine the risk factors of patients undergoing elective posterior lumbar decompression
- Provided statistical consulting for other researchers and clinicians at the institute
- Worked as a teaching assistant for biostatistics curriculum at Lerner College of Medicine

Skills

Programming: R / Python / MySQL / SAS / Perl / JMP

Relevant Modules: scikit-learn / scipy / mglearn / pillow/ nltk / spacy / numpy / pandas / matplotlib

Operating system: Windows / Linux / Mac OS

Languages: English (proficient), Chinese (native)

Version Control: Git

Publications

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.

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.

Presentations & Posters

- “Deconvolution reveals cell-type-specific transcriptional effects across cancer types,” iBright, Houston, 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,” ASHG, Houston, 2019
- “Deconvolution analysis to understand the tumor-stroma-immune environment in prostate cancer,” Q-bio, Houston, 2019