Jill V. Hagey, MS, PhD

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Education

University of California Davis, Davis CA
PhD, Animal Biology with a designated emphasis in Host-Microbe Interactions **09/20**
Dissertation Topic: Surveying the composition and function of the fecal microbiota of dairy cows across California.
MS, Animal Biology **12/15**
Thesis Topic: Modulation of Gut Microbes: Interplay between Peptidoglycan Recognition Proteins and Lysozyme.
BS, Cell Biology **12/11**

Select Professional Training

Machine Learning (Regression, Classification, Clustering & Retrieval) 10/21
University of Washington, Coursera
Summer Institute Stats for Big Data: Supervised & Unsupervised Methods for Machine Learning 7/21
University of Washington, School of Public Health, Department of Biostatistics
Python and Command Line Tools for Genomic Data Science 12/20
John Hopkins, Coursera
Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) 08/18
Marine Biological Laboratory, Woods Hole MA

Bioinformatics Skills

- Experience with **HPCs** (SLURM & SGE), **Linux** & troubleshooting bioinformatic tools on Microsoft systems.
- Deployed bioinformatic pipelines on Terra.bio (Google backend) using Dockstore and assisted CDC cloud team to deploy PHoeNIx on **AWS**.
- Proficient in **Python** and **R/R markdown** for data analysis (**ggplot2/Tidyverse**) & visualization (**Plotly** see here).
- Authored several pipelines in **Nextflow** and wrote tutorials for **WDL** and **Snakemake**
- Wrote tutorials for **Docker**/Singularity. Build & maintain Docker containers on quay.io & STaPH-B's repository.

Relevant Scientific Experience

Bioinformatics Domestic Lead for the Antimicrobial Resistance Laboratory Network 6/23 – present
CDC, Division for Healthcare Quality Promotion, Clinical and Environmental Microbiology Branch

- Primary point of contact for public health jurisdictions seeking bioinformatics technical assistance. These requests include troubleshooting programs, assistance interpreting results, aiding with validations, providing recommendations for capacity building, and training local staff on bioinformatic fundamentals.
- **Bioinformatics subject matter expert (SME)** reviewer for grant applications to The Epidemiology and Laboratory Capacity Program at CDC. My knowledge of state sequencing & bioinformatic capacity was critical in determining strategic sequencing investments for surveillance & ID of highly antibiotic-resistant pathogens.
- Regularly provide Antimicrobial Resistance Laboratory Network (ARLN) leadership updates on bioinformatic workflow developments and implementation across the network.
- Recognized as a "stellar and effective communicator", I was specifically requested by ARLN regional labs to train their staff on bioinformatics analysis and ensure use of NGS was aligned with ALRN objectives.
- As the lead developer for **outbreak analysis** pipeline PhyloPHoeNIx, I have demonstrated the capability to adapt to changing and additional priorities, delegate, and oversee the work of colleagues.
- Authored a version of our bioinformatic pipeline PHoeNIx for **CLIA validation**, requiring coordination with medical microbiologists & IT for automated Laboratory Information Management System **(LIMS) reporting**.
- Developed and presented training for partners in Eastern Europe, South America and Africa.
- Collaborate across the branch for data modernization efforts combing different data streams into **Databricks**.
- Create and ensure compliance with CI/CD standards and SOPs for routine procedures.
- Standardize methodologies for bioinformatic analysis of **long-read, metagenomic & wastewater data**.

Bioinformatian III Contractor for Goldbelt C6 LLC **2/22 – 6/23**
CDC, Division for Healthcare Quality Promotion, Clinical and Environmental Microbiology Branch

- **Lead developer** of PHoeNIx: a platform agnostic bioinformatic pipeline for healthcare-associated and antimicrobial resistant pathogens, which is used by >30 domestic and international public health jurisdictions.
- Rewrote the SNVPhyl pipeline in Nextflow to remove use of the Galaxy platform, which mitigated major security vulnerabilities from Log4J and significantly improved the speed of the pipeline.
- Triaged and closed GitHub issues by implementing feature enhancements, addressing bugs, and resolving containerization issues, all while collaborating with a distributed team via pull requests and issue tracking.
- Implemented documentation, version control with **Git**, SOPs, and citation software to bioinformatic team.

