

Gunars Osis, PhD

Bioinformatics Scientist | PhD Molecular Biologist | Public Health Genomics | Workflow Engineering | HPC

SUMMARY

PhD-trained Molecular Biologist and Bioinformatics Scientist with 10+ years of experience spanning genomics, computational biology, and public health. Author of 19 peer-reviewed publications and experienced in translating complex biological questions into scalable computational solutions. Combines deep biological expertise with production-scale software engineering to develop, validate, and optimize bioinformatics workflows and scientific software supporting mission-critical federal public health genomics.

TECHNICAL SKILLS

Programming & Workflow Development: Python • Bash • Nextflow • GitLab CI/CD • nf-core

NGS & Bioinformatics: Metagenomics • WGS • WES • RNA-seq • Variant Calling • Taxonomic Classification
Data & Automation: Power BI • Power Platform • SQL • Clarity LIMS

Infrastructure: Linux • HPC • Singularity • Conda

Laboratory: DNA/RNA • qPCR • Western • Cell Culture • Microscopy • Cre-Lox & Crispr Line Generation

WORK EXPERIENCE

Bioinformatician, Dec 2022 – Current,

CDC Biotechnology Core Facility via ASRT Inc., Smyrna, GA

- Supported mission-critical national pathogen surveillance by leading production-scale genomic and metagenomic analyses of more than 5,000 Illumina, PacBio, and Oxford Nanopore datasets (~200 TB) using Nextflow, Python, and Groovy on Linux HPC infrastructure. Working closely with scientists and Lab staff to define analytical requirements, validate workflows, and improve Core performance.
- Served as a scientific contributor throughout the software development lifecycle for the TaxTriage metagenomic pipeline, leading workflow validation, software testing, quality assurance, and performance optimization over a three-year development cycle. Improved runtime performance by 40–60%, reduced unclassified reads by more than 25%, achieved 99% reproducibility across collaborating laboratories, and co-authored the resulting Bioinformatics journal publication.
- Developed and deployed a PowerApps–PowerAutomate–GitLab Service Desk solution supporting 80+ scientists and 100+ monthly requests, streamlining operational support through automated routing, reporting, and stakeholder communication while reducing response time by ~60%.
- Built operational Power BI dashboards integrating sequencing metadata, QC metrics, and TaxTriage outputs, enabling real-time performance monitoring and supporting data-driven decision-making for genomic surveillance teams.
- Engineered and maintained scientific software, including 80+ automation scripts (Python, Bash, Groovy) and 12 production bioinformatics pipelines using Singularity and Conda, improving reproducibility, scalability, and maintainability across Linux HPC environments.
- Modernized production bioinformatics infrastructure by migrating four production servers and more than 30 automated workflows to RHEL8 with zero downtime, improving operational reliability (>99% uptime) while reducing maintenance workload by approximately 50%.
- Provided cross-functional bioinformatics and systems support by integrating new sequencing instruments into Clarity LIMS, improving automation reliability and reducing reagent usage by approximately 25% while training 15+ scientists in Nextflow, HPC workflows, and metagenomic analysis.

Graduate Research Assistant, Aug 2017 – Aug 2022

UAB, Birmingham, AL

- Designed and analyzed multi-omics experiments, integrating bulk & single-cell RNA-seq with untargeted LC-MS/MS metabolomics to identify biomarkers of renal injury; conducted data processing, differential expression (DESeq2, STAR), pathway analysis, and multi-omics integration using MetaboAnalyst.
- Developed and executed R scripts and Bash pipelines for RNA-seq preprocessing, QC, differential expression, pathway analysis, and metabolomics–transcriptomics integration, improving analytical reproducibility and automation.
- Investigated molecular mechanisms of acute kidney injury with a focus on LDHA metabolic regulation, generating multiple peer-reviewed publications and driving collaborative research across institutional partners.
- Engineered and managed multiple genetic mouse models using Cre-Lox and tamoxifen-inducible systems; maintained 100+ colonies, performed genotyping/phenotyping, and ensured compliance with IACUC protocols.
- Applied molecular biology (qPCR, Western blot), histology (IHC, fluorescence microscopy), and cell-culture assays to characterize metabolic reprogramming, inflammatory signaling, and renal injury responses.
- Delivered multiple poster and oral presentations at national conferences, including the American Society of Nephrology Kidney Week (2017–2021), presenting findings on LDHA regulation, macrophage polarization, renal metabolism, and ischemic injury.

