Zechuan Shi

Ph.D. Candidate in Bioinformatics | zechuas@uci.edu | GitHub: https://github.com/rootze

SUMMARY

Ph.D. Candidate in Bioinformatics with integrated dry and wet lab experience, spanning single-cell genomics, preclinical drug trials, and therapeutic target discovery. Developer of open-source bioinformatics tools and first/co-first author on multiple publications in neurodegeneration and immunology. Seeking bioinformatics Postdoc position.

EDUCATION

Ph.D. Candidate in Bioinformatics — Expected Jun 2026
University of California, Irvine, Department of Neurobiology and Behavior
Principal Investigator: Vivek Swarup, Ph.D.

- **Research Direction:** Bioinformatics, Genomics, GWAS, Single Cell, Big Data, Alzheimer's Diseases
- My thesis research focuses on leveraging statistical methods and computational tools to investigate Alzheimer's disease, with the ultimate goal of discovering new therapeutic targets

Master of Science in Biotechnology — Sep 2016 – May 2018
Johns Hopkins University
GPA: 3.92/4.0

- **Concentration:** Bioinformatics, Molecular Targets and Drug Discovery Technologies

SOFTWARE PACKAGES/TOOLS

Developer

compact — Github: compact

- an in silico module perturbation method that unlocks a functional understanding of the dynamic gene networks in single-cell data

scROAD — ShinyApp: scROAD

- a database that offers single-cell cCREs' transcription factor occupancy information generated from snATAC-seq analysis of human postmortem prefrontal cortex (PFC) tissue for dementia research

ArchRtoSignac — Github: ArchRtoSignac

- an R package that allows easier implementation of both ArchR and Signac scATAC-seq analysis pipelines

Contributor

hdWGCNA — Github: hdWGCNA

- an R package for performing weighted gene co-expression network analysis (WGCNA) in high dimensional transcriptomics data

FIRST/CO-FIRST AUTHOR PUBLICATIONS

* These authors contributed equally

5. **Shi, Z.***, Morabito, S.*, et al. (2025). In silico module perturbation analysis unlocks a functional understanding of the dynamic gene networks in single-cell data. (Manuscript in preparation)

4. Das, S.*, **Shi, Z.***, et al. (2025). Oligodendrocyte reprogramming ameliorates Alzheimer's disease by reestablishing intercellular communication. (Manuscript in preparation)

3. Childs, J.*, **Shi, Z.***, et al. (2025). Single nucleus RNA sequencing and spatial transcriptomics of mouse habenula after reinstatement of cocaine self-administration. (Manuscript in preparation)

2. **Shi, Z.***, Das, S.*, Morabito, S.*, Miyoshi, E., et al. (2024). Single-nucleus multi-omics identifies shared and distinct pathways in Pick's and Alzheimer's disease. **bioRxiv**, 2024.09.06.611761. DOI:

https://doi.org/10.1101/2024.09.06.611761 (Manuscript in review; **Science Advances**)

1. **Shi, Z.***, Das, S.*, Morabito, S., Miyoshi, E., & Swarup, V. (2022). Protocol for single-nucleus ATAC sequencing and bioinformatic analysis in frozen human brain tissue. **STAR Protocols**, 3(3), 101491. DOI: https://doi.org/10.1016/j.xpro.2022.101491

OTHER CO-AUTHOR PUBLICATIONS

8. Fotio, Y., Al Masri, S., **Shi, Z.**, et al. (2025). Metabolic reallocation in spinal cord oligodendrocytes drives chronic pain via neuronal β-amyloid production. (Manuscript in preparation)

7. Tran, K.M., Kwang, N.E., Butler, C.A., [et al., including **Shi, Z.**]. (2025). APOE Christchurch enhances a disease-associated microglial response to plaque but suppresses response to tau pathology. **Mol Neurodegeneration**, DOI: 10.1186/s13024-024-00793-x

6. Miyoshi, E., Morabito, S., Henningfield, C.M. [et al., including **Shi, Z.**]. (2024). Spatial and single-nucleus transcriptomic analysis of genetic and sporadic forms of Alzheimer's Disease. **Nature Genetics**, DOI: https://www.nature.com/articles/s41588-024-01961-x

