Jenna **Hamlin**

HEALTH SCIENTIST - INFORMATICS

Respiratory Diseases Laboratory Branch, Centers for Disease Control and Prevention, Atlanta, GA, USA

✉ jhamlin@cdc.gov | 🔘 jennahamlin

I am a scientist with over 10 years of experience in classical genetics, genomics, and evolutionary biology. My training spans a range of tools and approaches—including bioinformatics, population genetics, and species distribution modeling—with a strong emphasis on experimental design. As my computational skills increased, the genomes of the organisms I study have become smaller. Currently, I work at the intersection of public health (ph), ph tool development, and the study of pathogens, with a focus on reproducible research.

Education

University of Georgia   *Athens, GA*

PH.D. IN GENETICS   *2015*

University of North Carolina - Asheville   *Asheville, NC*

B.S. IN BIOLOGY   *2010*

Appointments

Centers for Disease Control and Prevention   *Atlanta, GA*

HEALTH SCIENTIST INFORMATICS   *22-Jun–Current*

- Led the Legionella International Typing Workgroup, organizing meetings, tracking progress, and fostering collaboration
- Maintained bioinformatics pipelines (el_gato, mashWrapper) including updates, validation, and troubleshooting
- Transferred pipelines to CDCgov GitHub, conducted code reviews, and supported SNP pipeline project development
- Streamlined Legionella genomics analyses and automated documentation to improve workflow efficiency
- Authored manuscripts, abstracts, and presentations for both internal and external audiences
- Implemented data management solutions for metadata
- Led workgroup meetings, mentored colleagues, and coordinated communications for Legionella bioinformatics projects

Centers for Disease Control and Prevention, Contractor with ASRT Inc.   *Atlanta, GA*

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES   *20-Nov–22-Jun*

- Refactored and validated pipelines (Perl ? Python, NextFlow) to ensure reproducible workflows for internal and external users
- Supported public health partners by onboarding tools, facilitating data transfers, analyzing datasets, and delivering actionable results
- 60-day detail on Data Analytics and Visualization for Vaccine Task Force (April - June 2021)
- Maintained bioinformatics infrastructure, legacy pipelines, and validation plans while troubleshooting technical issues.
- Produced scientific communications, including manuscripts, abstracts, figures, and presentations for ASM, CSTE, and Legionella conferences
- Managed data and analyses, including sequence uploads, wgMLST, dendrogram generation, and outbreak investigations
- Analyzed sequence type(ST) 213 and 222 genomes to track and report increases in Legionella cases

Centers for Disease Control and Prevention; Fellow with APHL   *Atlanta, GA*

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLLOW   *19-Sep–20-Nov*

- Developed tinselR - an Rshiny application for annotating outbreak trees
- Completed APHL core competency and leadership training
- Served a 30-day detail on Routine Reporting for COVID-19 Response (June - July 2020)

University of Georgia   *Athens, GA*

BENSASSON LAB POST-DOCTORAL RESEARCHER   *17-Oct–19-Aug*

- Directed collaborative research with graduate and undergraduate students
- Collated and streamlined genome mapping for 1,000 Saccharomyces cerevisiae isolates as a lab resource
- Applied iterative population genomics and phylogenetics methods to classify 400 genomes
- Resolved haplotypes for Candida albicans genomes using PacBio sequencing

Indiana University   *Bloomington, IN*

MOYLE LAB POST-DOCTORAL RESEARCHER   *15-Jun–17-Sep*

- Directed research with faculty, graduate students, and undergraduates at IU and collaborators at two external universities
- Conducted a genome-wide study on factors influencing introgression likelihood in Solanum species
- Streamlined genotyping to generate biological replicates; validated accuracy with technical replicates and statistical testing
- Applied linear mixed models and ANOVA to analyze targeting, rates, and floral traits across replicated large-scale crosses

Skills

Analytical

Data science, Experimental Design, Next Generation Sequencing, Genomics, High Performance Computing, Project Management, Quality Control, Reproducible research, Statistics, Technical writing and documentation

Programming

AWK - proficient, Bash - expert, Python - expert, R - expert, Rmarkdown - expert, NextFlow - proficient, GitHub - expert

