

Cory Gardner

PHD STUDENT · DEPARTMENT OF COMPUTER SCIENCE

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Education

Saint Louis University

Spring 2022 – Present

PHD IN COMPUTER SCIENCE, *St. Louis, MO*

- Advisor: Dr. Tae-Hyuk Ahn
- Dissertation Focus: Multimodal Deep Learning and HPC for Scalable Metagenomics
- Relevant Coursework: Software Engineering, Software Development, Machine Learning, Computer Vision, Natural Language Processing, Biometry, Data Structures, High Performance Computing, Parallel Programming, Distributed Computing, Computer Security

University of Wisconsin-Madison

2024

OPEN SCIENCE GRID (OSG) SCHOOL, *Madison, WI*

Saint Louis University

2020 – 2021

MS IN BIOINFORMATICS & COMPUTATIONAL BIOLOGY, *St. Louis, MO*

Colorado State University

2014 – 2017

BS IN SOCIOLOGY, *Pueblo, CO*

Research Interests

Computational Biology & Genomics in general, and in particular:

- Advanced sequence representation methods for genomic data analysis
- Multimodal deep learning approaches integrating genomic, transcriptomic, and phenotypic data
- Applications of deep learning to biological sequence understanding
- Development of efficient computational methods for metagenomic data processing, including taxonomic profiling and classification

High-Performance Computing & Parallel Processing in general, and in particular:

- GPU-accelerated image analysis for medical and biological applications
- Parallel algorithm optimization for processing large-scale genomic datasets
- Distributed computing strategies for computationally intensive bioinformatics tasks
- Memory-efficient implementations for handling terabyte-scale biological data

Machine Learning Privacy & Security in general, and in particular:

- Membership and property inference attack detection in biomedical ML
- Federated learning approaches for healthcare data privacy
- Privacy-preserving data fusion for multimodal medical data
- Adversarial model testing and vulnerability discovery frameworks

Academic/Professional Experience

GRADUATE RESEARCH ASSISTANT, St. Louis, MO

- CT-image analysis (GPU-based CUDA acceleration of CT images for quality control)
- Metagenomic Analysis (Critical Assessment of Massive Data Analysis)
- RNA-seq (Novel Candidate Genes Differentially Expressed in Glyphosate-Treated Horseweed)
- Long read *de-novo* assembly and annotation (First haplotype-resolved assembly of *Saccharomyces bayanus*).
- Computational Privacy (Privacy and Inference Attacks on Multimodal Machine Learning Models)
- T-Cell analysis (sequence diversity for pathogen exposure prediction)
- Anomaly detection (Novel methods for anomaly detection in images)
- ChipSEQ (CTCF regulates the long gene expression program in neurons)
- Federated learning for increased privacy in medical applications

Teaching Assistant

2023 – 2024

SAINT LOUIS UNIVERSITY

- Data Structures
- Distributed Computing
- Concurrent and Parallel Programming
- Introduction to Bioinformatics

Supplemental Instructor

2024

SAINT LOUIS UNIVERSITY

- Introduction to Bioinformatics II

Publications

Gardner, C., et al. "Chromosome-level subgenome-aware *de novo* assembly provides insight into *Saccharomyces bayanus* genome divergence after hybridization." *Genome Res.* 2024 Nov 20;34(11):2133–2146. doi: 10.1101/gr.279364.124.

Yang Y, **Gardner C**, Gupta P, Peng Y, Piasecki C, Millwood RJ, Ahn TH, Stewart CN Jr. "Novel Candidate Genes Differentially Expressed in Glyphosate-Treated Horseweed (*Conyza canadensis*)." *Genes.* 2021;12(10):1616. doi: 10.3390/genes12101616.

Sirasani JP, **Gardner C**, Jung G, Lee H, Ahn TH. "Bioinformatics approaches of blood and tissue microbiome analyses: challenges and perspectives." *Briefings in Bioinformatics* (under review).

