David K. Jacobson, PhD

(440) 334-4010
Atlanta, GA
davejacobson12@gmail.com

Bioinformatician

Google Scholar
LinkedIn
CDC Git Repos: Upon Request

PROFESSIONAL INTERESTS

Detail-oriented bioinformatician with expertise developing and managing bioinformatic workflows for microbial metagenomic and whole-genome sequencing analysis from a variety of sample types. Seeking to leverage expertise in next-generation sequencing, bioinformatics tools (Python, R, Nextflow, Singularity), and multi-omic research to advance public health impacts through innovative analytical approaches.

EDUCATION

Ph.D., Anthropology - Human Health and Biology, *University of Oklahoma*   Dec. 2020
Dissertation: Factors Influencing Ecological Dynamics of the Human Microbiome.

B.S., Anthropological Sciences, *The Ohio State University*. Magna Cum Laude.   May 2014
Minor: Molecular Genetics

PROFESSIONAL EXPERIENCE

Associate Service Fellow   March 2023 — March 2025
Division of Parasitic Diseases and Malaria, CDC   *Atlanta, GA*
- Led bioinformatic analysis for parasite genotyping in nationwide surveillance of *Cyclospora* and *Plasmodium* to resolve outbreak clusters, identify infectious disease trends, and inform epidemiologic decision making on parasitic disease.
- Developed and maintained Nextflow bioinformatic pipelines in CDC's HPC infrastructure by integrating nf-core modules with custom R, python, and bash scripts to ensure bioinformatic analyses incorporate state-of-the-art techniques and software, such as machine learning to identify geographic origin of *P. vivax* parasites.
- Worked closely with lab staff to identify improved genotyping markers / sequencing approaches for *Cyclospora* and *Plasmodium* nationwide surveillance efforts and optimized bioinformatic pipelines for new NGS data by validating accuracy and replicating published results.
- Spearheaded the creation and implementation of PowerBI and Rmarkdown dashboard / reports / visualizations to disseminate genotyping results and track KPIs for stakeholders with various levels of technical expertise (bioinformaticians, lab staff, epidemiologists, leadership).
- Held numerous technical discussions, 50-state calls, and 1-on-1 meetings with State Public Health Lab (SPHL) partners to provide details on *Cyclospora* and *Plasmodium* genotyping approaches and key insights made possible via bioinformatic analyses.
- Automated data entry process for updating internal tracking databases with specimen metadata, laboratory results, and bioinformatic analysis outputs to minimize data errors and improve cross-team collaboration.
- Wrote workflow documentation / SOPs and trained bioinformaticians to enhance quality management systems for bioinformatic analysis at CDC.

Postdoctoral ORISE Fellow   Jan. 2021 — March 2023
Division of Parasitic Diseases and Malaria, CDC   *Atlanta, GA*
- Converted *Cyclospora* genotyping bioinformatic pipeline from Mac-based bash script to linux-based Nextflow script, facilitating the use of CDC's HPC resources and improving turnaround time for public health responses.
- Improved informatics pipelines for combining epidemiologic and bioinformatic data by standardizing submission forms used by SPHLs and implementing QC checks, allowing for more accurate and timely outbreak investigations.
- Collaborated with federal agencies and SPHLs to standardize and disseminate genotyping protocols and tools for active public health response efforts.
- Conducted research on the genetic population structure of *Cyclospora* resulting in peer-reviewed publications.

Graduate Research Assistant   Jan. 2016 — Dec. 2020
Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma   *Norman, OK*
- Led bioinformatic analysis for projects related to the human microbiome, ovarian cancer, and ancient DNA, resulting in peer-reviewed publications.
- Developed bioinformatic workflows for metagenomic datasets; including genome assembly, phylogenetics, functional characterization, and innovative statistical analysis.
- Generated amplicon and whole-genome NGS data in the wet-lab, from extraction to sequencing, giving years of hands-on experience generating NGS data.
- Managed international research collaborations, overseeing sample collection, data sharing, and compliance with regulatory standards.

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TECHNICAL SKILLS

Tools and Languages	Python, R, Nextflow, Bash, Containerization (Singularity, Docker), Git, linux/unix, bioinformatic tools (e.g., BBTools, Bowtie2, Samtools, GATK, nf-core), high-performance computing environments, Rmarkdown, Rshiny, PowerBI, SQL
Bioinformatic Analyses	WGS analysis, SNP calling, molecular epidemiology, microbiome community profiling (shotgun metagenomics, 16S rRNA), phylogenetic trees, hierarchical clustering, mapping, microbial genome assemblies, quality control, marker identification, drug resistance screening (*Plasmodium*)
Additional Skillsets	Scientific communication, report generation, bioinformatic training, international collaborations, interagency government collaborations, standard operating procedures (bioinformatics), adherence to laboratory quality management standards, Microsoft Office

PUBLICATIONS

Peterson, A. C., **Jacobson, D. K.**, Richins, T., Barratt, J. L.N., and Qvarnstrom, Y. (Accepted). Assessing the sequencing success and analytical specificity of a targeted amplicon deep sequencing workflow for genotyping the foodborne parasite Cyclospora. Journal of Clinical Microbiology.