5. Tiwari, V., Prajapati, B., Asare, Y. [et al., including **Shi, Z.**]. (2024). Innate immune training restores pro-reparative myeloid functions for remyelination in the aged central nervous system. **Immunity**, 57(9), 2173–2190.e8. DOI: https://doi.org/10.1016/j.immuni.2024.07.001

4. O'Shea, T.M., Ao, Y., Wang, S. [et al., including **Shi, Z.**]. (2024). Derivation and transcriptional reprogramming of border-forming wound repair astrocytes after spinal cord injury or stroke in mice. **Nat Neurosci**. DOI: https://doi.org/10.1038/s41593-024-01684-6

3. Garcia-Agudo, L.F., **Shi, Z.**, et al. (2024). BIN1K358R suppresses glial response to plaques in mouse model of Alzheimer's Disease. **Alzheimer's & dementia**: the journal of the Alzheimer's Association, 20(4), 2922–2942. DOI: https://doi.org/10.1002/alz.13767

2. Tran, K.M., Kawauchi, S., Kramár, E.A. [et al., including **Shi, Z.**]. (2023). A Trem2R47H mouse model without cryptic splicing drives age- and disease-dependent tissue damage and synaptic loss in response to plaques. **Mol Neurodegeneration**. DOI: https://doi.org/10.1186/s13024-023-00598-4

1. Ma, Z., Flynn, J., Libra, G., & **Shi, Z.** (2018). Elevated CO2 Accelerates Phosphorus Depletion by Common Bean (Phaseolus vulgaris) in Association with Altered Leaf Biochemical Properties. **Pedosphere**, 28(3), 422–429. DOI: https://doi.org/10.1016/S1002-0160(17)60420-X

PRESENTATION

Oral Session

- "In Silico Module Perturbation Analysis unlocks a functional understanding of the dynamic gene networks in single-cell data". **Annual Meeting of American Society of Human Genetics**, Denver, CO. Nov 2024.
- "Single-nucleus open chromatin accessibility landscape of Pick's and Alzheimer's disease". **Alzheimer's Association International Conference**, San Diego, CA. Jul-Aug 2022.

Poster Session

- "Single-nucleus multi-ome profiling of epigenomic modifications and transcriptome characterization of heterogeneity in early and late-stage Alzheimer's disease". **Alzheimer's Association International Conference**, Philadelphia, PA. Jul-Aug 2024.
- "Epigenetic dysregulation in Pick's and Alzheimer's disease". **15th Annual Emerging Scientists Symposium**, Irvine, CA. Mar 2024.
- "Characterizing BIN1K358R SNP rs138047593 effects in 5xFAD plaque pathology of Alzheimer's disease using snRNA-seq". **Annual Meeting of American Society of Human Genetics**, Washington DC. Nov 2023.
- "Effect of Elevated CO_2 on Growth, Biomass Partitioning, and Phosphorus Uptake in Common Bean (Phaseolus vulgaris) under Varied Nitrogen or Phosphorus Availability.". **The Annual Conference of Missouri Academy of Science**, St. Joseph, MO. Apr 2015.

INDUSTRY & TRANSLATIONAL EXPERIENCE

Biotech Investment Fellow, BlueRun Ventures – Beijing, China (Remote)   Nov 2021 – Jan 2022

- Participated in a selective Bio2X venture program focused on biotechnology innovation and commercialization strategy
- Delivered bi-monthly reports on biotech industry trends, investment landscapes, and startup evaluations
- Collaborated with venture analysts to conduct due diligence and generate scientific insight for early-stage investment decisions
- Awarded for exceptional performance in biotechnology innovation analysis and startup evaluation

Preclinical Research Specialist, University of Pennsylvania – Philadelphia, PA   Jul 2018 – Jul 2020
Advisor: Lewis Chodosh, M.D., Ph.D.
Project: Recurrent Breast Cancer Preclinical Drug Development

- Led preclinical oncology studies using MTB/TAN bi-transgenic HER2+ mouse models to evaluate therapeutic response and tumor recurrence
- Managed in vivo studies involving >600 mice across 11 transgenic lines to support target validation and efficacy profiling
- Performed RNA-Seq analysis to characterize minimal residual disease and identify prognostic biomarkers in disseminated tumor cells
- Collaborated cross-functionally with molecular biologists and pharmacologists to integrate transcriptomic data with phenotypic drug response

