

Jenna A. P. Hamlin

HEALTH SCIENTIST - INFORMATICS

✉ jennahamlin@gmail.com | 📱 jennahamlin

I am a scientist with over 10 years of experience in classical genetics, genomics, and evolutionary biology. My training spans a range of tools and approaches—including bioinformatics, population genetics, and species distribution modeling—with a strong emphasis on experimental design. 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

Appointments

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

Mosphere

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

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
Talks

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| mashWrapper | Atlanta, GA |
| GENOMICS INTEREST GROUP - TECHINCAL | 2022 |
| 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 | |
| Advancing Legionella pneumophila genomic surveillance with a high-resolution cg/wgMLST schema for outbreak detection and investigation | Porto, Portugal |
| ESCMID MICROBIAL TYPING | 2025 |
| • Mixao V, Ginevra C, Tewolde R, Afshar B, Jacqueline C, Kozak-Muiznieks NA, Willby MJ, Hamlin JAP, Borges V | |
| Updating Legionella pneumophila typing scheme and nomenclature using whole genome data | Dresden, Germany |
| ESCMID STUDY GROUP FOR LEGIONELLA INFECTIONS | 2024 |
| • Ginevra C, Tewolde R, Afshar B, Borges V, Goncalves P, Henderson KC, Jacqueline C, Kozak-Muiznieks NA, Willby MJ, Hamlin JAP | |
| Expanded Geographic Distribution for Two Legionella pneumophila Sequence Types of Clinical Concern | Puerto Vallarta, Mexico |
| SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION | 2024 |
| • Hamlin JAP, Kozak -Muiznieks NK, Mercante JW, Rishishwar L, Norris ET, Gaines AB, Ishaq MK, Winchell JM, and Willby MJ | |
| El_gato: accurate and rapid sequence-based typing for Legionella pneumophila | Hinxton, United Kingdom |
| APPLIED BIOINFORMATICS AND PUBLIC HEALTH MICROBIOLOGY | 2023 |
| • Hamlin JAP, Mashruwala D, Collins AJ, Gaines AB, Norris ET, Chivukula V, Rishishwar L, Overholt WA, Kozak-Muiznieks NK, Willby MJ, Winchell JM | |
| A Community Outbreak of Legionnaires' Disease Possibly Associated with an Outdoor Hotel Spa – California, 2021 | Salt Lake City, Utah |
| COUNCIL OF STATE AND TERRITORIAL EPIDEMIOLOGISTS | 2023 |
| • Burmester J, Evans S, Ferguson D, Lunsfordward R, Rutschmann S, Kimura A, Flores E, Mukhopadhyay R, Hannapel E, Bertumen JB, Hamlin JAP, and Miller, G | |
| Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Tool | Atlanta, GA |
| CDC LABORATORY SCIENCE SYMPOSIUM | 2023 |
| • Hamlin JAP, Willby MJ, and Winchell JM | |

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| Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Europe CDC LABORATORY SCIENCE SYMPOSIUM • Kozak-Muiznieks NA, Hamlin JAP, Lucas C, and Willby MJ | Atlanta, GA 2023 |
| Combining Mash and NCBI Datasets via Nextflow for a Legionella Species Identification Tool AMERICAN SOCIETY FOR MICROBIOLOGY • Hamlin JAP, Willby MJ, and Winchell JM | Baltimore, MD 2022 |
| Spread of Sequence Type ST222 from the Great Lakes Area to the US West Coast and Europe INTERNATIONAL CONFERENCE ON LEGIONELLA • Kozak-Muiznieks NA, Hamlin JAP, Lucas C, and Willby MJ | Yokohama, Japan 2022 |
| Tinsel - an Rshiny app for phylogenetic tree annotation ASSOCIATION OF PUBLIC HEALTH LABORATORIES ANNUAL MEETING • Hamlin JAP and Williams-Newkirk A | Virtual 2020 |
| Tinsel - an Rshiny application for annotating outbreak trees INTEGRATED FOODBORNE OUTBREAK RESPONSE AND MANAGEMENT • Hamlin JAP and Williams-Newkirk A | Canceled - Atlanta, GA 2020 |
| Genetic admixture and the origins of clinical Saccharomyces cerevisiae yeast FUNGAL GENETICS CONFERENCE • Hamlin JAP and Bensasson D | Pacific Grove, CA 2019 |
| Clinical Saccharomyces cerevisiae are admixed domesticated yeast CELLULAR AND MOLECULAR FUNGAL BIOLOGY: GORDON RESEARCH CONFERENCE • Hamlin JAP and Bensasson D | Holderness, NH 2018 |
| Higher Prevalence of Genetic Exchange Given Geographic Proximity SOUTHEASTERN POPULATION ECOLOGY & EVOLUTIONARY GENETICS. • Hamlin JAP and Moyle LC | Laural Hill, NC 2017 |
| Two Loci Contribute Epistatically to Heterospecific Pollen Tube Rejection, a Postmating Isolating Barrier Between Species SOLANACEAE CONFERENCE • Hamlin JAP and Moyle LC | Davis, CA 2016 |
| What Drives Phenotypic and Genetic Divergence for Iris hexagona BOTANICAL SOCIETY OF AMERICA • Hamlin JAP and Arnold ML | Boise, ID 2014 |
| Comparative Phylogeography of Two Louisiana Iris Species: Iris fulva and Iris brevicaulis AMERICAN GENETIC ASSOCIATION • Hamlin JAP, Brothers AN, Ballerini ES, and Arnold ML | Guanajuato, Mexico 2011 |

Packages

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| tinselR - An R package for visulizing 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/CDCgov/mashwrapper 2022 |
| el_gato - Sequence Based Typing of Illumina data for Legionella pneumophila MAINTAINER AND AUTHOR | https://github.com/CDCgov/el_gato 2025 |