

Jenna Hamlin

BIOINFORMATICIAN II

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 emphasis of developing 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, Contractor with ASRT Inc.

Atlanta, GA

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES

November 2020 - Current

- * Interfacing with state public health laboratories (PHL)
 - Communicated with members of state PHL to provide guidance regarding bioinformatics 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 for 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

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

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 UNIVERSITY 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

Tinsel - an Rshiny app for phylogenetic tree annotation.

ASSOCIATION OF PUBLIC HEALTH LABORATORIES ANNUAL MEETING

Virtual

2020

Tinsel - an Rshiny application for annotating outbreak trees.

INTEGRATED FOODBORNE OUTBREAK RESPONSE AND MANAGEMENT

Canceled - Atlanta, GA

2020

Genetic admixture and the origins of clinical *Saccharomyces cerevisiae* yeast.

FUNGAL GENETICS CONFERENCE

Pacific Grove, CA

2019

Clinical *Saccharomyces cerevisiae* are admixed domesticated yeast.

CELLULAR AND MOLECULAR FUNGAL BIOLOGY: GORDON RESEARCH CONFERENCE

Holderness, NH

2018

Higher Prevalence of Genetic Exchange Given Geographic Proximity.

SOUTHEASTERN POPULATION ECOLOGY & EVOLUTIONARY GENETICS.

Laural Hill, NC

2017

Two Loci Contribute Epistatically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species.

SOLANACEAE CONFERENCE

Davis, CA

2016

What Drives Phenotypic and Genetic Divergence for *Iris hexagona*?

BOTANICAL SOCIETY OF AMERICA

Boise, ID

2014

Comparative Phylogeography of Two Louisiana Iris Species: *Iris fulva* and *Iris brevicaulis*.

AMERICAN GENETIC ASSOCIATION

Guanajuato, Mexico

2011

R-Packages

tinselR - An R package for visualizing and annotating phylogenetic trees

AUTHOR AND MAINTAINER

<https://github.com/jennahamlin/tinselR>

2019

mashwrapper - a Python tool for parsing mash results

AUTHOR AND MAINTAINER

<https://github.com/jennahamlin/mashwrapper>

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