

Jenna Hamlin

HEALTH SCIENTIST - INFORMATICS

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

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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

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

HEALTH SCIENTIST INFORMATICS

Atlanta, GA

22-Jun–Current

- Led development of a cg/wgMLST 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 junior staff in bioinformatics best practices and pipeline development helping scale team capabilities

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

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES

Atlanta, GA

20-Nov–22-Jun

- Supported national COVID-19 vaccination strategy with the Vaccine Task Force for 60 days
- 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

Centers for Disease Control and Prevention; Fellow with APHL

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLOW

Atlanta, GA

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

University of Georgia

BENSASSON LAB POST-DOCTORAL RESEARCHER

Athens, GA

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

MOYLE LAB POST-DOCTORAL RESEARCHER

Bloomington, IN

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

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	<i>Mosphere</i> 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	<i>MMWR. Morbidity and Mortality Weekly Report</i> 2023
JAP Hamlin, T Nakov, A Williams-Newkirk TINSEL—AN R SHINY APPLICATION FOR ANNOTATING PHYLOGENETIC TREES	<i>Microbiology Resource Announcements</i> 2021
JAP Hamlin, MS Hibbins, LC Moyle ASSESSING BIOLOGICAL FACTORS AFFECTING POSTSPECIATION INTROGRESSION	<i>Evolution letters</i> 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 EPISTASTICALLY 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	<i>Biological Journal of the Linnean Society</i> 2017
JAP Hamlin, ML Arnold NEUTRAL AND SELECTIVE PROCESSES DRIVE POPULATION DIFFERENTIATION FOR IRIS HEXAGONA	<i>Journal of Heredity</i> 2015
ML Arnold, AN Brothers, JAP Hamlin, SJ Taylor, NH Martin DIVERGENCE-WITH-GENE-FLOW—WHAT HUMANS AND OTHER MAMMALS GOT UP TO	<i>Reticulate Evolution</i> 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

GENOMICS INTEREST GROUP - TECHINCAL

Atlanta, GA

2022

tinselR - An RShiny App for Phylogenetic Tree Annotation

CDC DATA VIZ DAY

Atlanta, GA

2020

Start Writing Manuscripts in Rmarkdown

GENOMICS INTEREST GROUP - TECHINCAL

Atlanta, GA

2020

Build Shiny Apps

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

Athens, GA

2018

Population Genomics of wild and domesticated yeast

UNIVERSITY OF GEORGIA ENTHUSIASTS OF DIVERSITY GENETICS AND EVOLUTION

Athens, GA

2018

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

SOCIETY FOR THE STUDY OF EVOLUTION

Portland, OR

2017

Epistasis for Postmating Prezygotic Isolation

SOCIETY FOR THE STUDY OF EVOLUTION

Austin, TX

2016

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

INDIANA UNVIVERSITY BROWN BAG

Bloomington, IN

2015

What Drives Phenotypic and Genetic Divergence for Iris hexagona

SOCIETY FOR THE STUDY OF EVOLUTION

Raleigh, NC

2014

Comparative Phylogeography of Two Louisiana Irises

SOCIETY FOR THE STUDY OF EVOLUTION

Snowbird, UT

2013

Posters

Advancing Legionella pneumophila genomic surveillance with a high-resolution cg/wgMLST schema for outbreak detection and investigation

ESCMID MICROBIAL TYPING

Porto, Portugal

2025

Updating Legionella pneumophila typing scheme and nomenclature using whole genome data

ESCMID STUDY GROUP FOR LEGIONELLA INFECTIONS

Dresden, Germany

2024

Expanded Geographic Distribution for Two Legionella pneumophila Sequence Types of Clinical Concern

SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION

Puerto Vallarta, Mexico

2024

El_gato: accurate and rapid sequence-based typing for Legionella pneumophila	Hinxton, United Kingdom
APPLIED BIOINFORMATICS AND PUBLIC HEALTH MICROBIOLOGY	2023
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
Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Tool	Atlanta, GA
CDC LABORATORY SCIENCE SYMPOSIUM	2023
Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Europe	Atlanta, GA
CDC LABORATORY SCIENCE SYMPOSIUM	2023
Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Tool	Baltimore, MD
AMERICAN SOCIETY FOR MICROBIOLOGY	2022
Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Europe	Yokohama, Japan
INTERNATIONAL CONFERENCE ON LEGIONELLA	2022
Tinsel - an Rshiny app for phylogenetic tree annotation	Virtual
ASSOCIATION OF PUBLIC HEALTH LABORATORIES ANNUAL MEETING	2020
Tinsel - an Rshiny application for annotating outbreak trees	Canceled - Atlanta, GA
INTEGRATED FOODBORNE OUTBREAK RESPONSE AND MANAGEMENT	2020
Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast	Pacific Grove, CA
FUNGAL GENETICS CONFERENCE	2019
Clinical Saccharomyces cerevisiae are admixed domesticated yeast	Holderness, NH
CELLULAR AND MOLECULAR FUNGAL BIOLOGY: GORDON RESEARCH CONFERENCE	2018
Higher Prevalence of Genetic Exchange Given Geographic Proximity	Laural Hill, NC
SOUTHEASTERN POPULATION ECOLOGY & EVOLUTIONARY GENETICS.	2017
Two Loci Contribute Epistatically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species	Davis, CA
SOLANACEAE CONFERENCE	2016
What Drives Phenotypic and Genetic Divergence for Iris hexagona	Boise, ID
BOTANICAL SOCIETY OF AMERICA	2014
Comparative Phylogeography of Two Louisiana Iris Species: Iris fulva and Iris brevicaulis	Guanajuato, Mexico
AMERICAN GENETIC ASSOCIATION	2011

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

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