

Cory Gardner

PHD CANDIDATE • DEPARTMENT OF COMPUTER SCIENCE

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Education

PhD Candidate in Computer Science, Saint Louis University (St. Louis, MO)

2022 – May 2027 (expected)

- Advisor: Dr. Tae-Hyuk Ahn
- Dissertation Focus: Multimodal Deep Learning and HPC for Scalable Metagenomics
- PhD Candidacy: April 2025

MS in Bioinformatics & Computational Biology, Saint Louis University (St. Louis, MO)

2020 – 2021

Open Science Grid (OSG) School, University of Wisconsin (Madison, WI)

2024

BS in Sociology, Colorado State University (Pueblo, CO)

2014 – 2017

Research Interests

- Multimodal learning for genomics/metagenomics and biomedical data integration
- GPU/HPC acceleration for scalable bioinformatics and data-intensive ML pipelines
- Privacy and inference attacks on biomedical ML (membership/property inference) and mitigations
- Memory- and compute-efficient methods for deployment on heterogeneous systems (CPU/GPU)

Academic/Professional Experience

Graduate Research Assistant – Ahn Lab (BioHPC Lab)

Saint Louis University, 2020 – Present

- Research across metagenomics, RNA-seq, long-read genome assembly/annotation, and GPU-accelerated analysis.
- Current focus: scalable multimodal ML + HPC for large biological datasets; privacy evaluation of biomedical ML models.
- RNA-seq analysis for a study of persistent neuronal stress signaling in an Angelman syndrome mouse model (*Nature*, 2026).
- Prior projects include: haplotype-resolved assembly of *Saccharomyces bayanus*; GPU-accelerated CT image QC; ChIP-seq analysis.

Graduate Assistant

Reinert Center for Transformative Teaching & Learning, SLU, July 2025 – May 2026

- Supported faculty and graduate students in adopting evidence-based teaching practices and learning technologies.
- Designed and facilitated instructional-development workshops and resources.

Teaching Assistant

Saint Louis University, 2023 – 2024

- Courses: Data Structures; Distributed Computing; Concurrent & Parallel Programming; Intro to Bioinformatics.

Publications and Presentations

Peer-reviewed / Proceedings

Kim, K. S., **Gardner, C.**, Cullen, A., Stelzer, J. A., Cho, K., Sharma, A., Nemera, M. T., Law, T., Naz, H., Zhao, G., Gabel, H. W., Patti, G. J., Musiek, E. S., Ahn, T.-H., & Yi, J. J. "Persistent neuronal stress signaling underlies phenotypes in a mouse model of Angelman syndrome." *Nature*, 2026. (Accepted)

Gardner, C., Dhiren, A., Min, B., & Ahn, T.-H. "Wavelet-Enhanced PaDiM for Industrial Anomaly Detection." *IEEE Access*, 14: 37702–37718, 2026. DOI: 10.1109/ACCESS.2026.3669882.

Kang, J., Jung, S., Kim, K., **Gardner, C.**, Yeom, J. S., Ahn, T.-H., & Kim, J. "HPC-CARLA: Closed-Loop Evaluation of Autonomous Driving Agents as a Resilient, Schedulable HPC Workload." *SC'26 Workshops (WORKS)*, 2026. (Accepted)

Gardner, C., Jeong, S., Khatavkar, O., Moon, A., Cao, Q., & Ahn, T.-H. "Evaluating Accuracy and Performance Tradeoffs in GPU-Accelerated Single-Cell RNA-seq Analysis." *Proceedings of the SC'25 Workshops of the International Conference for High Performance Computing, Networking, Storage and Analysis (DRBSD-11)*, 349–358, 2025. DOI: 10.1145/3731599.3767378.

Sirasani, J. P.* **Gardner, C.***, Jung, G., Lee, H., & Ahn, T.-H. “Bioinformatic approaches to blood and tissue microbiome analyses: challenges and perspectives.” *Briefings in Bioinformatics*, 26(2): bbaf176, 2025. DOI: 10.1093/bib/bbaf176. *Co-first authors.

