

# Jennifer Hamlin

BIOINFORMATICIAN

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

✉ [jhamlin@cdc.gov](mailto:jhamlin@cdc.gov) | [🌐 jennahamlin](https://www.linkedin.com/in/jennahamlin)

*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 Ureaplasma genome sequences
- Migrated bioinformatic work to use github as a lab notebook

### 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

BIOINFORMATICS, 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

## Tools

BCFTOOLS, BLAST, BWA, CONDA/ANACONDA, FASTQC, GIT/GITHUB, PROKKA, QUASt, RSHINY, SAMTOOLS, SEQTK, SHOVILL, SNIPPY, SPADES, TRIMMOMATIC, VCFTOOLS

# Publications

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## 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

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

## 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

*The Bulletin of the Ecological Society of America*

2011

# 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 - TECHINICAL

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

Portland, OR

2020

### **Tinsel - an Rshiny application for annotating outbreak trees**

INTEGRATED FOODBORNE OUTBREAK RESPONSE AND MANAGEMENT

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