# Xinyu Guo

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## EDUCATION

**University of Southern California,** GPA 3.95/4.0
**Doctor of Philosophy, Computational Biology and Bioinformatics**
Los Angeles, CA
August 2022 - Current
- Andrew J. Viterbi Fellowship, awarded to outstanding Ph.D. students in computational sciences

**Johns Hopkins University**
**Master of Science, Biostatistics,** GPA 3.97/4.0
Baltimore, MD
August 2020 - May 2022
- Selected member of the Delta Omega Public Health Honorary Society

**Washington University in St. Louis**
**Bachelor of Art, Mathematics Major & Computer Science Minor**, GPA 3.89/4.0
St. Louis, MO
August 2018 - May 2020
- Cum Laude, Dean's List

## RESEARCH EXPERIENCE

**Lab Member, Statistical Genetics and Genomics Studies**
Advisor: Dr. Liang Chen, University of Southern California
- Developed a **self-supervised contrastive learning method** with GNN/GCN architectures to analyze spatial transcriptomics data, optimizing performance, enabling integration with large-scale multi-omics datasets, and genetical risk evaluation.
- Identified novel potential genetic drivers of nonsense-mediated mRNA decay with downstream regulatory implications, **adopted in multi-omics pipelines at peer institutions**.
- Conducted large-scale analysis of single-cell RNA-seq data to study cell cycle phases across tissues and cell types, leading to **publication in *Briefings in Bioinformatics* (2024)**.

**Lab Member, Statistical Genetics Studies**
Advisor: Dr. Nilanjan Chatterjee & Dr. Diptavo Dutta, Johns Hopkins University
- Developed a cross-tissue subset-based meta-analysis method (CSTWAS) to identify a set of potential "active" tissues with improved power, leading to **publication in *Human Genetics and Genomics Advances* (2024)**.
- Performed transcriptome-wide and single cell level association studies to identify genes linked to renal cell carcinoma. Results **published in *The American Journal of Human Genetics* (2024)**.
- Modeled genome-wide association study (GWAS) results with single-cell ATAC-seq data to interpret etiology for human diseases at the cellular level.

**Lab Member, Statistical Genomics Studies**
Advisor: Dr. Hongkai Ji & Dr. Eneda Toska, Johns Hopkins University
- Built a comprehensive RNA-seq, ChIP-seq, and ATAC-seq analysis **pipeline**, enabling robust differential analysis, gene set enrichment, and motif discovery, **adopted cross labs**.
- Elucidated how transcriptional and epigenetic regulators mediate hormone-driven cancer tumor resistance to therapeutics, with **findings published in *Cell Reports* (2024), *Oncogene* (2023), and *Cancer Research* (2023)**.

**Research Assistant, Alzheimer's Disease Biomarkers Studies**
Advisor: Dr. Chenguang Wang & Dr. Zheyu Wang, Johns Hopkins University
- Developed an **R package (publicly available)** that integrates biomarker datasets from BIOCARD, NACC, and ADNI, producing harmonized analysis sets that enable cross-study replication in Alzheimer's disease research and are accessible for use by other investigators in the field.

**Research Assistant, Respiratory Failure Prediction**
Advisor: Dr. Andrew Michelson, Washington University in St. Louis, Institute for Informatics
- Built lasso and logistic regression models to predict respiratory failure in COVID-19 patients, which were **implemented in the Barnes-Jewish Hospital EHR system** to enable early identification of high-risk patients and timely ICU resource deployment.

**Research Assistant, Bootstrap Method Research**
Advisor: Dr. Todd Kuffner, Washington University in St. Louis
- Investigated properties of bootstrap methods and created a **novel density smoothing approach** with optimized bandwidth selection, improving accuracy in resampling-based inference.

## PAPERS & PUBLICATIONS

- **From G1 to M: a comparative study of methods for identifying cell cycle phases.** *Briefings in Bioinformatics.*
  **Guo, X.**, Chen, L.
  17 cited. (doi: https://doi.org/10.1093/bib/bbad517)
- **Cell-autonomous Cxcl1 sustains tolerogenic circuitries and stromal inflammation via neutrophil-derived TNF in pancreatic cancer.** *Cancer Discovery.*
  Bianchi, A., …, **Guo, X.**, …, Merchant, N.
  102 cited. (doi: https://doi.org/10.1158/2159-8290.cd-22-1046)
- **Subset-based method for cross-tissue transcriptome-wide association studies improves power and interpretability.** *Human Genetics and Genomics Advances.*
  **Guo, X.**, Chatterjee, N., Dutta, D.
  1 cited. (doi: https://doi.org/10.1016/j.xhgg.2024.100283)
- **Transcriptome-and proteome-wide association studies identify genes associated with renal cell carcinoma.** *The American Journal of Human Genetics.*
  Dutta, D, **Guo, X.**, …, Purdue, R.
  3 cited. (doi: https://doi.org/10.1016/j.ajhg.2024.07.012)
- **Methylation of the chromatin modifier KMT2D by SMYD2 contributes to therapeutic response in hormone-dependent breast cancer.** *Cell Reports.*
  Blawski, R., …, **Guo, X.**, …, Toska, E.
  7 cited. (doi: https://doi.org/10.1016/j.celrep.2024.114174)
- **ERK hyperactivation serves as a unified mechanism of escape in intrinsic and acquired CDK4/6 inhibitor resistance in acral lentiginous melanoma.** *Oncogenes.*
  Jagirdar, K., …, **Guo, X.**, …, Rebecca, V.
  8 cited. (doi: https://doi.org/10.1038/s41388-023-02900-6)
- **SMYD2 Regulates Chromatin Modifier KMT2D in ER+/PIK3CA Mutant Breast Cancer.** *Cancer Research.*
  Blawski, R., …, **Guo, X.**, …, Toska, E. (dio: https://doi.org/10.1158/1538-7445.AM2022-2955)
- **The histone methyltransferase KMT2D mediates subtype-specific transcriptional regulation and therapeutic response in prostate cancer.** *Cancer Research.*
  Kittane, S., …, **Guo, X.**, …, Toska, E. (dio: https://doi.org/10.1158/1538-7445.AM2024-1245)

## LEADERSHIP AND COMMUNITY INVOLVEMENTS

**Founder, EYE Public Welfare**                                          June 2016 – Current
- Founded an NGO with more than 50 people and raised a donation online while holding charity book fairs in schools and parks.
- Went to middle schools in impoverished areas and donated 100 brand new desks with many other teaching equipment.

## HONORS, TEACHING AND PRESENTATIONS

- **Andrew J. Viterbi Fellowship**, awarded to **outstanding Ph.D. students in computational science**. (August 2023)
- **Selected member** of the Alpha chapter of the **Delta Omega Society**—Honorary Society in Public Health. (May 2022)
- **Teaching Assistant**, *Statistics for Biosciences*, University of Southern California — Led weekly discussion sessions and guided students in statistical methods. (2025)
- **Presenter**, **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)
- Patent—Multifunctional Shared Printer. [201821510016.7]
- Patent—Portable Shared Printer. [201821494888.9]