Bioinformatian: COVID-19 Emergency Response **1/22 – 2/22**
CDC, International Lab Task Force: Pathogen Genomics

- Evaluated cloud, command line, web-based software for SARS-CoV-2 genomic analysis and provided recommendations for capacity building tailored to our international partner's needs.
- Provided data analysis to partner countries on an as-need basis.
- Reviewed proposed research projects and provided key feedback for their implementation.

American Public Health Laboratories Bioinformatics Fellow **9/20 – 2/22**
CDC, Clinical Detection and Surveillance Lab Team: Water Borne Disease Prevention Branch

- Developed a custom **Snakemake** workflow on a high-performance computing **cluster to identify SNPs** differentiating *Cryptosporidium* genomes infecting humans and cattle, leveraging **machine learning algorithms** to pinpoint **key genomic variations (SNPs).** This pipeline could be used to replace current wet lab methods that have poor resolution allowing accurate tracking of outbreaks.
- Created **R shiny** application to visualize and compare the similarity of 18S rRNA gene sequences of *Cryptosporidium* species for quick look up and searching of our genomic database.
- Evaluated performance of assembly and alignment software on sequenced *Cryptosporidium* genomes.
- Nominated for The Fellows Collective Exemplary Contributions to Public Health Award

Deputy Team Lead/Bioinformatian: COVID-19 Emergency Response **3/21 – 7/21**
CDC, Laboratory and Testing Task Force: Technical Outreach and Assistance for States Team (TOAST)

- Authored protocols on protocols.io for sequence submission to public repositories, pipeline implementation and troubleshooting for **SARS-CoV-2 genomic characterization** that are utilized nationwide in public health labs.
- Collaborated with state public health bioinformatians to develop a pipeline for genomic characterization of SARS-CoV-2, which lead to the availability of this pipeline on command line and **Terra.bio**.
- Coordinated with public health staff to bring together a diverse advisory group on server and cloud computing purchasing & resource requirements for a state public health lab, which was critical for their sequencing & bioinformatic infrastructure development.
- Communicated guidance for **CLIA validation** of bioinformatic pipelines.
- Meet weekly with NCBI staff to elevate barriers for submission of sequences to public repositories.
- Synchronized needs of bioinformatic regional resources at public health labs with the objectives of the Office of Advanced Molecular Detection at the Center for Disease Control and Prevention.

PhD Dissertation UC Davis **9/15 – 09/20**

- Wrote pipeline for **16S rRNA analysis** (AVS ID, diversity, differential abundance & variability analysis):
    - Identified farm variation in microbial communities of feces and milk from dairy cattle.
    - Evaluated differences in microbial populations due to sampling method from the rumen of cattle.
- Analyzed **metagenomic data** to determine functional differences of the microbiome of cattle and identification of taxonomy contributing to nitrogen cycling and antibiotic resistance.
- Engineering *Lactococcus lactis* to secrete SodA for therapeutic use against *Salmonella* and *E. coli* in daily calves.
- J. B. Russel Young Scientist Award for Best Poster Presentation

Masters Thesis UC Davis **8/13 – 12/15**

- Solid foundation in study design and statistical analysis with SAS, R, Adobe Illustrator and GraphPad Prism.
- Used an intestinal cell line, IPEC-J2, to determine expression of peptidoglycan recognition protein-3/4 in response to milk products, commensal and pathogenic bacteria.

- Analyzed gene expression of cytokines and immune receptors via qRT-PCR in a malnourished swine model.

