

HEALTH SCIENTIST - INFORMATICS

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

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 Athens, GA

Ph.D. IN GENETICS

University of North Carolina - Asheville

Asheville, NC

B.S. IN BIOLOGY

2010

2015

Appointments

Centers for Disease Control and Prevention

Atlanta, GA

HEALTH SCIENTIST INFORMATICS

22-Jun-Current

- General data analyses for Legionella
- · International collaboration: Legionella International Typing (LIT) group developing a new typing scheme

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

Atlanta, GA

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES

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 phylodyanamic 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

Atlanta, GA

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLLOW

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 Athens, GA

BENSASSON LAB POST-DOCTORAL RESEARCHER

Atnens, 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 Unversity Bloomington, IN

Moyle Lab Post-Doctoral Researcher

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

JUNE 2025

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,	Msphere
EXPANDED GEOGRAPHIC DISTRIBUTION FOR TWO LEGIONELLA PNEUMOPHILA SEQUENCE TYPES OF CLINICAL CONCERN	2024
NV Grossmann	MMWR. Morbidity and Mortality Weekly Report
Large Community Outbreak of Legionnaires Disease Potentially Associated with a Cooling Tower—Napa County, California, 2022	2023
JAP Hamlin, T Nakov, A Williams-Newkirk	Microbiology Resource Announcements
TINSELR—AN R SHINY APPLICATION FOR ANNOTATING PHYLOGENETIC TREES	2021
JAP Hamlin, MS Hibbins, LC Moyle Assessing Biological factors affecting postspeciation introgression	Evolution letters 2020
JAP Hamlin, GB Dias, CM Bergman, D Bensasson	G3
PHASED DIPLOID GENOME ASSEMBLIES FOR THREE STRAINS OF CANDIDA ALBICANS FROM OAK TREES	2019
JAP Hamlin, G Dias, CM Bergman, D Bensasson	
Phased diploid genome assemblies for three strains of Candida albicans from oak trees	2019
JAP Hamlin, NA Sherman, LC Moyle	G3
TWO LOCI CONTRIBUTE EPISTASTICALLY TO HETEROSPECIFIC POLLEN REJECTION, A POSTMATING ISOLATING BARRIER BETWEEN SPECIES	2017
JAP Hamlin, TJ Simmonds, ML Arnold	Biological Journal of the Linnean Society
NICHE CONSERVATISM FOR ECOLOGICAL PREFERENCE IN THE LOUISIANA IRIS SPECIES COMPLEX	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	Reticulate Evolution: Symbiogenesis, Lateral Gene Transfer, Hybridization
DIVERGENCE-WITH-GENE-FLOW—WHAT HUMANS AND OTHER MAMMALS GOT UP TO	2015
JAP Hamlin, ML Arnold	Ecology and Evolution
DETERMINING POPULATION STRUCTURE AND HYBRIDIZATION FOR TWO IRIS SPECIES.	2014
ML Arnold, JAP Hamlin, AN Brothers, ES Ballerini, RS Singh, J Xu,	Rapidly evolving genes and genetic systems
NATURAL HYBRIDIZATION AS A CATALYST OF RAPID EVOLUTIONARY CHANGE	2012
ML Arnold, JAP Hamlin, AN Brothers, ES Ballerini, RS Singh, J Xu, RAPIDLY EVOLVING GENES AND GENETIC SYSTEMS	Oxford University Press 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
Paresentations	
mashWrapper	Atlanta, GA
GENOMICS INTEREST GROUP - TECHINCAL	2022
tinselR - An RShiny App for Phylogenetic Tree Annotation CDC DATA VIZ DAY	Atlanta, GA 2020

Build Shiny Apps WARNELL SCHOOL OF FORESTRY & NATURAL RESOURCES DATA MANIPULATION AND MANAGEMENT COURSE Population Genomics of wild and domesticated yeast University of Georgia Enthusiasts of Diversity Genetics and Evolution No Easy D: Little Evidence for Introgression from Whole-Genome Data in Wild Solanum Society for the Study of Evolution Athens, GA Portland, OR 2017
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
No Easy D: Little Evidence for Introgression from Whole-Genome Data in Wild Solanum Portland, OR
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 Bloomington, IN
Species complex 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
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, Miller, G
Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Atlanta, GA
Tool 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 • Hamlin JAP, Willby MJ, and Winchell JM
Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Yokohama, Japan
Europe International Conference on Legionella 2022
Kozak-Muiznieks NA, Hamlin JAP, Lucas C, and Willby MJ
Tinsel - an Rshiny app for phylogenetic tree annotationVirtualAssociation of Public Health Laboratories Annual Meeting2020

• Hamlin JAP and Williams-Newkirk A

Tinsel - an Rshiny application for annotating outbreak trees

INTEGRATED FOODBORNE OUTBREAK RESPONSE AND MANAGEMENT

• Hamlin JAP and Williams-Newkirk A

Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast

Pacific Grove, CA

2020

2019

Canceled - Atlanta, GA

FUNGAL GENETICS CONFERENCE

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

2014

BOTANICAL SOCIETY OF AMERICA

• 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/jennahamlin/mashwrapper

AUTHOR AND MAINTAINER

MAINTAINER 2022

Mentaring eorgia 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