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 — Houston, TX
Ph.D., Biostatistics — Anticipated in May 2023
Case Western Reserve University — Cleveland, OH
M.S., Biostatistics — January 2018
Purdue University — West Lafayette, IN
B.S., Mathematical Statistics — 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 monitoring 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 July 2017 – July 2018
Cleveland Clinic 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