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.

Leonard, S. R., Mammel, M. K., Almeria, S., Gebru, S. T., **Jacobson, D. K.**, Peterson, A. C., Barratt, J. L.N., and Musser, S. M. (2024). Evaluation of the Increased Genetic Resolution and Utility for Source Tracking of a Recently Developed Method for Genotyping Cyclospora cayetanensis. Microorganisms 12(5), 848.

Kahler, A. M., Hofstetter, J., Arrowood, M., Peterson, A. C., **Jacobson, D. K.**, Barratt, J., da Silva, A. L. B. R., Rodrigues, C., and Mattioli, M. C. (2024). Sources and prevalence of Cyclospora cayetanensis in southeastern US growing environments. Journal of food protection 87(7), 100309.

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 Pfcpmp 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.

Peterson, A. C., Richins, T., Houghton, K., Mishina, M., Sharma, S., Sambhara, S., **Jacobson, D. K.**, Qvarnstrom, Y., and Cama, V. (2023). The limit of detection of the BioFire® FilmArray® gastrointestinal panel for the foodborne parasite Cyclospora cayetanensis. Diagnostic Microbiology and Infectious Disease 107(2), 116030.

Honap, T. P., Monroe, C. R., Johnson, S. J., **Jacobson, D. K.**, Abin, C. A., Austin, R. M., Sandberg, P., Levine, M., Sankaranarayanan, K., and Lewis Jr, C. M. (2023). Oral metagenomes from native American ancestors reveal distinct microbial lineages in the pre-contact era. American Journal of Biological Anthropology 182(4), 542-556.

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.

Haffner, J. J., Katemauswa, M., Kagone, T. S., Hossain, E., **Jacobson, D. K.**, Flores, K., Parab, A. R., Obregon-Tito, A. J., Tito, R. Y., Reyes, L. Marin., Troncoso-Corzo, L., Meda, N., Carabin, H. Honap, T. P, Guijo-Pomo E., Sankaranarayanan, K., Lewis Jr, C. M. and McCall, L. (2022). Untargeted fecal metabolomic analyses across an industrialization gradient reveal shared metabolites and impact of industrialization on fecal microbiome-metabolome interactions. MSystems 7(6), e00710-22.

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.

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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.

Borry, M., Cordova, B., Perri, A., Wibowo, M., Honap, T.P., Ko, J., Yu, J., Britton, K., Girdland-Flink, L., Power, RC., Stuijts, I., Salazar-García, D.C., Hofman, C., Hagan, R., Kagone, T. S., Meda, N., Carabin, H., **Jacobson, D. K.**, Reinhard, K., Lewis, C.M., Kostic, A., Jeong, C., Herbig, A., and Warinner, C. (2020). CoproID predicts the source of coprolites and paleofeces using microbiome composition and host DNA content. . PeerJ 8(), e9001.

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.

In preperation and under review

Barratt, J. L.N., **Jacobson, D. K**, Pierre-Louis, E., Bajic, M., Kelley, J., Patel, D. S., Goldman, I., Zhou, Z., Shi, Y. P., Ridpath, A., Mace, K., Carlson, C., Sutcliffe, A., Butler, Q., Morrison, A., Stanek, D., Tomson, K., Blackmore, B., Cannons, A., Rollo, S., Wang, C., Tuladhar, R., Clemons, B., Antenucci, S., Mergen, K., White, J., Antwi, M., Rothfeldt, L., Lazenby, K., Hedges, S., Shray, J., Courtney, A., Boyanton, B., Qvarnstrom, Y., Freeman, M., and Raphael, B. (Under Review). Genetic characterization of Plasmodium vivax linked to autochthonous malaria transmission in the US (2023) using Illumina AmpliSeq technology: a genetic epidemiology study. Lancet Regional Health - Americas.

White J. L., Ridpath A. D., Guzzardi E., Smith K., Slavinski S., Antwi M., Lee E., Barrett K., Southwick K. L., Gayen S., Quinn M. J., Mace K. E., Williams S., Raphael B., **Jacobson, D. K.**, Barratt J. L. N., McElroy P., Antenucci S., Clemons B. M., McKinney K. and Backenson B. (In Preperation). Case Report and Epidemiological Investigation of Healthcare-associated Plasmodium falciparum Malaria Transmission in Westchester County, New York- 2023

Matlock B., Qvarnstrom Y., Watson B., Neja M., Austin R. M., Barratt J. L. N., **Jacobson D.K.**. (In Preperation). Implementation of automated and customizable QC steps in a bioinformatic pipeline for NGS-based diagnostic tests

POSTERS AND PRESENTATIONS

Conference Posters and Presentations

Jacobson, D. K., Zheng, Y., Peterson, A. C., Qvarnstrom, Y., Richins, T., Cama, V., and Barratt, J. L.N. (2022). Optimization of CDC's Cyclospora cayetanensis Genotyping Workflow Yields More Accurate Genetic Clustering Results. International Association of Food Protection Annual Meeting.

