(314) 680-8961

xinyug@usc.edu Xinyu Guo www.linkedin.com/in/xinyu-guo-5408 **EDUCATION University of Southern California** Los Angeles, CA Doctor of Philosophy, Computational Biology and Bioinformatics Current Andrew J. Viterbi Fellowship Baltimore, MD Johns Hopkins University Master of Science, Biostatistics, GPA 3.97/4.0 August 2020 - May 2022 Member of the Delta Omega Public Health Honorary Society St. Louis, MO Washington University in St. Louis August 2018 - May 2020 Bachelor of Art, Mathematics Major & Computer Science Minor, GPA 3.89/4.0 Cum Laude Dean's List Shanghai, China East China University of Science and Technology Sep 2016 - June 2018 Mechanical Engineering Major, GPA 3.7/4.0 China National Scholarship Highest Academical Scholarship of Each China University of Science and Technology Berkeley, CA University of California in Berkeley, Summer Institute June – August 2017 RESEARCH EXPERIENCE

Lab Member, Statistical Genetics and Genomics Studies	Los Angeles, CA
Advisor: Dr. Liang Chen, University of Southern California	Aug 2022 – Present
• Analyzing cell cycle phases distributions with single cell RNA-seq data at tissue-specific and cell	
type-specific level	
 Accurately predicting cell cycle phases with single-cell RNA-seq data 	
Analyzing disease-related alternative splicing at cell-type level	
Lab Member, Statistical Genetics Studies	Baltimore, MD

Advisor: Dr. Nilanjan Chatterjee & Dr. Diptavo Dutta, Johns Hopkins University

Oct 2020 – Present Developed a cross-tissue subset-based meta-analysis method (CSTWAS) to identify a set of

Integrating genome-wide association study (GWAS) results with single-cell ATAC-seq data to interpret etiology for human diseases at the cellular level

Research Assistant, Statistical Genomics Studies

potential "active" tissues with improved power

Advisor: Dr. Hongkai Ji & Dr. Eneda Toska, Johns Hopkins University

Analyzing RNA-seq and ChIP-seq/ATAC-seq data: Align and map sequence reads to the genome; Implement downstream analysis such as differential analysis, gene set enrichment analysis, and motif analysis

Elucidating how transcriptional and epigenetic regulators mediate hormone-driven cancer tumor resistance to therapeutics

Research Assistant, Alzheimer's Disease Biomarkers

Advisor: Dr. Chenguang Wang & Dr. Zheyu Wang, Johns Hopkins University

Created a R package to collect Alzheimer's Disease biomarkers form BIOCARD, NACC, and ADNI databases, and create an analysis dataset

Researcher Assistant, Respiratory Failure Prediction

Advisor: Dr. Andrew Michelson, Washington University in St. Louis, Institute for Informatics

Modeled with lasso and logistic regression to predict respiratory failure probability of COVID-19 tested patients. This model is implemented in the Barnes-Jewish Hospital Electronic Health Record system to early identify patients' risks for respiratory decompensation, facilitating timely resource deployment

Researcher, Bootstrap Method Research

Advisor: Dr. Todd Kuffner, Washington University in St. Louis

Investigated the properties of bootstrap method in R and visualizing its resampling process and evaluated a new method to smooth data density curve and focusing on finding an optimal bandwidth

Baltimore, MD

Feb 2021 – Present

Baltimore, MD Aug 2020 – Oct 2022

St. Louis, MO

June 2020 – Dec 2020

St. Louis, MO May 2019 – May 2020

TECHNICAL SKILLS

- Computer languages: R, Python, Java, HTML, CSS, Java Script, Latex, MATLAB, SQL
- Computer programs: Cluster Computing, SolidWorks, Auto CAD, Microsoft Office, Wind, Amazon AWS
- Other: Shiny App Building, Statistical Model Building, Web Design, Data Collection from APIs

PAPERS & PUBLICATIONS

• Subset-based method for cross-tissue transcriptome-wide association studies improves power and interpretability.

Guo, X., Chatterjee, N, Dutta, D.

(doi: https://doi.org/10.1101/2023.01.11.23284454)

• PI3K pathway regulates AR-dependent transcription in breast cancer through the epigenetic regulator KMT2D.

Kittane, S*., Ladewig, E*., Arruabarrena-Aristorena, A*., Guo, X^., Sallalku, M^., Karthaus, W., Blawski, R., Ji, H., Leslie, C., Sawyers, C., Toska, E#.

*^ these authors contributed equally #corresponding

(Manuscript in submission)

• SMYD2 Regulates Chromatin Modifier KMT2D in ER+/PIK3CA Mutant Breast Cancer.

Blawski, R., Sallaku, M., Guo, X., Kittane, S., Scaltriti, M., Luo, M., Toska, E. (Manuscript in submission)

LEADERSHIP AND COMMUNITY INVOLVEMENTS

Founder, China EYE Public Welfare

Shanxi, China

• Founded an NGO with more than 50 people and raised a donation online while holding charity book fairs in schools and parks

June 2016 – Present

 Went to middle schools in impoverished areas and donated 100 brand new desks with many other teaching equipment

HONORS AND CERTIFICATIONS

- Be elected a member of the Alpha chapter of the Delta Omega Society—Honorary Society in Public Health (May 2022)
- Present at the Second Annual Data Science Workshop at Augusta University (October 2021)
- Poster Presentation in MSSISS at University of Michigan (February 2020)
- Summer Undergraduate Research Award (Summer 2019)
- Poster Presentation in Undergraduate Research Symposium (November 2019)
- Math tutor of Washington University in St. Louis Arts & Science school (August 2019)
- First prize in the 7th Advanced Graphing Technology and Innovation Design Competition (June 2017)
- Outstanding Student Leaders of East China University of Science and Technology (June 2018)
- Professional Certification of Auto CAD Graphing
- Patent—Multifunctional Shared Printer [201821510016.7]; Patent—Portable Shared Printer [201821494888.9]

Personal Website: https://www.brian-guo.com GitHub: https://github.com/Thewhey-Brian