Jenna **Hamlin**

Bioinformatician II

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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*

Bioinformatician with Division of Bacterial Diseases — *20-Nov–Current*

- Interfacing with state public health laboratories for bioinformatics help
- Test and development of reproducible and validated binformatics tools (NextFlow, validation using simulated NGS data)
- Phylogenetic and phylodyanamic analyses for a Leginella sequence type of public health concern
- Generating additional analyses and ideas for Legionella research questions
- 60-day detail on Data Analytics and Visualization for Vaccine Task Force (April - June 2021)

Centers for Disease Control and Prevention — *Atlanta, GA*

Association of Public Health Laboratories Bioinformatics Felllow — *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 — *Athens, GA*

Bensasson Lab Post-Doctoral Researcher — *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 Unversity — *Bloomingto, IN*

Moyle Lab Post-Doctoral Researcher — *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, NextFlow - expert, 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 epistastically 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

University of Georgia

Spatial, temporal, and genome-wide patterns of differentiation for the Louisiana iris species complex

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

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

Bulletin of the Ecological Society of America

Science for a social revolution: ecologists entering the realm of action

2011

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

Tinsel - an Rshiny app for phylogenetic tree annotation. *Virtual*
Association of Public Health Laboratories Annual Meeting *2020*

Tinsel - an Rshiny application for annotating outbreak trees. *Canceled - Atlanta, GA*
Integrated Foodborne Outbreak Response and Management *2020*

Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast. *Pacific Grove, CA*
Fungal Genetics Conference *2019*

Clinical Saccharomyces cerevisiae are admixed domesticated yeast. *Holderness, NH*
Cellular and Molecular Fungal Biology: Gordon Research Conference *2018*

Higher Prevalence of Genetic Exchange Given Geographic Proximity. *Laural Hill, NC*
Southeastern Population Ecology & Evolutionary Genetics. *2017*

Two Loci Contribute Epistastically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species. *Davis, CA*
Solanaceae Conference *2016*

What Drives Phenotypic and Genetic Divergence for Iris hexagona? *Boise, ID*
Botanical Society of America *2014*

Comparative Phylogeography of Two Louisiana Iris Species: Iris fulva and Iris brevicaulis. *Guanajuato, Mexico*
American Genetic Association *2011*

R-Packages

tinselR - An R package for visulizing and annotating phylogenetic trees *https://github.com/jennahamlin/tinselR*

Author and maintainer *2019*

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