

JOHNATHAN JIA

Currently searching for fulltime position

I am currently working fulltime as a data analyst in the Liu lab at Baylor College



PROFESSIONAL EXPERIENCE

- 2023

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Data Analyst
Baylor College of Medicine

• QC and analyzed scRNA-seq data from brain organoid tissues

• Developed pipelines in Python and R for use

• Pipeline for IMC Data Analysis

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Houston, TX

2020
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2019

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Research Assistant I
MD Anderson Cancer Center

• Collected and prepared samples of blood, bone marrow, and tumor for storage and analysis

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Houston, TX

RESEARCH EXPERIENCE

2023
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2020

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Graduate Research Assistant
UTHSC Houston Graduate School of Biomedical Sciences

• Developed DeepHTLV

• Analyzed COVID-19 scRNA-seq data transcriptional programs using DrivAER

• Wrote review of current COVID-19 scRNA-seq research

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Houston, TX

EDUCATION

2022
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2020

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M.S. in Quantitative Sciences
UTHSC Houston Graduate School of Biomedical Sciences

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

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Houston, TX

2018
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2015

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M.D.
UTHSC Houston McGovern School of Medicine

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Houston, TX

2015
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2011

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B.S. in Biology
Emory University

• Investigating heterogeneity in the dynamics of virus and immune response

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Atlanta, GA

HONORS AND AWARDS

2022

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Best presentation at QS Seminar
Best QS seminar presentation

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Houston, TX

2022

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

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Houston, TX

2016

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Rheumatology Research Foundation Research Award
Awarded for Establishing Shenzhen Ankylosing Spondylitis Cohort

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Houston, TX

CONTACT INFO

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github.com/jjia1

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832-361-0388

SKILLS

Skill	Proficiency Level (0-100%)
R	100%
Python	100%
Bash	90%
Jupyter	100%
LaTeX	80%
Tensorflow	100%
Pytorch	80%
Git/Docker	100%

PUBLICATIONS

Deep learning for detecting and elucidating human T-cell leukemia virus type 1 integration sites (Cell Patterns 2023)

H.Xu and **J.Jia**, H.Jeong,Z.Z

Delineating COVID-19 immunological features using single-cell RNA sequencing (The Innovation 2022)

W.Liu, **J.Jia**, Y.Dai, W.Chen, G.Pei,Q.Yan, Z.Zhao

Investigating Cellular Trajectories in the Severity of COVID-19 and Their Transcriptional Programs Using Machine Learning Approaches (Genes 2021)

H.Jeong and **J.Jia**, Y.Dai, L.Simon, Z.Zhao

What Controls the Acute Viral Infection Following Yellow Fever Vaccination? (Bulletin of Mathematical Biology 2016)

J.Moore, H.Ahmed, **J.Jia**, R.Akondy, R.Ahmed, R.Antia

This resume was made with the R package [pagedown](#).
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