# KELSI O. WEST, PHD, MPH

Translating complex bioinformatics and engineering insights into impactful scientific solutions.

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## 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**
- Atlassain
- 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 pharmaceutical and agriculture clients

- 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
- CLC and IPA

## 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 tuberculosi*s 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 pharmokinetic 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.