Publications

JAP Hamlin, NA Kozak-Muiznieks, JW Mercante, L Rishishwar, ET Norris, …
Expanded geographic distribution for two Legionella pneumophila sequence types of clinical concern

Msphere
2024

NV Grossmann, C Milne, MR Martinez, K Relucio, B Sadeghi, EN Wiley, …
Large Community Outbreak of Legionnaires Disease Potentially Associated with a Cooling Tower—Napa County, California, 2022

MMWR. Morbidity and Mortality Weekly Report
2023

JAP Hamlin, T Nakov, A Williams-Newkirk
tinselR—an R Shiny Application for Annotating Phylogenetic Trees

Microbiology Resource Announcements
2021

JAP Hamlin, MS Hibbins, LC Moyle
Assessing biological factors affecting postspeciation introgression

Evolution letters
2020

JAP Hamlin, GB Dias, CM Bergman, D Bensasson
Phased Diploid Genome Assemblies for Three Strains of Candida albicans from Oak Trees

G3
2019

JAP Hamlin, NA Sherman, LC Moyle
Two loci contribute epistatically to heterospecific pollen rejection, a postmating isolating barrier between species

G3
2017

JAP Hamlin, TJ Simmonds, ML Arnold
Niche conservatism for ecological preference in the Louisiana iris species complex

Biological Journal of the Linnean Society
2017

JAP Hamlin, ML Arnold
Neutral and Selective Processes Drive Population Differentiation for Iris hexagona

Journal of Heredity
2015

ML Arnold, AN Brothers, JAP Hamlin, SJ Taylor, NH Martin
Divergence-with-gene-flow—what humans and other mammals got up to

Reticulate Evolution
2015

JAP Hamlin, ML Arnold
Determining Population Structure and Hybridization for Two Iris Species.

Ecology and Evolution
2014

ML Arnold, JAP Hamlin, AN Brothers, ES Ballerini, RS Singh, J Xu, …
Natural hybridization as a catalyst of rapid evolutionary change

Rapidly evolving genes and genetic systems
2012

ML Arnold, ES Ballerini, AN Brothers, JAP Hamlin, CDA Ishibashi, …
The genomics of natural selection and adaptation: Christmas past, present and future (?).

Plant Ecology & Diversity
2012

Presentations

Talks

mashWrapper   *Atlanta, GA*

GENOMICS INTEREST GROUP - TECHINCAL   *2022*

tinselR - An RShiny App for Phylogenetic Tree Annotation   *Atlanta, GA*

CDC DATA VIZ DAY   *2020*

Start Writing Manuscripts in Rmarkdown   *Atlanta, GA*

GENOMICS INTEREST GROUP - TECHINCAL   *2020*

Build Shiny Apps   *Athens, GA*

WARNELL SCHOOL OF FORESTRY & NATURAL RESOURCES DATA MANIPULATION AND MANAGEMENT COURSE   *2018*

Population Genomics of wild and domesticated yeast   *Athens, GA*

UNIVERSITY OF GEORGIA ENTHUSIASTS OF DIVERSITY GENETICS AND EVOLUTION   *2018*

No Easy D: Little Evidence for Introgression from Whole-Genome Data in Wild Solanum   *Portland, OR*

SOCIETY FOR THE STUDY OF EVOLUTION   *2017*

Epistasis for Postmating Prezygotic Isolation   *Austin, TX*

SOCIETY FOR THE STUDY OF EVOLUTION   *2016*

Spatial, temporal, and genome-wide patterns of differentiation for the Louisiana iris species complex   *Bloomington, IN*

INDIANA UNVIVERSITY BROWN BAG   *2015*

What Drives Phenotypic and Genetic Divergence for Iris hexagona   *Raleigh, NC*

SOCIETY FOR THE STUDY OF EVOLUTION   *2014*

Comparative Phylogeography of Two Louisiana Irises   *Snowbird, UT*

SOCIETY FOR THE STUDY OF EVOLUTION   *2013*

Posters

Updating Legionella pneumophila typing scheme and nomenclature using whole genome data   *Dresden, Germany*

ESCMID STUDY GROUP FOR LEGIONELLA INFECTIONS   *2024*

- Ginevra C, Tewolde R, Afshar B,⌧Borges V, Goncalves P, Henderson KC, Jacqueline C, Kozak-Muiznieks NA, Willby MJ, Hamlin JAP

