

Jessica Zhou

Email: jlz014@eng.ucsd.edu
LinkedIn: jessica-l-zhou
GitHub: github.com/zrcjessica
Mobile: +1(858)776-4926

EDUCATION

University of California, San Diego
Ph.D., Bioinformatics and Systems Biology

La Jolla, CA
Sep. 2017–Present

University of Southern California
B.S., Biomedical Engineering

Los Angeles, CA
Aug. 2013–May 2017

EXPERIENCE

- **UC San Diego & Salk Institute for Biological Studies** La Jolla, CA
Ph.D. Candidate Sep. 2017 - Present
 - **Single-cell genomics analysis pipeline:** Developed computational pipelines for analyzing single-cell sequencing datasets, including scRNA-seq and scATAC-seq, as well as multiplexed single-cell CRISPR regulatory screens.
 - **Modeling enhancer activity:** Designed generalized linear models for discovering enhancer gene pairs from single-cell CRISPR regulatory screens and studying interactions between enhancers
 - **Machine learning for genomics:** Developed neural networks for predicting cell type-specific chromatin accessibility from scATAC-seq data.
 - **Science communication:** Wrote successful research grant applications (e.g. Fulbright, NIH F31) and presented research at numerous conferences. Highly skilled at clearly communicating research to various audiences.
- **Hasso-Plattner Institute & Max Delbrück Center for Molecular Medicine** Berlin, Germany
Fulbright Scholar Sep. 2019 - Mar. 2020
 - **Statistical modeling:** Developed statistical models for identifying regulatory elements from single-cell CRISPR regulatory screens
 - **Collaboration:** Led a highly collaborative project between lab at home and abroad as multilingual visiting researcher.
- **University of Southern California** Los Angeles, CA
Undergraduate Researcher Feb. 2015 - Jun. 2017
 - **Cancer metabolism:** Performed integrative statistical analysis of multi-omics datasets to study cancer metabolism
 - **Gene set enrichment analysis:** Identified genes driving dysregulation of oxidative phosphorylation across breast, ovarian and uterine cancers
 - **Pipeline design:** Designed Rscript pipeline to study correlation between tumor copy number alterations and protein levels
- **Harvard Medical School** Boston, MA
Research Intern Jun. 2016 - Aug. 2016
 - **Summer Bioinformatics Program:** Accepted into prestigious Harvard-MIT Health Sciences and Technology (HST) Summer Bioinformatics Program
 - **Algorithm development:** Developed algorithm for identifying enrichment of transcription factor binding motifs in ChIP-seq data

SKILLS

- Programming languages & tools: Python, R, Bash, awk/sed, Snakemake, MATLAB, SQL
- Machine learning & statistics: scikit-learn, scipy, numpy, generalized linear models, maximum likelihood estimation, hypothesis testing/AB testing, PyTorch, Tensorflow
- Data analysis and visualization: ggplot, matplotlib, seaborn, pandas, dplyr
- High performance computing (HPC): Microsoft Azure, SGE, slurm

TEACHING & OUTREACH

- **American Society of Human Genetics** USA
Public Education and Awareness Committee Member Jan. 2020 - Dec. 2022
 - Brainstorm subjects for public-facing online Discover Genetics fact sheets and advise on content
 - Run and judge annual ASHG DNA Day Essay Contest for high schoolers
 - Participate in AskScience Reddit panels
- **Fleet Science Center** San Diego, CA
Volunteer Sep. 2017 -
 - Volunteer with Two Scientists Walk Into a Bar program, where pairs of local scientists visit local breweries and invite the public to ask questions about science
 - Volunteer with BE WiSE program, which engages local young women (grades 7-12) in STEM
- **UC San Diego** La Jolla, CA
Bioinformatics Bootcamp Instructor Sep. 2018 - Sep. 2019
 - Designed and taught lectures on statistical concepts (e.g. p-values, statistical distributions, OLS, MLE) paired with interactive Jupyter notebooks to incoming first year students in the Bioinformatics PhD program
 - Planned and organized welcome week events for the Bioinformatics PhD program
- **University of Southern California** Los Angeles, CA
MATH 226 Supplemental Instructor Aug. 2015 - May 2017
 - Designed and taught weekly lectures (3x/week) to supplement undergraduate vector calculus course

AWARDS

NIH Ruth L. Kirschstein Predoctoral Individual National Research Service Award (F31)
ASHG 2022 Reviewer's Choice Recipient
UCSD Interdisciplinary Research Award
Fulbright Study/Research Award
National Science Foundation Graduate Research Fellowship Program Honorable Mention
University of California Trustee Scholar
University of Southern California Provost's Research Fellowship
Women in Science and Engineering Research Fellowship
Rose Hills Foundation Research Fellowship

PUBLICATIONS

- [1] **Zhou, J. L.**, G. d. Guglielmo, A. J. Ho, M. Kallupi, H.-R. Li, A. S. Chitre, L. L. Carrette, O. George, A. A. Palmer, G. McVicker, and F. Telese, “Cocaine addiction-like behaviors are associated with long-term changes in gene regulation, energy metabolism, and GABAergic inhibition within the amygdala,” *bioRxiv*, Sep. 2022.
- [2] Flores, A., J. Schell, A. S. Krall, D. Jelinek, M. Miranda, M. Grigorian, D. Braas, A. C. White, **J. L. Zhou**, N. A. Graham, T. Graeber, P. Seth, D. Evseenko, H. A. Coller, J. Rutter, H. R. Christofk, and W. E. Lowry, “Lactate dehydrogenase activity drives hair follicle stem cell activation,” *Nat Cell Biol*, vol. 19, no. 9, pp. 1017–1026, Sep. 2017, Number: 9 Publisher: Nature Publishing Group, ISSN: 1476-4679.

PRESENTATIONS

- *Single-cell sequencing links reduced glucose metabolism to cocaine addiction-like behavior in rats.* Poster presentation at the American Society of Human Genetics Annual Meeting. Oct. 25-29, 2022.
- *Cocaine addiction is associated with long-term changes in gene regulation, metabolic pathways, and GABAergic inhibition within the amygdala.* Talk presented at the Complex Traits Community conference. September 29-30, 2022.
- *snRNA-seq reveals that reduced glucose metabolism is linked in cocaine addiction in HS rats.* Talk presented at the NIDA P50 Center for GWAS in Outbred Rats Retreat. Nov. 4, 2022.
- *Cell type-specific multiomic analysis of substance use disorders in outbred rats.* Talk presented at the Probabilistic Modeling in Genomics conference. May 14-16, 2021.
- *A novel statistical method for identifying combinatorial regulatory elements from multiplexed single-cell CRISPR regulatory screens.* Poster presentation at the Probabilistic Modeling in Genomics conference. October 6-9, 2019.
- *Enhanced breast cancer risk prediction from imputed gene expression.* Poster presentation at the American Society of Human Genetics Annual Meeting. October 17, 2018.