Biological Scientist, October 2012 – June 2017

University of Florida, Gainesville, FL

- Conducted NIH-funded research on renal ammonia metabolism and transporter regulation using genetically modified mouse models, supporting mechanistic studies of renal physiology.
- Developed a novel 2- μ L ammonia quantification assay, authored SOP, validated the workflow, and maintained Blood Gas Analyzer instrumentation.
- Led molecular and histological analyses (qPCR, Western, IHC, fluorescence imaging) and performed quantitative image analysis using ImageJ to support transporter physiology studies.
- Directed research for the NaDC1 (SLC13A2) transporter project, resulting in a first-author publication (PMID: 31188034).
- Contributed to manuscript development, figure generation, and experimental design for multiple peer-reviewed publications across renal physiology and transporter biology.
- Trained and mentored junior researchers, including future MD/PhD trainees, in molecular assays, imaging, and data analysis.
- Developed and maintained SOPs for genotyping, histology, and assay workflows, improving reproducibility and laboratory efficiency.

EDUCATION

University of Alabama at Birmingham, 2022
PhD in Biochemistry/Molecular Genetics

University of Florida, 2012
BA in Biological Sciences

SELECTED PUBLICATIONS (19 TOTAL)

1. ***TaxTriage: An Open-Source Metagenomic Sequencing Data Analysis Pipeline Enabling Putative Pathogen Detection***
 - Brian Merritt; Jeremy D Ratcliff; Stanley Ta; **Gunars Osis**; Matthew R. Mauldin; Peter M Thielen
 - Bioinformatics, Volume 42, Issue 4, April 2026, btag119, <https://doi.org/10.1093/bioinformatics/btag119>
2. ***Increased Proportions of Invasive Pneumococcal Disease Cases Among Adults Experiencing Homelessness Sets the Stage for New Serotype 4 Capsular-Switch Recombinants.***
 - Beall B, Chochua S, Metcalf B, Lin W, Tran T, Li Z, Li Y, Bentz ML, Sheth M, **Osis G**, McGee L.
 - J Infect Dis. 2025 Apr 15;231(4):871-882. doi: 10.1093/infdis/jiae453. PMID: 39259351
3. ***Macrophage-Specific Lactate Dehydrogenase Expression Modulates Inflammatory Function In Vitro.***
 - Lu Y*, **Osis G***, Zmijewska AA, Traylor A, Thukral S, Wilson L, Barnes S, George JF, Agarwal A.
 - Kidney360. 2025 Feb 1;6(2):197-207. doi: 10.34067/KID.00000000630. Epub 2024 Nov 12. PMID: 39531318
4. ***Expression of Lactate Dehydrogenase A and B isoforms in the mouse kidney.***
 - **Gunars Osis**, Amie M Traylor, Laurence M Black, Daryll Spangler, James F George, Abolfazl Zarjou, Jill W Verlander, Anupam Agarwal
 - Am J Physiol Renal Physiol. 2021 May 1;320(5):F706-F718. doi: 10.1152/ajprenal.00628.2020 PMID: 33719570
5. ***Effect of NBCe1 deletion on renal citrate and 2-oxoglutarate handling.***
 - **Osis G**, Handlogten ME, Lee HW, Hering-Smith KS, Huang W, Romero MF, Verlander JW, Weiner ID.
 - Physiol Rep. 2016 Apr;4(8). pii: e12778. doi: 10.14814/phy2.12778. PMID: 27117802

For full publication history, please visit ORCID: 0000-0002-0613-737X