Gardner, C., et al. “Chromosome-level subgenome-aware de novo assembly provides insight into *Saccharomyces bayanus* genome divergence after hybridization.” *Genome Research*, 34(11): 2133–2146, 2024. DOI: 10.1101/gr.279364.124.

Yang, Y., **Gardner, C.**, Gupta, P., Peng, Y., Piasecki, C., Millwood, R. J., Ahn, T.-H., & Stewart, C. N. Jr. “Novel Candidate Genes Differentially Expressed in Glyphosate-Treated Horseweed (*Conyza canadensis*).” *Genes (Basel)*, 12(10): 1616, 2021. DOI: 10.3390/genes12101616.

Preprints

Nguyen, V. D., Gao, C., **Gardner, C.**, Wang, Z., Margenot, A. J., Huang, L., & Ahn, T.-H. “First Metagenome-Assembled Genomes from the Historic Morrow Plots Reveal Management-Associated Dominance of Archaeal Ammonia Oxidizers.” *bioRxiv*, 2026. In revision at *Scientific Data*. DOI: 10.64898/2026.03.24.714042.

Posters / Talks

Gardner, C. “Practical Strategies for UDL in PowerPoint.” *Teaching Essentials Workshop, Reinert Center for Transformative Teaching & Learning*, Saint Louis University, Mar 31, 2026.

Gardner, C., Jeong, S., Khatavkar, O., Moon, A., Cao, Q., & Ahn, T.-H. “Evaluating Accuracy and Performance Tradeoffs in GPU-Accelerated Single-Cell RNA-seq Analysis.” *Talk / workshop presentation, DRBSD-11 at SC’25 Workshops*, November 2025. *Best Paper Runner-Up Award*.

Gardner, C. “Practical Considerations when Choosing Digital Learning Tools.” *Teaching Essentials Workshop, Reinert Center for Transformative Teaching & Learning*, Saint Louis University, Oct 28, 2025.

Gardner, C. “Effective Teaching Practices for First-Time Teachers.” *Graduate Assistant Orientation, Reinert Center for Transformative Teaching & Learning*, Saint Louis University, Aug 14, 2025.

Gardner, C., Min, B., & Ahn, T.-H.* “PaDiM-Wavelet: Memory-Efficient Anomaly Detection for Heterogeneous Computing Systems.” *Poster presentation, GCASR 2025*, Chicago, IL, 2025. (Saint Louis University; Sejong University).

Gardner, C. “Long-read Genome Assembly.” *Lightning talk, Donald Danforth Plant Science Center*, 2023.

Gardner, C., Ahmad, S., & Ahn, T.-H. “Metagenomic Data Analysis with Probability-Based Reduced Dataset Representation.” *Presentation, CAMDA (ISMB)*, 2020. *Best Presentation Award*.

Awards & Honors

Alpha Sigma Nu	2026
The Honor Society of Jesuit Colleges and Universities (SLU); inducted February 2026.	
Best Paper Runner-Up Award (DRBSD-11, SC’25 Workshops)	2025
Recognized for “Evaluating Accuracy and Performance Tradeoffs in GPU-Accelerated Single-Cell RNA-seq Analysis.”	
Best Presentation Award	2020
CAMDA (ISMB): metagenomic sample origin prediction / classification presentation.	
Conference Fellowship	2020
International Society of Computational Biology (ISCB).	
BITWISE Scholarship	2019 – 2020
National Science Foundation merit-based scholarship supporting research in bioinformatics and high-performance computing.	

Skills

- **Programming:** Python, C++, R, CUDA
- **HPC/Systems:** Slurm, MPI, HTC/OSG, GPU optimization, profiling/benchmarking
- **ML:** PyTorch, TensorFlow; multimodal learning; representation learning
- **Bioinformatics:** RNA-seq, metagenomics pipelines, assembly workflows