

# Jenna A. P. Hamlin

HEALTH SCIENTIST - INFORMATICS

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*I am a scientist with over 10 years of experience in bioinformatics, genomics, and classical genetics. My training includes a broad set of skills and approaches including programming and experimental design to evolutionary biology and species distribution modeling. Currently, I work at the intersection of public health (ph), ph tool development, and the study of pathogens, with a focus on reproducible research.*

## Education

### University of Georgia

PH.D. IN GENETICS

Athens, GA

2010 - 2015

### University of North Carolina - Asheville

B.S. IN BIOLOGY

Asheville, NC

2006 - 2010

## Work Experience

### Centers for Disease Control and Prevention

Atlanta, GA

HEALTH SCIENTIST INFORMATICS WITH DIVISION OF BACTERIAL DISEASES

22-Jun–Current

- Led development of Legionella pneumophila typing scheme for international workgroup in coordination with four European countries
- Streamlined workflows and ensured reproducibility by developing automated report scripts and documentation
- Delivered validated, QC-compliant, and regulatory-ready L. pneumophila computational tools: el\_gato and mashWrapper
- Improved scalability and responsiveness to evolving infrastructure and user needs by integrating computational tools into shared environments
- Mentored three laboratory staff in bioinformatics best practices and pipeline development helping scale team capabilities
- Translated scientific findings for national and international audiences with 2 manuscripts and 7 posters

BIOINFORMATICIAN II WITH DIVISION OF BACTERIAL DISEASES (CONTRACTOR WITH ASRT, INC.)

20-Nov–22-Jun

- Supported national COVID-19 vaccination strategy with the Vaccine Task Force during an emergency response
- Refactored and validated legacy pipelines (Perl to Python with Nextflow) to ensure reproducibility, scalability, and regulatory compliance
- Delivered genomic insights for outbreak response by partnering with state public health agencies to deploy tools and secure data
- Reduced downtime for routine analyses by maintaining and optimizing bioinformatics infrastructure and troubleshooting pipeline failures
- Translated scientific findings for diverse national audiences with 2 posters and 1 conference talk

ASSOCIATION OF PUBLIC HEALTH LABORATORIES (APHL) BIOINFORMATICS FELLOW

19-Sep–20-Nov

- Developed tinselR - an Rshiny application for annotating outbreak trees
- Trained in APHL Core Competencies, including laboratory management, communication, and quality systems
- Translated scientific findings for diverse national audiences with 1 manuscript, 2 posters, and 2 conference talks
- Generated and improved routine reports during COVID-19 emergency response, informing decisions by the Coronavirus Task Force

### University of Georgia

Athens, GA

BENSASSON LAB POST-DOCTORAL RESEARCHER

17-Oct–19-Aug

- Directed collaborative research with two graduate and three undergraduate students
- Developed a genomic reference resource for 1,000 Saccharomyces cerevisiae isolates through streamlined mapping workflows
- Achieved genomic classification of 400 S. cerevisiae isolates through iterative population genomics and phylogenetic analysis
- Resolved haplotypes for three Candida albicans genomes using PacBio sequencing
- Translated scientific findings for national and international audiences with 1 manuscript, 1 poster, and 2 conference talks

### Indiana University

Bloomington, IN

MOYLE LAB POST-DOCTORAL RESEARCHER

15-Jun–17-Sep

- Directed research with two graduate students, and seven undergraduates at IU and collaborators at two external universities
- Conducted a genome-wide study on factors influencing introgression likelihood in Solanum (tomato) species
- Streamlined genotyping to generate biological replicates and validated accuracy using technical replicates and statistical testing
- Analyzed targeting, rates, and floral traits across replicated large-scale crosses using linear mixed models and ANOVA
- Translated scientific findings for diverse audiences with 2 manuscripts, 2 posters, and 2 conference talks

## Skills

### Bioinformatics

NGS DATA ANALYSIS (ILLUMINA AND PACBIO), SNP CALLING WORKFLOWS, PUBLIC DATABASES (NCBI, ENA, PUBMLST),

COMPUTATIONAL BIOLOGY TOOLS FOR ALIGNMENT (BWA & MINIMAP), VARIANT CALLING (SAMTOOLS & BCFTOOLS),

PHYLOGENETICS (RAXML & IQ-TREE), GENOME ASSEMBLY (SPADES & QUAST), ALLELE TYPING SCHEME DEVELOPMENT,

OUTBREAK INVESTIGATION SUPPORT

Programming & Automation

PYTHON, BASH AND R, WORKFLOW AUTOMATION (NEXTFLOW AND SHELL), PIPELINE REFACTORING AND VALIDATION, MAINTENANCE OF LEGACY PIPELINES, VERSION CONTROL WITH GIT/GitHub

Compute Infrastructure

HIGH PERFORMANCE COMPUTING (HPC) CLUSTER, LINUX, WINDOWS, MACOS, CONTAINERIZED ENVIRONMENTS (DOCKER, SINGULARITY), SYSTEM TROUBLESHOOTING AND OPTIMIZATION

Documentation & Communication

SCIENTIFIC MANUSCRIPTS, ABSTRACTS, AND FIGURES, KNOWLEDGE TRANSFER MATERIALS FOR INTERNAL TEAMS AND COLLABORATORS, CONFERENCE PRESENTATIONS, STANDARD OPERATING PROCEDURES (SOPS), JOB AIDS, AND README FILES

Standards & Compliance

PUBLIC HEALTH DATA STANDARDS AND REGULATORY REQUIREMENTS, GENOMIC SURVEILLANCE WORKFLOWS, VALIDATION DATASETS AND QUALITY CONTROL REPORTING, VERSION-CONTROLLED DEPLOYMENT OF PIPELINES AND TOOLS

Publications

**JAP Hamlin, NA Kozak-Muiznieks, JW Mercante, L Rishishwar, ET Norris, ...**  
EXPANDED GEOGRAPHIC DISTRIBUTION FOR TWO LEGIONELLA PNEUMOPHILA SEQUENCE TYPES OF CLINICAL CONCERN

Msphere  
2024

**NV Grossmann, C Milne, MR Martinez, K Relucio, B Sadeghi, EN Wiley, ...**  
LARGE COMMUNITY OUTBREAK OF LEGIONNAIRES DISEASE POTENTIALLY ASSOCIATED WITH A COOLING TOWER—NAPA COUNTY, CALIFORNIA, 2022

MMWR. Morbidity and Mortality  
Weekly Report  
2023

**JAP Hamlin, T Nakov, A Williams-Newkirk**  
TINSELR—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