
PROFESSIONAL GOALS

Detail-oriented bioinformatician with years of experience developing and managing bioinformatic workflows to analyze complex datasets. Seeking to leverage expertise in next-generation sequencing, bioinformatics pipeline development, and multi-omic datasets to advance biomedical research.

TECHNICAL SKILLS

Tools and Languages	Python, R (Rmarkdown, Rshiny), Nextflow, Bash, bioinformatic tools (e.g., GATK, bowtie2, samtools, nf-core, etc.), containerization (Singularity, Docker), Git, linux/unix command line, high-performance computing environments, cloud computing, PowerBI, SQL
Bioinformatic Analyses	Whole genome analysis, genome assembly, SNP calling, gene prediction, microbiome community profiling (16s rRNA amplicon, shotgun metagenomics), clustering, database management and curation, machine learning, molecular epidemiology, phylogenetics, drug resistance screening
Communication	Collaboration with interdisciplinary teams, scientific manuscript preparation and grant writing, dashboards/reports to communicate findings with senior leadership and non-technical stakeholders
Additional Skillsets	NGS wet lab (DNA/RNA extraction, qPCR, dPCR, PCR, library preparation, sequencing), bioinformatic troubleshooting, Data visualization (Rmarkdown, Rshiny, PowerBI), SOP development / laboratory quality management standards, intergovernmental collaborations

EDUCATION

Ph.D., Anthropology - Human Health and Biology , <i>University of Oklahoma</i> <i>Dissertation: Factors Influencing Ecological Dynamics of the Human Microbiome.</i>	Dec. 2020
B.S., Anthropological Sciences , <i>The Ohio State University</i> . Magna Cum Laude. <i>Minor: Molecular Genetics</i>	May 2014

PROFESSIONAL EXPERIENCE

Associate Service Fellow <i>Division of Parasitic Diseases and Malaria, CDC</i>	March 2023 — March 2025 <i>Atlanta, GA</i>
<ul style="list-style-type: none">Led bioinformatic surveillance of parasitic pathogens, identifying outbreak clusters and detecting genetic signals of drug resistance to inform epidemiologic investigations and track infectious disease spread.Developed and optimized bioinformatic pipelines using Nextflow, Python, and R to analyze NGS data by integrating open-source tools with custom scripts and statistical analyses, enhancing the detection of drug resistance-associated SNPs, outbreak clusters, and geographic origin of infectious diseases.Automated data integration workflows for clinical and epidemiologic datasets, improving interdisciplinary collaboration and streamlining communication of key findings to global public health stakeholders, supporting anti-malarial drug efficacy monitoring and epidemiologic decision-making.Ensured high performance of bioinformatic workflows by curating database, managing and improving bioinformatic software environments, and troubleshooting bugs in HPC infrastructure/code.Authored SOPs and workflow documentation, training junior scientists to enhance bioinformatics quality management systems and compliance with quality control standards.	
Postdoctoral ORISE Fellow <i>Division of Parasitic Diseases and Malaria, CDC</i>	Jan. 2021 — March 2023 <i>Atlanta, GA</i>
<ul style="list-style-type: none">Optimized genotyping pipelines for infectious disease surveillance, accelerating variant detection and enabling timely interventions.Partnered with federal agencies and public health labs to standardize and deploy bioinformatic pipelines via GitHub, ensuring alignment between federal agencies and state/local/territorial health departments.Improved data harmonization strategies for integrating epidemiologic and genomic data, facilitating real-time insights for public health applications.Conducted population genetics research on parasitic pathogens, contributing to peer-reviewed publications	

Graduate Research Assistant

Jan. 2016 — Dec. 2020

Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma

Norman, OK

- Led bioinformatics research documenting human microbiome variation between lifestyles and disease state, taxonomically and functionally profiling human gut, oral, and vaginal microbiomes.
- Developed scalable bioinformatics workflows that integrated published software with custom R and Python scripts to merge bioinformatic results with dietary recall surveys and clinical metadata.
- Performed genome assembly, phylogenetics, and functional annotation from shotgun metagenomic data to uncover variation in bacterial genomes constructed from samples originating on different continents.
- Conducted hands-on NGS library preparation and sequencing for microbiome and cancer research, ensuring data integrity from wet lab to computational analysis.
- Managed international research collaborations, overseeing data sharing, regulatory compliance, and publication strategy, strengthening interdisciplinary partnerships in biomedical research.

