Shaurita D. Hutchins, MS

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Summary

Computational biologist specializing in rare disease genomics, systems biology, biomedical knowledge engineering, and scientific software development. Integrates multi-omics analysis and gene regulatory network inference with biomedical databases and ontologies to investigate disease mechanisms and develop reproducible research tools.

Education

2020 – Present	PhD Candidate, Genetics, Genomics, and Bioinformatics, University of Alabama at Birmingham
2010 – 2012	MS, Biological Sciences, Mississippi College
2006 – 2010	BS, Biology Premed, Xavier University of Louisiana

Skills

Biomedical Knowledge Engineering	BioCypher, Neo4j, Cypher, HPO, MONDO, MeSH; schema design, identifier normalization, provenance tracking, graph validation
Programming & Data Engineering	Python, R, JavaScript, Bash, SQL, pandas, Polars, NumPy, SciPy, Pydantic, Flask, API development (FastAPI), pytest
Workflow Automation & HPC	Nextflow, Snakemake, Docker, Git, CI/CD, Slurm, Linux, HPC
Genomics & Transcriptomics	VEP, Hail, bcftools, FastQC, MultiQC, DESeq2, WGS/WES, bulk RNA-seq, splicing analysis
Systems Biology	WGCNA, PANDA/netZoo, STRING, BioGRID, JASPAR, networkx

Research & Professional Experience

2020 – Present | PhD Candidate, University of Alabama at Birmingham, Birmingham, AL
Department of Genetics; Center for Computational Genomics and Data Science
Mentor: Dr. Elizabeth A. Worthey

- Conceptualized an ME/CFS knowledge graph for nutritional hypothesis generation and co-developed its **BioCypher and Neo4j** integration workflows.
- Contributed to the CHARMomics schema and prototyped ontology-constrained clinical summarization workflows integrating HPO-guided validation for LLM-assisted interpretation.
- Developed a containerized GPU workflow using the **Evo 2 genomic foundation model** to score candidate variants in heritable pulmonary arterial hypertension.
- Identified seven co-expression modules distinguishing HPAH from IPAH and 16 pathways with differential regulatory targeting to prioritize candidate genetic modifiers for functional follow-up.
- Integrated whole-genome sequencing, RNA-seq, differential expression, and splicing analyses to characterize a candidate disease-causing splicing mechanism in a rare VMA21-associated X-linked myopathy.
- Implemented and maintained workflow orchestration with **Nextflow and Snakemake** for large-scale data processing, annotation, quality control, and multi-omics integration on HPC systems.
- Built internal workflow infrastructure and documentation for provenance tracking, reproducibility, and FAIR-aligned project handoff.
- Developed Streamlit, Flask, R Shiny, and workflowr resources for data exploration, variant interpretation, and cohort-level analysis.

2015 – 2020 | Researcher III, University of Mississippi Medical Center, Jackson, MS
Department of Psychiatry and Human Behavior
Mentor: Dr. Eric J. Vallender

- Designed, deployed, and administered the laboratory's CentOS-based computational cluster, managing system configuration, software, user access, and storage to support genomic and bioinformatic analyses.
- Implemented memory-aware genomics pipelines in Python and Bash to analyze sequencing datasets exceeding 1 TB on shared computing infrastructure.
- Refactored computational pipelines using multiprocessing, increasing throughput **approximately six-fold**.
- Built *OrthoEvolution*, an object-oriented Python library for orthology inference and comparative genomics. github.com/datasnakes/OrthoEvolution
- Co-developed *MicrobiomeR*, an R package providing simplified, standardized microbiome-analysis workflows, resulting in a peer-reviewed software publication. github.com/vallenderlab/MicrobiomeR

Selected Projects

ME/CFS Knowledge Graph for Nutritional Hypothesis Generation 2026 – Present

- Conceptualized an ME/CFS knowledge graph for nutritional hypothesis generation and co-developed its BioCypher and Neo4j integration workflows.
- Extended the FoodAtlas-based graph with **CTD gene–chemical interactions**, connecting genes to food-associated chemicals.
- Developed the ME/CFS Food–Gene Explorer, a **React app** linking participant-specific regulatory networks to ranked chemicals and supporting gene, pathway, and food-composition evidence.
- Processed 222,732 entities and 557,210 relationships from FoodAtlas v4.1 into Neo4j-ready graph data.
- Implemented BioCypher schema configuration, Pydantic-based data validation and graph integrity checks, MeSH identifier handling, provenance tracking, and reproducible graph ingestion to support ME/CFS hypothesis-generation research.

