JOHNATHAN JIA

Third year MS student seeking fulltime position

I am currently a 3rd year MS student enrolled at the University of Texas Health Science Center (UTHSC) Graduate School of Biomedical Sciences (GSBS) Quantitative Sciences (QS) program. I have an interest in bioinformatics and data mining. I am seeking a full-time position as a data analyst or data scientist. I am proficient in both R and Python, and I believe my background allows me to connect both data science and traditional biology.

CONTACT INFO

✉ jdjia93@gmail.com

⊙ github.com/jjia1

SKILLS

Experienced in data mining, machine learning, and deep learning.

Proficient with Tensorflow/Keras, Pandas, Numpy, and Scikit-learn libraries.

Skilled in R and Python.

🖥 RESEARCH EXPERIENCE

2012-2015

Undergraduate Research Assistant
Emory University, Department of Biology   📍 Atlanta, GA

- Studied within-host dynamics of infection between viruses and the immune system using a population biology approach with predator-prey interactions.
- Implemented deterministic (differential) and stochastic models in R to find the host factors that cause variation in immune response after administration of the yellow fever vaccine (live-attenuated virus).

2015 | 2018

Medical School Research Assistant
UTHSC McGovern Medical School, Department of Rheumatology
📍 Houston, TX; Shenzhen, China

- Collaborated with physicians in China to establish new ankylosing spondylitis (AS) patient cohort for comparative analysis with the US cohort.
- Translated and transcribed patient information from Chinese into English and performed statistical analysis (ANOVA, t-test) on the new patients. - Helped perform analysis and write abstract regarding the effect of NSAID indices on AS disease progression and pathology

2020 | Current

Graduate Research Assistant
UTHSC GSBS, Center for Precision Health   📍 Houston, TX

- Currently building a deep learning prediction model using TensorFlow and Keras with 4,000,000 samples that can be used in vaccine development and cancer immunotherapy treatment.
- Developed a convolutional neural network with self-attention architecture using TensorFlow and Keras for identifying high confidence transcription factor targets for human T-cell leukemia virus. Available on Github.
- Performed pseudotime analysis to infer which transcription factor programs drive the trajectory of COVID-19 infection severity using both Seurat and Slingshot in R with machine learning models in Python.
- Regularly collaborates with various colleagues to conduct research, build models, and perform statistical analysis on large datasets.

*This resume was made with the R package **pagedown**.*

Last updated on 2022-11-10.

💼 PROFESSIONAL EXPERIENCE

2019-2020

Research Assistant I
MD Anderson Cancer Center, Immunotherapy Platform 📍 Houston, TX
- Analyzed scRNA-seq data from patient cancer samples using CellRanger and Seurat in R. Used PCA and tSNE projections to look for any characteristics or unique cell populations. Performed differential gene expression analysis and generated volcano plots.
- Processed and prepared blood, bone marrow, and cancer tissue samples from patients for storage or subsequent analysis such as flow cytometry, staining, and sequencing.

📄 PUBLICATIONS

2017

What Controls the Acute Viral Infection Following Yellow Fever Vaccination?
Bulletin of mathematical biology
James Moore, Hasan Ahmed, **Johnathan Jia**, Rama Akondy, Rafi Ahmed, Rustom Antia DOI: 10.1007/s11538-017-0365-3

2021

Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches.
Genes
Hyun-Hwan Jeong and **Johnathan Jia** (co-first author), Yulin Dai, Lukas Simon, Zhongming Zhao DOI: 10.3390/genes12050635

2022

Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches.
The Innovation
Wendao Liu, **Johnathan Jia**, Yulin Dai, Wenhao Chen, Guangsheng Pei, Qiheng Yan, Zhongming Zhao DOI: 10.1016/j.xinn.2022.100289

2022

Detecting and elucidating human T-cell leukemia virus type 1 integration sites with deep learning
Patterns *(currently under review)*
Haodong Xu and **Johnathan Jia** (co-first author), Hyun-Hwan Jeong, Zhongming Zhao Preprint DOI: 10.2139/ssrn.4208345

🎓 EDUCATION

2011-2015

Emory University
B.S. in Biology with High Honors and B.A. in Chemistry 📍 Atlanta, GA

Thesis: Investigating heterogeneity in the dynamics of virus and immune response following a yellow fever vaccination

2015-2018   • **UTHSC McGovern Medical School**

📍 Houston, TX

2020-2022 (Expected)   • **UTHSC Graduate School of Biomedical Sciences**
M.S. in Quantitative Sciences   📍 Houston, TX

Thesis: DeepHTLV: a deep learning model for detecting and elucidating
human T-cell leukemia virus type 1 integration sites

🔖 HONORS AND AWARDS RECEVED

2016   • **Rheumatology Research Foundation Research Award**
Awarded for Shenzhen AS cohort research

2022   • **First prize at UTH GSBS Quantitative Sciences Retreat
Poster Presentation**
First prize for pre-candidacy students