Gardner C, Ahmad S, Ahn TH. "Metagenomic Data Analysis with Probability-Based Reduced Dataset Representation," *CAMDA Conference Proceedings*, 2020.

Research Projects

De Novo Haplotype-Level Assembly of Hybrid Yeast

2021 – 2024

Project Description:

The accurate assembly of hybrid genomes presents unique computational challenges due to the presence of multiple subgenomes with varying levels of divergence. This project focused on generating a chromosome-level subgenome-aware *de novo* assembly of the *Saccharomyces bayanus* yeast genome to study post-hybridization genome evolution. The resulting assembly revealed novel insights into subgenome divergence following hybridization events.

My Role:

- Designed and executed a comprehensive assembly pipeline including read quality control, *de novo* sub-genome aware assembly, and sequence polishing
- Developed methods for subgenome discrimination and parental haplotype attribution
- Validated assembly results via phylogenetic analysis
- Published findings in *Genome Research*

Required Skills:

- Oxford Nanopore long-read sequencing data analysis
- Genome assembly tools
- High-performance computing for parallel processing
- Bioinformatics workflow design and implementation

Privacy-Preserving Machine Learning for Biomedical Data

2024 – Present

Project Description:

Medical data present challenges for machine learning applications due to strict privacy requirements. This project addresses membership and property inference attacks (MIA/PIA) against machine learning models trained on biomedical data, where adversaries may extract private information about training data or individuals. The work focuses on developing privacy-preserving techniques that maintain accuracy while protecting sensitive information.

My Role:

- Investigated differential susceptibility to privacy attacks between multimodal models their component unimodal models.

Required Skills:

- Privacy-preserving machine learning techniques
- Deep learning for medical imaging
- Adversarial machine learning and attack simulation

GPU-Accelerated CT Image Analysis

June 2020 – August 2021

Project Description:

Quality control of imaging data, particularly CT scans, is computationally demanding and often traditionally performed on CPU architectures with significant processing time requirements. This research collaboration with Xavis focused on developing optimized CUDA implementations for image preprocessing, image quality assessment, and CT rotation to achieve substantial performance improvements while maintaining accuracy.

My Role:

- Implemented parallel algorithms for CT image analysis tasks
- Designed CUDA kernels for noise level estimation, artifact detection, and contrast evaluation
- Integrated accelerated components into existing workflows

Required Skills:

- CUDA programming and GPU architecture knowledge
- Medical image processing techniques
- Parallel algorithm design and optimization
- Performance benchmarking and validation

Metagenomic Analysis & Sample Origin Prediction

September 2019 – August 2020

Project Description:

Environmental metagenomic samples contain complex, interacting microbial communities that can serve as biological signatures of their origin location. This project focused on developing computational methods for analyzing low-biomass microbial samples and predicting their geographical origins using machine learning techniques applied to taxonomic profiles generated through next-generation sequencing.

My Role:

- Implemented taxonomic classification pipeline
- Designed and trained ensemble machine learning models for geolocation prediction
- Presented the work at CAMDA 2020, receiving the Best Presentation Award

Required Skills:

- Metagenomic data analysis and taxonomic classification
- Machine learning for biological data
- High-performance computing for large-scale datasets

- Scientific communication and visualization

Awards & Honors

BITWISE Scholarship	2019–2020
NATIONAL SCIENCE FOUNDATION,	
Conference Fellowship	2020
INTERNATIONAL SOCIETY OF COMPUTATIONAL BIOLOGY,	
ISBM/CAMDA	2020
BEST PRESENTATION AWARD,	

Skills

- Programming Languages: C++, Python, R, CUDA
- Technologies & Frameworks: High-Performance Computing, PyTorch/TensorFlow, Bioinformatics Tools, Distributed Computing
- Analysis Skills: Statistical Modeling, Data Visualization
- Soft Skills: Technical Writing, Leadership & Mentoring, Research Presentation, Collaborative Research