GRNIntegrate 2026 – Present

Developing a Nextflow pipeline for **gene regulatory network inference** with PANDA and LIONESS. Combines bulk gene expression data with regulatory priors to compare networks across conditions and individual samples. Proposal accepted by nf-core.

Open OnDemand HPC Dashboard github.com/sdhutchins/ood-hpc-dash 2025 – Present

Developed a Flask-based Open OnDemand dashboard with the UAB Research Computing team to support HPC workflow visibility, Slurm resource monitoring, software environment review, and user-facing research computing support.

AutoCAB github.com/stjude-biohackathon/KIDS26-Team6 2026

Co-developed AutoCAB, a St. Jude BioHackathon 2026 prototype that captures computational workflows and turns recurring analysis steps into reusable agent skills for human review. Contributed workflow recording, session provenance, dashboard interfaces, and sensitive-data redaction, including benchmarking on synthetic data.

BioWrappers github.com/biowrappers Present

Founded an open-source effort developing wrappers around common bioinformatics tools and APIs.

Selected Publications

2026 Birch CL, Wilk BM, Gajapathy M, **Hutchins SD**, et al. Uncovering the genetic architecture of ME/CFS: a precision approach reveals impact of rare monogenic variation. *Journal of Translational Medicine*. 24:168.

2019 Gilmore RA, **Hutchins SD**, Zhang X, Vallender EJ. MicrobiomeR: An R Package for Simplified and Standardized Microbiome Analysis Workflows. *Journal of Open Source Software*. 4(35):1299.

Selected Presentations & Invited Talks

Dec 2026 **Hutchins SD**. Building HPC Interfaces with Flask and Open OnDemand. Oral presentation, PyData Global 2026, Virtual. *(Forthcoming)*

Nov 2026 Gattas M*, **Hutchins S***, Tammineni MK*, John J, Owusu P, Niu B, Rosikiewicz W. AutoCAB: Turning Everyday Scientific Workflows into Reusable AI Agent Skills. Poster presentation, Knowledge in Data Science Symposium (KIDS26), St. Jude Children's Research Hospital, Memphis, Tennessee. *(Forthcoming)* * *Joint first authors.*

Oct 2026 **Hutchins SD**, Wilk BM, Bharti S, Mamidi T, Worthey EA. Integrative multi-omics reveals regulatory network rewiring and candidate genetic modifiers in heritable pulmonary arterial hypertension. Poster presentation, American Society of Human Genetics Annual Meeting, Montréal, Canada.

Oct 2026 **Hutchins SD**. Who Owns Your DNA? Invited lightning talk, Advocates in Action: ACGT Presentations and Networking Event, American Society of Human Genetics Annual Meeting, Montréal, Canada.

Jul 2026 **Hutchins SD**. Invited career journey speaker, Decoding the Data Ecosystem (DeCoDE) Institute Capstone Event, Common Fund Data Ecosystem Training Center, Virtual.

Selected Funding & Awards

2026 **CFDE Training Module Development Award**, Common Fund Data Ecosystem. $5,000.

2026 **St. Jude BioHackathon Travel Award**, St. Jude Children's Research Hospital. Covered airfare and accommodations.

2024 **JXTX+CSHL Biological Data Science Conference Travel Scholarship**. Conference registration and CSHL housing.

2023 **Inclusive Campus Commitment Award**, UAB Office of Student Involvement & Leadership

2022 **XSEDE Cloud Computing Allocation**, co-PI. $66,150 for Hackin' Omics 2022; MED220019.

2018 **hackseq18 Winner**, beRi, University of British Columbia.

Professional Service

2026 **Abstract Reviewer**, American Society of Human Genetics Annual Meeting

2022 – Present **Reviewer**, Journal of Open Source Software