Shu (Lisa) Liao

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EDUCATION

Washington University in St. Louis St. Louis, MO
Fifth Year Ph.D. candidate in Computer Science Sep 2021-Present

Washington University in St. Louis St. Louis, MO
B.S. in Computer Science Sep 2017-May 2021

RESEARCH EXPERIENCE

Center For Genome Sciences and Systems Biology St. Louis, MO
Graduate Research Assistant Sep 2021-Present

- Conducted statistical analysis for the Long Life Family Study Cohort (LLFS), including GWAS, TWAS, and rare variant analysis for 11 cardiovascular traits.
- Performed extensive quality control on WGS and chip genotypes from the Framingham Heart Study (FHS), which was used as the replication cohort in our publication.
- Implemented and maintained code for phenotype covariates adjustment.
- Implemented machine learning models for predicting complex traits from genomic and transcriptomic data.
- Presented posters at 3 conferences, and participated in manuscript preparation and submission for 5 paper.

Center For Genome Sciences and Systems Biology St. Louis, MO
Undergraduate Research Assistant May 2019-May 2021

- Inferred yeast transcription factor activity from observed gene expression levels across various conditions with matrix factorization to gain a deeper understanding of cellular state.
- Reformated microarray and ChIP expression data for transcription factor network construction and parameter inference.
- Implemented network construction module and inference pipeline using Python on a HPC cluster.
- Visualized and interpreted results with python and R, and deliver progress reports in lab meeting weekly.

Washington University in St. Louis, Department of Biological Sciences St. Louis, MO
Undergraduate Research Assistant Jan 2021-May 2021

- Engaged in analysis and annotations of unexplored regions of *Drosophila Bipectinata.*
- Utilize BLAST, BLAT, Genome Browser, RepeatMasker, Genscan, Clustal, NCBI and other genomic database, gene prediction or comparative analysis tools to explore next-generation sequencing data.

POSTER PRESENTATIONS

Acharya, S., **Liao, S.**, Jung, W., Kang, E., Moghaddam, V.A., Feitosa, M., Wojczynski, M.K., Lin. S., Anema, J.A., Schwander, K., O'Connell, J., Province, M., Brent, M.R. *Multi-omics Integration to Identify Genes Affecting Cardiovascular Diseases Related Traits.* Poster presented at

- Annual Conference of the American Society of Human Genetics (ASHG), Washington DC. (2023, November)
- Annual Scientific Meeting of the Gerontology Society of America (GSA), Tampa, FL. (2023, November)
- Annual Meeting of the International Genetic Epidemiology Society (IGES), Denver, CO. (2024, November)

Liao, S., Erdenebaatar, Z., Acharya, S., Jung W., M., Brent, M.R. *Deciphering pathway contributions to complex traits with a biologically informed neural network.* Poster presented at NHGRI Research Training & Career Meeting.

TEACHING EXPERIENCE

Washington University in St. Louis, Department of Computer Science St. Louis, MO
Graduate Assistant Instructor – one semester Sep 2023-Present

- Presented 3 lectures on Gibbs sampling and systems biology.

- Held weekly office hours and monitored online discussion boards to help students in resolving questions concerning course material for Computational Biology.
- Managed communications with student graders and created grading guidelines and expectations.

Washington University in St. Louis, Department of Computer Science St. Louis, MO

Undergraduate Teaching Assistant – two semesters Jan 2019-Dec 2020

- Held weekly office hours to help students in resolving questions concerning course material for Rapid Prototype Development & Creative Programming and Introduction to Data Science.
- Assisted students in trouble shooting HTML, PHP and Javascript web applications and evaluate student work to provide feedback in grades and comments.

PUBLICATIONS

Acharya, S., **Liao, S.**, Jung, W. J., Kang, Y. S., Moghaddam, V. A., Feitosa, M. F., Wojczynski, M. K., Lin, S., Anema, J. A., Schwander, K., Connell, J. O., Province, M. A., & Brent, M. R. (2024). A methodology for gene level omics-WAS integration identifies genes influencing traits associated with cardiovascular risks: The Long Life Family Study. Human Genetics, 143(9), 1241–1252. https://doi.org/10.1007/s00439-024-02701-1

Li, M., Song, Z., Reed, E., Karagiannis, T. T., Andersen, S., Brent, M., Mateusiak, C., Acharya, S., Jung, W. J., **Liao, S.**, Wojczynski, M. K., Feitosa, M. F., O'Connell, J. R., Montasser, M. E., Thorpe, R. J., Jr, Arbeev, K., Milman, S., Tai, A., Perls, T. T., Sebastiani, P., … Monti, S. (2026). Whole blood transcriptional signatures of age and survival identified in long life family and integrative longevity omics studies. *GeroScience*, 10.1007/s11357-025-02090-x. Advance online publication. https://doi.org/10.1007/s11357-025-02090-x

Acharya, S., Moghaddam, V. A., Jung, W. J., Kang, Y. S., **Liao, S.**, Province, M. A., & Brent, M. R. (2026). Finding Significant Hits in Networks: a network-based tool for analyzing gene-level P-values to identify significant genes missed by standard methods. *Briefings in bioinformatics*, *27*(2), bbag061. https://doi.org/10.1093/bib/bbag061

Moghaddam, V. A., Acharya, S., Schwaiger-Haber, M., **Liao, S.**, Jung, W. J., Thyagarajan, B., Shriver, L. P., Daw, E. W., Saccone, N. L., An, P., Brent, M. R., Patti, G. J., & Province, M. A. (2025). Gene-Embedded Multi-Modal Networks for Population-Scale Multi-Omics Discovery. *bioRxiv : the preprint server for biology*, 2025.01.22.634403. https://doi.org/10.1101/2025.01.22.634403. **Submitted**

Jung, W. J., Acharya, S., Ruskin, D. P., Liao, S., Moghaddam, V. A., Erdenebaatar, Z., & Brent, M. R. (2025). Combining Motifs, CRE Activity, And Gene Expression Data Using ML Greatly Improves the Accuracy of Tissue-Specific TF Network Maps. *bioRxiv : the preprint server for biology*, 2025.10.10.681634. https://doi.org/10.1101/2025.10.10.681634. **Submitted**