

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, application development, and the study of organisms that pose risks to human health, 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

- General bioinformatics development for Legionella team
- Leading the Legionella International Typing (LIT) workgroup to develop a new typing scheme
- Providing computational skills mentorship to individuals without a bioinformatics background

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

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES

Atlanta, GA

20-Nov–22-Jun

- Interfacing with state public health laboratories for bioinformatics and genomics help
- Refactored Species ID tool with Nextflow wrapped around for future deployment on Nextflow tower
- Phylogenetic and phylodynamic analyses for a Leginella sequence types of public health concern
- Development of validation for Species ID tools using simulated NGS data
- 60-day detail on Data Analytics and Visualization for Vaccine Task Force (April - June 2021)

Centers for Disease Control and Prevention; Fellow with APHL

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLOW

Atlanta, GA

19-Sep–20-Nov

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

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 1000 *Saccharomyces cerevisiae* isolates as lab resource
- Applied iterative population genomics and phylogenetics methods to classify 400 genomes
- Resolved haplotypes for *Candida albicans* genomes with PacBio sequencing

Indiana University

MOYLE LAB POST-DOCTORAL RESEARCHER

Bloomington, IN

15-Jun–17-Sep

- Directed research with faculty, graduate, and undergraduates at IU and with two external universities
- Genome-wide study of factors that determine the likelihood of introgression for *Solanum* species
- Generated biological replicates via streamlined genotyping; confirmed accuracy with technical replicates and statistics
- 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

Mosphere
2024

NV Grossmann
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 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

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, 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*

Guanajuato, 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

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