Expanded Geographic Distribution for Two Legionella pneumophila Sequence Types of Clinical Concern   *Puerto Vallarta, Mexico*

SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION   *2024*

- Hamlin JAP, Kozak -Muiznieks NK, Mercante JW, Rishishwar L, Norris ET, Gaines AB, Ishaq MK, Winchell JM, and Willby MJ

El_gato: accurate and rapid sequence-based typing for Legionella pneumophila   *Hinxton, United Kingdom*

APPLIED BIOINFORMATICS AND PUBLIC HEALTH MICROBIOLOGY   *2023*

- Hamlin JAP, Mashruwala D, Collins AJ, Gaines AB, Norris ET, Chivukula V, Rishishwar L, Overholt WA, Kozak-Muiznieks NK, Willby MJ, Winchell JM

A Community Outbreak of Legionnaires' Disease Possibly Associated with an Outdoor Hotel Spa – California, 2021   *Salt Lake City, Utah*

COUNCIL OF STATE AND TERRITORIAL EPIDEMIOLOGISTS   *2023*

- Burmester J, Evans S, Ferguson D, Lunsforward R, Rutschmann S, Kimura A, Flores E, Mukhopadhyay R, Hannapel E, Bertumen JB, Hamlin JAP, and Miller, G

Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Tool   *Atlanta, GA*

CDC LABORATORY SCIENCE SYMPOSIUM   *2023*

- Hamlin JAP, Willby MJ, and Winchell JM

Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Europe

Atlanta, GA

CDC Laboratory Science Symposium

2023

- Kozak-Muiznieks NA, Hamlin JAP, Lucas C, and Willby MJ

Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Tool

Baltimore, MD

American Society for Microbiology

2022

- Hamlin JAP, Willby MJ, and Winchell JM

Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Europe

Yokohama, Japan

International Conference on Legionella

2022

- Kozak-Muiznieks NA, Hamlin JAP, Lucas C, and Willby MJ

Tinsel - an Rshiny app for phylogenetic tree annotation

Virtual

Association of Public Health Laboratories Annual Meeting

2020

- Hamlin JAP and Williams-Newkirk A

Tinsel - an Rshiny application for annotating outbreak trees

Canceled - Atlanta, GA

Integrated Foodborne Outbreak Response and Management

2020

- Hamlin JAP and Williams-Newkirk A

Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast

Pacific Grove, CA

Fungal Genetics Conference

2019

- Hamlin JAP and Bensasson D

Clinical Saccharomyces cerevisiae are admixed domesticated yeast

Holderness, NH

Cellular and Molecular Fungal Biology: Gordon Research Conference

2018

- Hamlin JAP and Bensasson D

Higher Prevalence of Genetic Exchange Given Geographic Proximity

Laural Hill, NC

Southeastern Population Ecology & Evolutionary Genetics.

2017

- Hamlin JAP and Moyle LC

Two Loci Contribute Epistastically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species

Davis, CA

Solanaceae Conference

2016

- Hamlin JAP and Moyle LC

What Drives Phenotypic and Genetic Divergence for Iris hexagona

Boise, ID

Botanical Society of America

2014

- Hamlin JAP and Arnold ML

Comparative Phylogeography of Two Louisiana Iris Species: Iris fulva and Iris brevicaulis

Guanajuato, Mexico

American Genetic Association

2011

- Hamlin JAP, Brothers AN, Ballerini ES, and Arnold ML

Packages

tinselR - An R package for visulizing and annotating phylogenetic trees

https://github.com/jennahamlin/tinselR

Author and maintainer

2019

mashwrapper - a Python tool for parsing mash results

https://github.com/CDCgov/mashwrapper

Author and maintainer

2022

Mentoring

University of Georgia graduate students

E. Scopel Ferreira Da Costa

J. Pena

University of Georgia undergraduate students

T. Simmonds

K. Miller

J. Foley

S. Duque

B. Webb

Indiana University graduate students

C. Jewell

M. Gibson

Indiana University undergraduate students

A. Huh

J. Breisch

S. Henderson

L. Howser

C. Plasterer

D. Shukla

S. Seo