Consultant, PBG Healthcare Consulting – Philadelphia, PA   Sep 2018 – Dec 2018
Wharton School of the University of Pennsylvania

- Collaborated with data scientists and medical researchers to optimize drug development pipelines
- Conducted market research and due diligence in partnership with business teams to assess therapeutic positioning
- Designed and distributed a primary research survey, identified key opinion leaders, and conducted interviews to define unmet clinical needs

R&D Intern, Gracomics LLC (Startup), MO   Jan 2016 – May 2016
Advisor: Wayne Zhou, Ph.D.
Project: ELISA-based Diagnostic Kit Development

- Contributed to the development of an in-cell ELISA-based diagnostic kit aimed at improving applications in biomedical research and clinical diagnostics
- Gained hands-on experience in tissue culture, western blotting, ELISA, and DAMA staining techniques
- Supported assay optimization efforts to enhance sensitivity and reproducibility of ELISA in cellular contexts

EARLY RESEARCH EXPERIENCE

Undergraduate Research Fellow, Truman State University – Kirksville, MO   May 2014 - Dec 2015
Advisor: John Ma, Ph.D.
Project: Effect of Elevated CO_2 on Growth, Biomass Partitioning, and Phosphorus Uptake in Common Bean (Phaseolus Vulgaris) under Varied Nitrogen or Phosphorus Availability

- Investigated the impact of elevated CO_2 on growth, biomass allocation, and phosphorus uptake in Phaseolus vulgaris under varying nitrogen and phosphorus conditions
- Performed phosphatase assays and nutrient uptake experiments to assess physiological responses to environmental changes
- Conducted statistical analyses to identify optimal nutrient regimes for enhanced plant growth
- Designed and executed experiments simulating climate change effects on crop nutrient dynamics
- Awarded the Gerhardt Research Fellowship and Grants-in-Aid of Scholarship and Research, recognizing research excellence and proposal merit

Summer Research Fellow, University of Pennsylvania – Philadelphia, PA   May 2013 - August 2013
Advisor: Andy Minn, MD., Ph.D.

Project: Stromal Regulation of Breast Cancer DNA Damage Resistance

- Elucidated a DNA damage resistance mechanism against radiation by activating STAT1 and NOTCH3 due to the interaction between stromal cells and BrCa cells
- Performed tissue culture, siRNA knockdown, flow cytometry, RNA extraction and Q-RT PCR
- Tested Interferon antibody efficiency and analyzed the optimal range of interferon concentration

TEACHING & OUTREACH EXPERIENCE

Program Manager, genPALs and UCI GPS – STEM Data Science Cohort – Irvine, CA   Jul 2022 – Jun 2024
- Organized bi-weekly seminars to promote the research in genomics and epigenomics
- Foster connections with invited speakers and industry professionals
- Coordinate with board members to organize professional networking events

Graduate Teaching Assistant, University of California – Irvine, CA   Mar 2022 – Mar 2024
Classes: Bio 38: Mind, Memory, and Brain; Bio 48: The Mind-Body Connection in the Neuroscience of Well-Being; N 138: Sex Influences on Brain; NEURBIO 227. Bioinformatics and Systems Biology
- Graded 200+ students' writing assignments, programming tasks and exams
- Facilitated in-class discussion sections and answered students' questions

Cell Biology Teaching Assistant, Truman State University – Kirksville, MO   Aug 2013 – Dec 2014
- Collected and analyzed biological data from weekly lab classes and assisted professors in preparing lab materials
- Interpreted research findings from 2 lab sessions per semester and helped students summarize data into reports
- Assisted 100+ students with their lab assignments and verified their operation procedures

Fellowship & Awards

Dunlop School of Biological Sciences Travel Award (2024-2025): University of California Conference Travel Award ($300)

Biological Sciences Travel Award (2023-2024): University of California Conference Travel Award ($300)

Bio2X Outstanding Trainee Award (2021-2022): BlueRun Ventures Winter 2021 - 2022 Bio2X Life Sciences Ideation Fellowship

Cum Laude (2015): Graduating with Honor, TSU

Gerhardt Research Funding (2015): a competitive research award ($3,000)

Grants-in-Aid of Scholarship and Research (GIASR) (2014): a competitive research grant for the initial stage of an individual student research project ($750)

President's Honorary Scholarship (2011-2015): an annual academic achievement scholarship ($4,500), TSU