Jill Hagey

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Areas of Specialization:

I am passionate about creating reproducible pipelines to make biological "big data" easy to understand, visually appealing, and useful for decision making. I employ a combination of bioinformatics analysis and wet lab techniques to inform our understanding of pathogens important to public health. My unique background in and bioinformatics, cell biology, microbiology, immunology and animal science is specially tailored for a career improving public health.

Education:

University of California Davis, Davis CA
PhD, Animal Biology with a designated emphasis in Host-Microbe Interactions September 2020

MS, Animal Biology December 2015

BS, Cell Biology December 2011

Bioinformatic/Statistical Training:

Summer Institute in Stats for Big Data: Supervised & Unsupervised Methods for Machine Learning 7/21
University of Washington, School of Public Health, Department of Biostatistics
Python 3 Programing Specialization 12/20
University of Michigan, Coursera
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 HPC (SLURM & SGE), Unix/Linux & troubleshooting bioinformatic tools on Microsoft systems
- Proficient in R: an example can be found here. Built R Shiny applications.
- Adept in Python for scrapping data on NCB/GISAID, data analysis and wrangling, Examples here, here and here.
- Workflow languages: Wrote tutorials for WDL and Snakemake, ran hands on training for CDC Bioinformatians
- Containers: Wrote tutorial for Docker and Singularity containers.
- Genomic characterization of SARS-CoV-2
- 16S rRNA amplicon analysis with AVS identification, diversity, differential abundance and variability analysis.
- Metagenomics: examples here.
    - Custom scripts using snakemake, python, bash and R for data manipulation and analysis.
    - Tree formation and read/contig placement.
    - Functional annotation, taxonomic classification, assembly, binning and genome annotation.

Relevant Experience:

Deputy Team Lead: COVID-19 Emergency Response 3/2021 – present

CDC, Laboratory and Testing Task Force, Technical Outreach and Assistance for States Team (TOAST)

- Authored protocols.io pages for sequence submission to public repositories, pipeline implementation and troubleshooting for SARS-CoV-2 genomic characterization.
- Collaborated with state public health bioinformatians on SARS-CoV-2 sequence pipeline development and conducted comprehensive pipeline evaluations.
- Advised state public health labs on server and cloud computing purchasing and resource requirements.
- Communicated guidance for CLIA validation of bioinformatic pipelines.
- Meet weekly with NCBI to elevate barriers for submission of sequences to public repositories.
- Synchronized needs of bioinformatic regional resources at PHL labs with the objectives of the Office of Advanced Molecular Detection at the Center for Disease Control and Prevention.

APHL Bioinformatics Fellow (PI: Dawn Roellig, PhD) 9/2020 – present
CDC, Clinical Detection and Surveillance Lab Team in the Water Borne Disease Prevention Branch

- Identified SNPs that differentiate between genomes of *Cryptosporidium* that infected humans and cattle by implementing custom workflows on a high-performance computing cluster.
- Created R shiny application to visualize and compare the similarity of 18S rRNA gene sequences of *Cryptosporidium* species.
- Evaluated performance of assembly and aligning software after sequencing *Cryptosporidium*.

PhD Dissertation UC Davis (PI: Elizabeth Maga, PhD) 9/15 – 9/2020
Dissertation Topic: Surveying the composition and function of the fecal microbiota of dairy cows across California.

- Created custom pipelines and analyzed several 16S amplicon-based projects:
  - 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 identified taxonomy contributing to nitrogen cycling and antibiotic resistance.
- Scripts and description of projects can be found at jvhagey.github.io
- Engineering *Lactococcus lactis* for therapeutic use against *Salmonella* and *E. coli* in daily calves.

Masters Thesis UC Davis (PI: Elizabeth Maga, PhD) 8/13 – 12/15
Thesis Topic: Modulation of Gut Microbes: Interplay between Peptidoglycan Recognition Proteins and Lysozyme.

- Solid foundation in study design and statistical analysis with SAS, R, Adobe Illustrator and GraphPad Prism.
- Utilized 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 (PI: Munashe Chigerwe, BVSc, MPH, PhD) 1/13 – 9/14
University of California Davis, Department of Medicine and Epidemiology

- Effectively managed administrative all aspects of research projects including budget management, maintained adherence to Standard Operation Procedures 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.

Business/Leadership Training:

Innovation Access Intern 04/2020
University of California, Davis Office of Research
UC Entrepreneurship Academy 09/19
University of California, Davis Graduate School of Management
Leadership Challenge Workshop: Leadership Practices Inventory 02/19
University of California, Davis Graduate School of Management

Publications:

Hagey, J. V., Bhatnagar, S., Heguy, J. M., Karle, B. M., Price P. L., Meyer, D., Maga, E. A. (2020). Metagenomic Analysis of the Fecal Microbiome in Dairy Cows Reveal Species Involved in the Nitrogen Cycle. *In Prep*.

Hagey, J. V.*, Laabs, M.*, DePeters, E. J. (2020). Rumen Sampling Methods Bias Microbial Communities. *In Review*.

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.

Chigerwe, M., & **Hagey, J. V.** (2014). Refractometer assessment of colostral and serum IgG and milk total solids concentrations in dairy cattle. *BMC Veterinary Research*, *10*(1), 178. doi:10.1186/s12917-014-0178-7

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.

Chigerwe, M., Coons, D. M., & **Hagey, J. V.** (2012). Comparison of colostrum feeding by nipple bottle versus oroesophageal tubing in Holstein dairy bull calves. *Journal of the American Veterinary Medical Association*, *241*(1), 104–9.

Select Fellowships and Awards:

- Little Bang! Business Poster Competition Winner 2020
- Business Development Fellow with the Institute for Innovation and Entrepreneurship 2019-2020
- J. B. Russel Young Scientist Award for Best Poster Presentation 2019

Poster Presentations:

Congress on Gastrointestinal Function
Identification of Microbes Involved in Nitrogen Fixation in Dairy Cow Manure on Farms across California 04/19
International Society of Microbial Ecology
Prevalence of Nitrogen Fixation Genes in Dairy Cattle Feces 08/18
Animal Biology Graduate Group Colloquium
Survey of Microbial Fecal Populations across California Dairies 10/16
Keystone Symposia: "Gut Microbiota Modulation of Host Physiology: The Search for Mechanism"
Lysozyme Transgenic Goat Milk Regulates Expression of Peptidoglycan Recognition Protein 3 & 4 04/15