

Jenna A. P. Hamlin

HEALTH SCIENTIST - INFORMATICS

✉ jennahamlin@gmail.com | 📱 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. 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

PH.D. IN GENETICS

Athens, GA

2015

University of North Carolina - Asheville

B.S. IN BIOLOGY

Asheville, NC

2010

Appointments

Centers for Disease Control and Prevention

Atlanta, GA

HEALTH SCIENTIST INFORMATICS WITH DIVISION OF BACTERIAL DISEASES

22-Jun–Current

- Led development of typing scheme for *Legionella pneumophila* for an international genomics consortium
- Created automated reporting scripts and documentation to streamline workflows and ensure reproducibility
- Led development and maintenance of validated genomic pipelines (el_gato, mashWrapper) for Illumina-based typing
- Liaised between informatics and wet lab teams, translating scientific goals into computational solutions
- Integrated pipelines into shared computational environments, responding to evolving infrastructure requirements, and user needs
- Improved compute workflows, boosted reproducibility with containerization, and updated documentation (README, SOPs, job aids)
- Directed annual updates to databases and tools, ensuring validation, QC, and regulatory readiness
- Mentored laboratory staff (n = 3) in bioinformatics best practices and pipeline development helping scale team capabilities

NA–NA

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES (CONTRACTOR WITH ASRT, INC.)

20-Nov–22-Jun

- Supported national COVID-19 vaccination strategy with the Vaccine Task Force during an emergency response
- Refactored and validated legacy pipelines (Perl to Python with Nextflow) to ensure reproducibility, scalability, and regulatory compliance
- Partnered with public health agencies to deploy tools, secure data, and deliver genomic insights for outbreak response
- Maintained and optimized bioinformatics infrastructure, troubleshooting pipeline failures and reducing downtime for routine analyses
- Produced scientific communications (manuscripts, abstracts, figures, conference talks) that translated technical results for diverse audience
- Managed data and analyses, including sequence uploads, wgMLST, dendrogram generation, and outbreak investigations
- Analyzed ST213 and ST222 genomes to flag emerging genetic types

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLOW

19-Sep–20-Nov

- Developed tinselR - an Rshiny application for annotating outbreak trees
- Trained in APHL Core Competencies, including laboratory management, communication, and quality systems
- Generated and improved routine reports during COVID-19 emergency response, informing decisions by the White House Coronavirus Task Force
- Test line test line test line

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* (yeast) 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* (tomato) 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

Bioinformatics

NGS DATA ANALYSIS, CGMLST AND wgMLST DEVELOPMENT, SNP CALLING WORKFLOWS, OUTBREAK INVESTIGATION SUPPORT,

PUBLIC DATABASES (NCBI, ENA, PUBMLST), COMPUTATIONAL BIOLOGY TOOLS FOR ALIGNMENT, VARIANT CALLING,

PHYLOGENETICS, GENOME ASSEMBLY

Scripting & Automation

PYTHON, BASH AND R SCRIPTING, WORKFLOW AUTOMATION, PIPELINE REFACTORING AND VALIDATION, MAINTENANCE OF LEGACY PIPELINES, VERSION CONTROL WITH GIT/GITHUB

Compute Infrastructure

OPERATING SYSTEMS: LINUX, WINDOWS, MACOS, CONTAINERIZED ENVIRONMENTS (DOCKER, SINGULARITY), SYSTEM TROUBLESHOOTING AND OPTIMIZATION

Documentation & Communication

STANDARD OPERATING PROCEDURES (SOPS), JOB AIDS, AND README FILES, SCIENTIFIC MANUSCRIPTS, ABSTRACTS, AND FIGURES, KNOWLEDGE TRANSFER MATERIALS FOR INTERNAL TEAMS AND COLLABORATORS, CONFERENCE PRESENTATIONS

Standards & Compliance

PUBLIC HEALTH DATA STANDARDS AND REGULATORY REQUIREMENTS, GENOMIC SURVEILLANCE WORKFLOWS, VALIDATION DATASETS AND QUALITY CONTROL REPORTING, VERSION-CONTROLLED DEPLOYMENT OF PIPELINES AND TOOLS

Publications

JAP Hamlin, NA Kozak-Muiznieks, JW Mercante, L Rishishwar, ET Norris, ...
EXPANDED GEOGRAPHIC DISTRIBUTION FOR TWO LEGIONELLA PNEUMOPHILA SEQUENCE TYPES OF CLINICAL CONCERN

Mosphere
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
TINSEL—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	
Advancing Legionella pneumophila genomic surveillance with a high-resolution cg/wgMLST schema for outbreak detection and investigation	Porto, Portugal
ESCMID MICROBIAL TYPING	2025
• Mixao V, Ginevra C, Tewolde R, Afshar B, Jacqueline C, Kozak-Muiznieks NA, Willby MJ, Hamlin JAP, Borges V	
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, Lunsfordward 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 Epistatically 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*

Guajuato, Mexico

AMERICAN GENETIC ASSOCIATION

2011

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

Packages

tinselR - An R package for visualizing 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

el_gato - Sequence Based Typing of Illumina data for *Legionella pneumophila*

https://github.com/CDCgov/el_gato

MAINTAINER AND AUTHOR

2025

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