HONORS AND AWARDS

Performance Award: SOP Development, Division of Parasitic Diseases and Malaria, CDC	2024
Excellence in Epidemiology: 2023 Domestic Malaria Response, Global Health Center, CDC	2023
Performance Award: Domestic Malaria Response, Division of Parasitic Diseases and Malaria, CDC	2023
Grant: Doctoral Dissertation Research Improvement Grant, National Science Foundation	2019
Grant: Robberson Research and Creative Endeavors Grant, University of Oklahoma	2016
Grant: Opler Research Award, University of Oklahoma	2015
Phi Beta Kappa, The Ohio State University	2013

SELECTED PUBLICATIONS

- Shen, J., Cama, V. A., **Jacobson, D. K.**, Barratt, J. L.N., and Straily, A. (2025). Cyclospora Genotypic Variations and Associated Epidemiologic Characteristics, United States, 2018–2021. *Emerging Infectious Diseases* 31(2), 256.
- Pierre-Louis, E., Kelley, J., Patel, D., Carlson, C., Talundzic, E., **Jacobson, D. K.**, and Barratt, J. L.N. (2024). Geo-classification of drug-resistant travel-associated *Plasmodium falciparum* using Pfs47 and Pfcmp gene sequences (USA, 2018–2021). *Antimicrobial Agents and Chemotherapy* 68(12), e01203-24.
- Jacobson, D. K.**, and Barratt, J. L.N. (2023). Optimizing hierarchical tree dissection parameters using historic epidemiologic data as ‘ground truth’. *Plos one* 18(2), e0282154.
- Jacobson, D. K.**, Peterson, A. C., Qvarnstrom, Y., and Barratt, J. L.N. (2023). Novel insights on the genetic population structure of human-infecting *Cyclospora* spp. and evidence for rapid subtype selection among isolates from the USA. *Current Research in Parasitology and Vector-Borne Diseases* 4(), 100145.
- Ahart, L., **Jacobson, D. K.**, Rice, M., Richins, T., Peterson, A. C., Zheng, Y., Barratt, J. L.N., Cama, V., Qvarnstrom, Y., Montgomery, S., and Straily A. (2023). Retrospective evaluation of an integrated molecular-epidemiological approach to cyclosporiasis outbreak investigations—United States, 2021. *Epidemiology and Infection* 151(), e131.
- Jacobson, D. K.**, Low, R., Plucinski, M. M., and Barratt, J. L.N. (2023). An improved framework for detecting discrete epidemiologically meaningful partitions in hierarchically clustered genetic data. *Bioinformatics Advances* 3(1), vbad118.
- Jacobson, D. K.**, Zheng, Y., Plucinski, M. M., Qvarnstrom, Y., and Barratt, J. L. N. (2022). Evaluation of various distance computation methods for construction of haplotype-based phylogenies from large MLST datasets. *Molecular phylogenetics and evolution* 177(), 107608.
- Jacobson, D. K.**, Honap, T. P., Ozga, A. T., Meda, N., Kagone, T. S., Carabin, H., Spicer, P., Tito, R. Y., Obregon-Tito, A. J., Reyes, L. M., Guijo-Pomo E., Sankaranarayanan, K., and Lewis Jr, C. M. (2021). Analysis of global human gut metagenomes shows that metabolic resilience potential for short-chain fatty acid production is strongly influenced by lifestyle. *Scientific reports* 11(1), 1724.
- Jacobson, D. K.**, Moore, K., Gunderson, C., Rowland, M., Austin, R., Honap, T. P., Xu, J., Warinner, C., Sankaranarayanan, K., and Lewis Jr C. M. (2021). Shifts in gut and vaginal microbiomes are associated with cancer recurrence time in women with ovarian cancer. *PeerJ* 9(), e11574.
- Jacobson, D. K.**, Honap, T. P., Monroe, C., Lund, J., Houk, B. A., Novotny, A. C., Robin, C., Marini, E., and Lewis Jr C. M. (2020). Functional diversity of microbial ecologies estimated from ancient human coprolites and dental calculus. *Philosophical Transactions of the Royal Society B* 375(1812), 20190586.