

# 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, SALARY - 95,000 (USD)

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 statically sound validation plan for tool that uses next generation sequencing data
- \* Phylogenetic and phylogenetic 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

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## 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

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## 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

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## Talks

## tinselR – An RShiny App for Phylogenetic Tree Annotation.

CDC DATA VIZ DAY

Atlanta, GA  
2020

## Start Writing Manuscripts in Rmarkdown.

GENOMICS INTEREST GROUP - TECHNICAL

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

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### 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

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### 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