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 10+ years of experience in classical genetics, genomics, and evolutionary biology. My training includes using a range of tools - bioinformatics, population genetics, molecular evolution all with experimental design in mind. Over the years as my computational skills increased, the genomes of the organisms I work on have gotten smaller. Now, I work at the interface of public health, application development, and understanding organisms that can cause harm to humans with an empahsis of developing reproduciable 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 · *June 2022 - Current*

* General informatics for Legionella
    - Continued projects from previous position with ASRT, inc.

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

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES · *November 2020 - June 2022*

* Interfacing with state public health laboratories (PHL)
    - Communicated with members of state PHL to provide guidance regarding bionformatics and genomics for Legionella species
* Refactored Legionella Species ID tool for broader compatibility and interfacing with Nextflow Tower
    - Removed structural design issues in original code that prevented expansion and adding of new functionalities
* Development of method validation plan for Legionella Species ID tool
    - Researched and proposed statistically sound validation plan to test tool that uses next generation sequencing data
* Phylogenetic and phylodynamic analyses for Legionella isolates of public health concern
    - Performing analyses and generating statistical summaries and visualizations
    - Writing and editing manuscripts for publication
    - Identifying scientific questions answerable with existing data
* Developing or testing scripts and pipelines as necessary
    - Generated script to interact with National Center of Biotechnology Information for downloading all available Legionella genomes
    - Evaluated using Nextflow pipeline for mapping Legionella genomes
* 60-day detail on Data Analytics and Visualization for Vaccine Task Force (April - June 2021)
    - Produced weekly reports and consolidated steps for document creation to be reproducible via one script

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

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLOW · *September 2019 - November 2020*

* Developing tinselR - an Rshiny application for annotating outbreak trees
    - tinselR is an open-source downloadable package in the R language used for phylogenetic tree analysis and visualization
* Participated in APHL core competency and leadership training
    - Gained skills and knowledge for a career in public health
* 30-day detail on Routine Reporting for COVID-19 Response (June - July 2020)
    - Produced daily and weekly reports for task force. Consolidated steps for document creation to be reproducible via one script

University of Georgia (UGA) · *Athens, GA*

BENSASSON LAB POST-DOCTORAL RESEARCHER · *October 2017 - August 2019*

* Directed collaborative research with UGA graduate and undergraduate students
* Collated and streamlined genome mapping for 1000 Saccharomyces cerevisiae isolates as lab resource
* Used iterative approach to assign 400 genomes to well-defined populations using best practices for population genomics and phylogenetics
* Resolved haplotypes for Candida albicans genomes with PacBio sequencing

Indiana University (IU)   *Bloomington, IN*
Moyle Lab Post-Doctoral Researcher   *June 2015 - September 2017*

* 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
* Streamlined genotyping to generate biological replicates. Validate data accuracy using technical replicates along with statistical analyses
* Identified targeting rates and floral trait differences with biological & technical replicates in large-scale crossing project via statistical analyses

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, T Nakov, A Williams-Newkirk   *Microbiology Resource Announcements*
tinselR—an R Shiny Application for Annotating Phylogenetic Trees   *2021*

JAP Hamlin, MS Hibbins, LC Moyle   *Evolution letters*
Assessing biological factors affecting postspeciation introgression   *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, NA Sherman, LC Moyle   *G3*
Two loci contribute epistatically 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   *Journal of Heredity*
Neutral and Selective Processes Drive Population Differentiation for Iris hexagona   *2015*

ML Arnold, AN Brothers, JAP Hamlin, SJ Taylor, NH Martin   *Reticulate evolution*
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, ES Ballerini, AN Brothers, JAP Hamlin, CDA Ishibashi, …   *Plant Ecology & Diversity*
The genomics of natural selection and adaptation: Christmas past, present and future (?).   *2012*

Presentations

Talks

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

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

2019

Author and maintainer

mashwrapper - a Python tool for parsing mash results

https://github.com/jennahamlin/mashwrapper

2022

Author and maintainer

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