

# Jenna Hamlin

BIOINFORMATICIAN

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

BIOINFORMATICIAN WITH DIVISION OF BACTERIAL DISEASES

Atlanta, GA

20-Nov–Current

- Maintenance and updating Legionella databases for sequencing types
- Developed pipeline for processing Legionella/Mycoplasma/Ureaplasma genome sequences using NextFlow
- Migrated bioinformatic work to use github as a lab notebook
- 60-day detail on Data Analytics and Visualization for Vaccine Task Force (April - June 2021)

### Centers for Disease Control and Prevention

ASSOCIATION OF PUBLIC HEALTH LABORATORIES BIOINFORMATICS FELLOW

Atlanta, GA

19-Sep–20-Nov

- Developing tinselR - an Rshiny application for annotating outbreak trees; hosted on github
- Worked with scientific computing group for tinselR to be hosted on CDC internal server
- 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
- Used an 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

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
- Streamlined genotyping to generate biological replicates. Validate data accuracy using technical replicates along with statistical analyses
- Used linear mixed models and ANOVA to identify differences in targeting, rates, and floral trait differences with biological and technical replicates for a large-scale crossing project

## 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

## Publications

## JAP Hamlin, T Nakov, A Williams-Newkirk

TINSEL—AN R SHINY APPLICATION FOR ANNOTATING PHYLOGENETIC TREES

## JAP Hamlin, MS Hibbins, LC Moyle

ASSESSING BIOLOGICAL FACTORS AFFECTING POSTSPECIATION INTROGRESSION

## JAP Hamlin, GB Dias, CM Bergman, D Bensasson

PHASED DIPLOID GENOME ASSEMBLIES FOR THREE STRAINS OF CANDIDA ALBICANS FROM OAK TREES

## JAP Hamlin, NA Sherman, LC Moyle

TWO LOCI CONTRIBUTE EPISTASTICALLY TO HETEROSPECIFIC POLLEN REJECTION, A POSTMATING ISOLATING BARRIER BETWEEN SPECIES

## JAP Hamlin, TJ Simmonds, ML Arnold

NICHE CONSERVATISM FOR ECOLOGICAL PREFERENCE IN THE LOUISIANA IRIS SPECIES COMPLEX

## JAP Hamlin, ML Arnold

NEUTRAL AND SELECTIVE PROCESSES DRIVE POPULATION DIFFERENTIATION FOR IRIS HEXAGONA

## ML Arnold, AN Brothers, JAP Hamlin, SJ Taylor, NH Martin

DIVERGENCE-WITH-GENE-FLOW—WHAT HUMANS AND OTHER MAMMALS GOT UP TO

## JAP Hamlin

SPATIAL, TEMPORAL, AND GENOME-WIDE PATTERNS OF DIFFERENTIATION FOR THE LOUISIANA IRIS SPECIES COMPLEX

## JAP Hamlin, ML Arnold

DETERMINING POPULATION STRUCTURE AND HYBRIDIZATION FOR TWO IRIS SPECIES.

## ML Arnold, JAP Hamlin, AN Brothers, ES Ballerini, RS Singh, J Xu, ...

NATURAL HYBRIDIZATION AS A CATALYST OF RAPID EVOLUTIONARY CHANGE

## ML Arnold, ES Ballerini, AN Brothers, JAP Hamlin, CDA Ishibashi, ...

THE GENOMICS OF NATURAL SELECTION AND ADAPTATION: CHRISTMAS PAST, PRESENT AND FUTURE (?).

## K Marshall, J Hamlin, M Armstrong, J Mendoza, C Lee, D Pieri, R Rivera, ...

SCIENCE FOR A SOCIAL REVOLUTION: ECOLOGISTS ENTERING THE REALM OF ACTION

Microbiology Resource

Announcements

2021

Evolution letters

2020

G3

2019

G3

2017

Biological Journal of the Linnean

Society

2017

Journal of Heredity

2015

Reticulate evolution

2015

University of Georgia

2015

Ecology and Evolution

2014

Rapidly evolving genes and genetic

systems

2012

Plant Ecology & Diversity

2012

Bulletin of the Ecological Society of

America

2011

## 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 UNVIVERSITY 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

## 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