Lab Manager **1/13 – 9/14**
University of California Davis, Department of Medicine and Epidemiology

- Effectively managed administrative aspects of research projects including budget management, maintained adherence to SOPs and university regulations, hiring, training and data acquisition.
- Achieved completion of multiple concurrent research projects in a timely manner while adhering to a budget.
- Accurately processed and measured immunoglobulins in colostrum and serum via ELISAs and RIDs.
- Designed and optimized new immunoassay protocol for measuring immunoglobulins in feces.

Relevant Business Experience

Innovation Access Intern **4/20-07/20**
University of California, Davis - Office of Research

- Reviewed university Record of Inventions to determine if they are patentable, scrutinized scientific merit, conducted technology marketability assessments and provided written recommendations to patent attorneys.

Business Development Fellow with the Institute for Innovation and Entrepreneurship **2019-2020**
University of California, Davis Graduate School of Management

- Completed courses including management of innovation, product development, and Entrepreneurship & Venture Investment alongside MBA students.
- Developed business plans, conducted market research & created pitch decks for Big Bang Business competition.

Select Poster/Oral Presentations and Trainings

NGS for Detecting Antimicrobial Resistance II: Navigating Genomic Sequencing Quality from PHoeNIx **02/25**
The American Public Health Laboratories webinars for continuing education programs
PHoeNIx: A Bioinformatic Pipeline for CDC's Antimicrobial Resistance Laboratory Network [Poster] **10/24**
ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines
SARS-CoV-2 Benchmark datasets for bioinformatics pipeline validation **09/21**
Technical Outreach & Assistance for States Team Office Hours for State Public Health Labs
Automating bioinformatic pipelines with Snakemake. **04/21**
Live demo and hands-on Workshop. Genome Interest Group, Technical. CDC
International Society of Microbial Ecology [Poster]
Prevalence of Nitrogen Fixation Genes in Dairy Cattle Feces **08/18**

Select Publications

Xiaoli, L., **Hagey, J. V.**, Lawsin, A., Winglee, K., Chen, J. C., … Katz, L. S. (2022) Benchmark datasets for bioinformatics pipeline validation: applications for SARS-CoV-2 Surveillance. *PeerJ*, Sep 5;10:e13821.

Hagey, J. V., Bhatnagar, S., Heguy, J. M., Karle, B. M., Price P. L., Meyer, D., Maga, E. A. (2022). Metagenomic Analysis of the Fecal Microbiome in Dairy Cows Reveal Species Involved in the Nitrogen Cycle.

Hagey, J. V., Laabs, M., Maga, E. A., DePeters, E. J. (2022). Rumen Sampling Methods Bias Bacterial Communities. *PLoS One*, May 5;17(5):e0258176.

Hagey, J. V., Bhatnagar, S., Heguy, J. M., Karle, B. M., Price P. L., Meyer, D., Maga, E. A. (2019). Fecal Microbial Communities in a Large Representative Cohort of California Dairy Cows. *Frontiers of Microbiology*, 10(May),1-14.

Garas, L. C., Feltrin, C., Hamilton, M. K., **Hagey, J. V.**, Murray, J. D., … Maga, E. A. (2016). Milk with and without lactoferrin can influence intestinal damage in a pig model of malnutrition. *Food & Function*, *7*(2), 665–678.

Chigerwe, M., **Hagey, J. V.**, & Aly, S. S. (2015). Determination of neonatal serum immunoglobulin G concentrations associated with mortality during the first 4 months of life in dairy heifer calves. *Journal of Dairy Research*, *82*(04), 400–406.

Pipkin, K. M., **Hagey, J. V.**, Rayburn, M. C., & Chigerwe, M. (2015). A Randomized Clinical Trial Evaluating Metabolism of Colostral and Plasma Derived Immunoglobulin G in Jersey Bull Calves. *Journal of Veterinary Internal Medicine*, 29, 961-966.

Murphy, J. M., **Hagey, J. V.**, & Chigerwe, M. (2014). Comparison of serum immunoglobulin G half-life in dairy calves fed colostrum, colostrum replacer or administered with intravenous bovine plasma. *Veterinary Immunology and Immunopathology*, *158*(3-4), 233–7.