Jacobson, D. K., Kagone, T.S., Meda, N., Carabin, H., Honap, T. P., Sankaranarayanan, K., Lewis Jr, C. M. (2019). Gut Microbiome Composition is Significantly Influenced by Shared Livin-Space in Rural Agriculturalists from Burkina Faso. American Journal of Physical Anthropology Annual Meeting.

Jacobson, D. K., Kagone, T.S., Meda, N., Carabin, H., Honap, T. P., Sankaranarayanan, K., Lewis Jr, C. M. (2020). Database bias hinders functional analysis of non-industrial populations' gut microbiomes. American Journal of Physical Anthropology Annual Meeting.

Jacobson, D. K., Sankaranarayanan, K., Larson, P.S., Watanabe, N., Tanihata, T., Lum, J.K., and Lewis Jr, C.M. (2017). Age is the primary factor structuring diversity of the oral microbiome. American Journal of Physical Anthropology Annual Meeting.

Jacobson, D. K., Sankaranarayanan, K., Lum, J.K., and Lewis Jr, C.M. (2016). Progression of the Oral Microbiome from Infancy to Adulthood. Oklahoma Academy of Sciences.

Presentations to U.S. and International Public Health Laboratories

Ahart, L., **Jacobson, D. K.** (2025). Summary of 2024 cyclosporiasis season. Presented to U.S. Food and Drug Administration Cyclospora Task Force.

Jacobson, D. K., Patel, D. (2024). Insights from Selective Whole Genome Amplification of P. falciparum. Presented to the Laboratory Science and Diagnostics Branch at CDC.

Jacobson, D. K.. (2024). The Cyclospora Genotyping Program: Initial Evaluation of Expanded Genotyping Panel. Presented to the Laboratory Science and Diagnostics Branch at CDC.

Jacobson, D. K., Peterson, A. (2024). The Cyclospora Genotyping Program: Summary and Updates. Presented in CDC's Advanced Molecular Detection Seminar Series.

Ahart, L., **Jacobson, D. K.**, Rice, M., Peterson, A. (2024). The Cyclospora Genotyping Program: Technical Discussion. Presented to U.S. State Public Health Laboratories.

Ahart, L., **Jacobson, D. K.**, Rice, M., Peterson, A. (2024). 2024 50-State Cyclosporiasis Kick-off Call. Presented to U.S. State Public Health Laboratories.

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Ahart, L., **Jacobson, D. K.**, Rice, M., Peterson, A. (2024). 2023 in the Rearview Mirror. Presented to U.S. Food and Drug Administration Cyclospora Task Force.

Ahart, L., **Jacobson, D. K.**, Rice, M., Peterson, A. (2023). 2023 50-State Cyclosporiasis Kick-off Call. Presented to U.S. State Public Health Laboratories.

Ahart, L., **Jacobson, D. K.**, Rice, M., Peterson, A. (2023). 2023 Cyclospora Outbreak Season Genotyping Results. Presented to U.S. State Public Health Laboratories.

Ahart, L., **Jacobson, D. K.**, Rice, M., Peterson, A. (2022) 50-State Cyclosporiasis Kick-off Call. Presented to U.S. State Public Health Laboratories.

Barratt, Joel, **Jacobson, D. K.**, Straily, A. (2022) An overview of Cyclospora cayetanensis genotyping at CDC. Presented to U.S. Food and Drug Administration Cyclospora Task Force.

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, *Universitiy of Oklahoma*	2016
Grant: Opler Research Award, *Universitiy of Oklahoma*	2015
Phi Beta Kappa, *The Ohio State University*	2013

SERVICE AND LEADERSHIP

Scientific Manuscript Reviewer, *Multiple Journals*	2019-2022
Trained and mentored 4 undegradate students in NGS wet lab protocols, *University of Oklahoma*	2016-2020
Founded and Directed Undergraduate Anthropology Mentorship Program, *University of Oklahoma*	2016-2020
Mentored high school student for their Advanced Placement Capstone Research Project, *University of Oklahoma*	2016-2017
Vice-President, Anthropology Graduate Student Association, *University of Oklahoma*	2016
Graduate Student Directing Committee, *Central Ecology and Evolution Conference*	2015-2016