Jingxiao Chen

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Summary

- Co-authored five peer-reviewed papers and collaborated on projects in clinical trials, electronic health records (EHR), COVID-19, and tumor microenvironment
- Extensive modeling experience in clinical trials, time series, longitudinal, high-throughput sequencing, and unstructured data
- Proficient in statistical computing: 6+ years of experience in R, 5+ years of experience in SAS, 3+ years of experience in Python

Education

University of Texas Health Science Center at Houston   Houston, TX
Ph.D., Biostatistics (**Minor**: Epidemiology; **Breadth**: Data Science)   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

Leveraging FITBIR Data to Improve Clinical Practice of Severe Traumatic Brain Injury
PI: Dr. Jose-Miguel Yamal

- Harmonize and curate data from various multi-center clinical trial studies
- Develop and validate statistical and machine learning methods (e.g., regularized regressions, discriminant analysis, random forests, support vector machines, etc.) that assess the association of multimodal longitudinal physiological variables with long-term neurological outcomes
- Cluster multivariate clinical patient trajectories with many missing values for patient stratification and optimize the personalized medicine

SARS-CoV-2 Surveillance Testing Program for Harris County
Co-PI: Dr. Jose-Miguel Yamal

- Adopt time-series models (e.g., Auto-Regressive Integrated Moving Average and neural network autoregression models) to predict COVID-19-related ICU and general bed usage for multiple Trauma Service Areas (TSAs) and Harris County in Texas for allocation of medical resources

- Perform geospatial analysis with the data monitoring the trend of daily and weekly SARS-CoV-2 infections and vaccinations to inform public health policy

Graduate Research Assistant   August 2018 – July 2020
The University of Texas MD Anderson Cancer Center   Houston, TX

Statistical Methods for Genomic Analysis of Heterogeneous Tumors
PI: Dr. Wenyi Wang

- Researched cell-type classification with high dimensional scRNA-seq data using dimensionality reduction techniques and unsupervised learning algorithms
- Simulated multimodal transcriptomic data and evaluated transcriptome decomposition performance with survival and time-dependent ROC analysis
- Established tumor transcriptome deconvolution analysis pipeline to understand the tumor microenvironment (TME) using available gene expression cancer consortium, i.e., TCGA
- 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

Risk Prediction for Li-Fraumeni Syndrome: A Practical Tool for Clinical Health Care Providers
PI: Dr. Wenyi Wang

- Built LFSPRO, an R package for TP53 germline mutation carrier estimation, and cancer risk predictions which outperformed typical clinical diagnostic criteria
- Validated the LFSPRO 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

Biostatistician   July 2017 – July 2018
Cleveland Clinic   Cleveland, OH

- Performed feature selection techniques, multiple regressions, tree-based methods, and regularization regressions to examine the risk factors of patients undergoing elective posterior lumbar decompression
- Provided statistical consulting for other researchers and clinicians at the institute

Skills

Programming: R / SAS / Python / MySQL / Perl
Coursework: Bayesian Data Analysis, Stochastic Process, Generalized Linear Models, Machine Learning, Survival Analysis, Categorical Data Analysis, Probability Theory, Statistical Inference
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. *Under review at Nature Biotechnology.*

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