

Detail oriented analyst with a strong background in developing and managing workflows for complex datasets. Skilled at blending technical expertise with effective stakeholder communication to drive informed decision making. Seeking to leverage background in identifying trends and optimizing workflows to support actionable solutions.

SKILLS AND COMPETENCIES

Process Optimization:	Expertise in using data-driven insights to align technical work with strategic goals and implement solutions that improve decision making speed and accuracy.
Stakeholder Communication:	Experience leading multidisciplinary collaborations and using dashboards/reports to communicate recommendations with senior leadership and non-technical stakeholders.
Data Analytics:	Data mining, cluster analysis, optimizing analytical performance, machine learning, extract, transform, load (ETL) processes
Technical Tools:	Python, R, Bash, SQL, GitHub, PowerBI, Tableau, Microsoft Office.

EDUCATION

Ph.D., Anthropology - Human Health and Biology , GPA 4.0, <i>University of Oklahoma</i> . <i>Dissertation: Factors Influencing Ecological Dynamics of the Human Microbiome.</i>	Dec. 2020
B.S., Anthropological Sciences , GPA 3.84, Magna Cum Laude, <i>The Ohio State University</i> . <i>Minor: Molecular Genetics</i>	May 2014

PROFESSIONAL EXPERIENCE

Associate Service Fellow <i>Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention</i>	March 2023 — March 2025 <i>Atlanta, GA</i>
<ul style="list-style-type: none">Led data-driven projects to improve nationwide disease surveillance, analyzing over 5,000 samples to optimize outbreak identification and improve public health responses, resulting in successful source-identification of 12 multistate foodborne disease outbreaks.Disseminated results to collaborators through over 200 reports/dashboards, 7 nationwide presentations, 7 scientific publications, and 5 technical discussions, demonstrating ability to communicate key takeaways to audiences with varying levels of technical expertise.Developed, implemented, and improved automated pipelines to reduce turnaround time and enhance quality control functionality, speeding up analysis by approximately 6 hours per week and filtering out samples with poor quality metrics (15% of total samples).Managed cross-functional collaboration with 11 lab teams, 3 teams of federal epidemiologists, and state health officials from 40+ jurisdictions to guide data-driven interpretations of infectious disease outbreak investigations, including confirmation of 10 malaria transmission cases in the United States.Spearheaded the creation of 2 standardized extract, transform, and load workflows that pulled from 8 previously unintegrated databases, increasing operational efficiency and reducing manual data entry/merging errors by 80% and allowing team members to focus on high-impact activities.	
Postdoctoral ORISE Fellow <i>Division of Parasitic Diseases and Malaria, Centers for Disease Control and Prevention</i>	Jan. 2021 — March 2023 <i>Atlanta, GA</i>
<ul style="list-style-type: none">Led process improvement initiatives by transitioning 6 legacy decentralized workflows to a single centralized repository, reducing software version inconsistencies across 30 individual scripts, increasing efficiency, and taking advantage of computing resources available at CDC.Designed interactive dashboards and reports distributed to 40+ state public health jurisdictions, enhancing accessibility of complex data for stakeholders, leading to improved data sharing between agencies and identification / resolution of pain points related to data generation and submission.Conducted advanced quantitative analyses to improve infectious disease outbreak detection, resulting in greater than 99% accuracy in linking outbreak cases together, enabling data-driven decision making for federal and state health agencies.Advised public health leadership (executive-level) at CDC, FDA, and state public health labs on strategic use of analytics, helping shape responses to major foodborne disease outbreaks.	

Graduate Research Assistant

Jan. 2016 — Dec. 2020

Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma

Norman, OK

- Extracted key insights from over 1,000 human microbiome samples, leveraging machine learning and statistical modeling to identify novel disease patterns relating to ovarian cancer and metabolic disease.
- Designed and implemented 5 scalable data pipelines for large-scale genetic datasets, using state-of-the-art analytical approaches to yield health related insights and 6 scientific publications.
- Led international research collaborations with partners in Italy and Burkina Faso, managing supply ordering and budgeting (\$60,000), compliance, and cross-border coordination, ensuring seamless data sharing and adherence to regulatory standards.

HONORS, AWARDS, AND LEADERSHIP

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 (\$19,982), *National Science Foundation* 2019

Phi Beta Kappa, *The Ohio State University* 2014

Leadership and Service

Founded and Directed Undergraduate Anthropology Mentorship Program, *University of Oklahoma* 2016-2020

Trained and mentored 10 graduate, undergraduate, and high school students, *University of Oklahoma* 2016-2020

Vice-President, Anthropology Graduate Student Association, *University of Oklahoma* 2016

Graduate Student Directing Committee, *Central Ecology and Evolution Conference* 2015-2016

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.

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.