

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 computational 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

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

- Reduced downtime for routine analyses by maintaining and optimizing bioinformatics infrastructure and troubleshooting pipeline failures
- 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
- Supported national COVID-19 vaccination strategy with the Vaccine Task Force during an emergency response
- 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

- Generated and improved routine reports during COVID-19 emergency response, informing decisions by the Coronavirus Task Force
- Trained in APHL Core Competencies and leadership training, including laboratory management, communication, and quality systems
- Developed tinselR an open-source R Shiny app for visualizing and annotating phylogenetic trees to explore relatedness
- Translated scientific findings for diverse national audiences with 1 manuscript, 2 posters, and 2 conference talks

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 (yeast) isolates using a streamlined genomic mapping workflow
- Resolved haplotype structure and examined structural variation for three Candida albicans (yeast) genomes using PacBio sequencing
- Achieved genomic classification of 400 S. cerevisiae isolates through iterative population genomics and phylogenetic analysis
- 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
- 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
- Conducted a genome-wide study on factors influencing introgression likelihood in Solanum (tomato) species
- 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

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

Programming & Automation

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

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 ...

MMWR

2023

JAP Hamlin, T Nakov, A Williams-Newkirk

TINSELR—AN R SHINY APPLICATION FOR ANNOTATING PHYLOGENETIC TREES

Microbiol. Resour. Announce.

2021

JAP Hamlin, MS Hibbins, LC Moyle

ASSESSING BIOLOGICAL FACTORS AFFECTING POSTSPECIATION INTROGRESSION

Evol. Lett.

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 EPISTATICALLY TO HETEROSPECIFIC POLLEN REJECTION, A POSTMATING ISOLATING ...

G3

2017

JAP Hamlin, TJ Simmonds, ML Arnold

NICHE CONSERVATISM FOR ECOLOGICAL PREFERENCE IN THE LOUISIANA IRIS SPECIES COMPLEX

Biol. J. Linn. Soc.

2017

JAP Hamlin, ML Arnold

NEUTRAL AND SELECTIVE PROCESSES DRIVE POPULATION DIFFERENTIATION FOR IRIS HEXAGONA

J. Hered.

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.

Ecol. Evol.

2014

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

NATURAL HYBRIDIZATION AS A CATALYST OF RAPID EVOLUTIONARY CHANGE

Rapidly Evol. Genes Genet. Syst.

2012

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

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

Plant Ecol. Divers.

2012

Packages

el_gato - Sequence Based Typing of Illumina data for Legionella pneumophila

[HTTPS://GITHUB.COM/CDCGOV/EL_GATO](https://github.com/CDCgov/el_gato)

Maintainer and author

2025

mashwrapper - a Python tool for parsing mash results

[HTTPS://GITHUB.COM/CDCGOV/MASHWRAPPER](https://github.com/CDCgov/mashwrapper)

Author and maintainer

2022

tinselR - An R package for visulizing and annotating phylogenetic trees

[HTTPS://GITHUB.COM/JENNAHAMLIN/TINSELR](https://github.com/JENNAHAMLIN/TINSELR)

Author and maintainer

2019