


KELSI O. WEST, PHD, MPH

Translating complex bioinformatics and engineering insights into impactful scientific solutions.

 Texas

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 kelsiwest.com

EDUCATION

PhD, Genetics

Texas A&M University

RNA Biology, Immunology
2016 - 2020

MPH, Epidemiology

East Tennessee State

2014 - 2016

BS, Health Education

Salisbury University

Minors: Biology, Chemistry
2010 - 2013

CERTIFICATIONS

NASA Open Science

EXPERTISE

Technical

- R/R Shiny
- Python
- Git
- Docker
- AWS
- Webflow
- Jekyll

Project Management

- Atlassian
- Presenting
- Problem-Solving
- Mentoring
- Organization
- Leadership
- Quality Assurance

PROFILE

Experienced Bioinformatics Scientist with a robust background in bioinformatic engineering, project management, and translational science. Proficient in designing comprehensive solutions, from conceptualizing and constructing data processing pipelines to designing intuitive user interfaces. Skilled in R, Python, AWS, and Docker. Exceptionally adept in bridging software engineering and science through effective communication, mentoring, facilitating collaboration, and solving complex problems at the intersection of these fields.

EXPERIENCE

Catalytic Data Science

2020 - June 2024

Bioinformatics Scientist II (2022 - 2024)

Bioinformatics Scientist (2020 - 2022)

Professional Highlight: Led efforts in successfully implementing 25+ specialized analytics in diverse genomics research areas for agriculture and pharmaceutical customers

- Executed a vigorous infrastructure for fault-tolerant NGS multi-omics analytics leveraging Docker, AWS, and a proprietary orchestrator
- Implemented containerization of genomic tools and Python API layers to deploy and maintain 60+ analytics modules and 90+ integrated pipelines
- Developed and presented innovative strategies to improve operational efficiency in executive leadership meetings and client-facing presentations
- Mentored team members in codebase and best practices, expediting high-quality analytics and pipeline delivery
- Analyzed molecular datasets for customers and team research needs using bioinformatics tools in diverse areas
- Developed internal documentation standards and biologically relevant QA test files to efficiently test and increase code maintainability

EXPERTISE

Analysis

- RNA-Seq
- scRNA-Seq
- WGS
- Quality Control
- Differential Isoforms
- Variant Detection
- Gene Fusions
- Annotation
- Gene-editing
- Cell Deconvolution
- Viral Integration
- Genome Assembly
- Metagenomics
- Gene Ontology
- Mass-Spectrometry
- Flow Cytometry
- ChIP-Seq
- ATAC-Seq
- File Conversion

Laboratory

- Tissue culture
- Infection models
- BSL3 trained
- Lentiviral production
- Protein constructs
- Site-directed mutagenesis
- shRNA knockdown
- RT-qPCR
- Western blots
- ChIP
- CRISPR/Cas9
- Immunofluorescence
- Cellular fractionation
- Confocal microscopy
- BioID

EXPERIENCE

Texas A&M University

2016 - 2020

PhD Researcher; Microbial Pathogenesis and Immunology

- Managed research projects investigating host-pathogen interactions, focusing on how RNA processing events affects host outcomes during *Salmonella* Typhimurium and *Mycobacterium tuberculosis* infection, leveraging diverse bioinformatics and molecular assays
- Spearheaded the creation and implementation of bioinformatic pipelines from scratch in a lab with no prior infrastructure, significantly improving data analysis while overseeing the integration of new tools
- Mentored and trained junior researchers, providing guidance in experimental techniques and data analysis
- Excelled in scientific communication through conference presentations, grants, and publications

East Tennessee State University

2015 - 2016

Research Assistant; Bill Gatton College of Pharmacy

- Characterized side effects of nanoparticle drug formulation in commonly used in nonsteroidal anti-inflammatory drugs (NSAIDs), Diclofenac and Celecoxib
- Analyzed gastrointestinal, urinary and pharmacokinetic parameters utilizing different statistical programs such as SAS, SPSS, and R

Research Assistant; Department of Epidemiology

- Collected epidemiological data through community surveys and interviews in Nueva Vida, Nicaragua
- Analyzed data using SAS and SPSS to conduct analysis about risk factors associated with many public health priorities around the world including type II diabetes, biosand water filters, HIV/AIDS, and pap smear utilization

SELECTED PUBLICATIONS

Global transcriptomics uncovers distinct contributions from splicing regulatory proteins to the macrophage innate immune responses.
Front. Immunol. 2021.

LRRK2 regulates innate immune responses and neuroinflammation during Mycobacterium tuberculosis infection.
eLife. 2020.

The splicing factor hnRNP M is a critical regulator of innate immune gene expression in macrophages.
Cell Reports. 2019.