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   *Athens, GA*

PH.D. IN GENETICS   *2010 - 2015*

University of North Carolina - Asheville   *Asheville, NC*

B.S. IN BIOLOGY   *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, ... — *Msphere*
Expanded geographic distribution for two Legionella pneumophila sequence types of clinical concern — *2024*

NV Grossmann, C Milne, MR Martinez, K Relucio, B Sadeghi, EN Wiley, ... — *MMWR*
Large Community Outbreak of Legionnaires Disease Potentially Associated with a Cooling Tower—Napa County, California, 2022 — *2023*

JAP Hamlin, T Nakov, A Williams-Newkirk — *Microbiol. Resour. Announce.*
tinselR—an R Shiny Application for Annotating Phylogenetic Trees — *2021*

JAP Hamlin, MS Hibbins, LC Moyle — *Evol. Lett.*
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 epistatically to heterospecific pollen rejection, a postmating isolating barrier between species — *2017*

JAP Hamlin, TJ Simmonds, ML Arnold — *Biol. J. Linn. Soc.*
Niche conservatism for ecological preference in the Louisiana iris species complex — *2017*

JAP Hamlin, ML Arnold — *J. Hered.*
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, ML Arnold — *Ecol. Evol.*
Determining Population Structure and Hybridization for Two Iris Species. — *2014*

ML Arnold, JAP Hamlin, AN Brothers, ES Ballerini, RS Singh, J Xu, ... — *Rapidly Evol. Genes Genet. Syst.*
Natural hybridization as a catalyst of rapid evolutionary change — *2012*

ML Arnold, ES Ballerini, AN Brothers, JAP Hamlin, CDA Ishibashi, ... — *Plant Ecolog. Divers.*
The genomics of natural selection and adaptation: Christmas past, present and future (?). — *2012*

Packages

tinselR - An R package for visulizing and annotating phylogenetic trees — *https://github.com/jennahamlin/tinselR*
Author and maintainer — *2019*

mashwrapper - a Python tool for parsing mash results — *https://github.com/CDCgov/mashwrapper*
Author and maintainer — *2022*

el_gato - Sequence Based Typing of Illumina data for Legionella pneumophila

Maintainer and Author