

TRACE LAIL, MS

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BIOINFORMATICS SCIENTIST

Expert In RNA Sequencing • Nextflow • Pipeline Curation

Industry-trained bioinformatics scientist with five years at BridgeBio building computational genetics workflows, including custom GTF pipelines, nf-core/rnaseq on Seqera Platform, and R Shiny dashboards for experimental decision support. Now completing an MS in Bioinformatics at Northeastern (expected 2027), contributing to nf-core as both an Ambassador and active module developer.

Seqera | Nextflow | nf-test | nf-core | Python | Python OOP | R | Differential Abundance | Functional Enrichment | Gene Ontology | Data Visualization, Wrangling | AWS | Slurm | Docker | Podman

PROFESSIONAL EXPERIENCE

Nextflow, Remote **Jan. 2026 – Present**

Nextflow Ambassador

- Authored *From Confused to Contributing: My First nf-core PR Journey*
- Hosted Introductory to Nextflow session for Northeastern Bioinformatics students

Seanome, Remote **May 2025 – Present**

Bioinformatics Engineer ~ Volunteer

- Designed and implemented a DIAMOND blastp subworkflow for the nf-core/proteinannotator pipeline, enabling protein homology search against the full NCBI RefSeq protein database at scale (up to 10,000x faster than BLAST on large datasets)
- Authored two new local modules: ncbirefseqdownload for automated RefSeq FASTA retrieval and diamondpreparetaxa for NCBI taxonomy file preparation
- Wrote nf-test suites for all new modules and subworkflows, covering live and stub modes across four test scenarios; CI-tagged for pipeline integration testing

NCSU, College of Veterinary Medicine, Remote **March 2025 – May 2025**

Bioinformatics Consultant

- Providing RNA-seq analysis support to a canine oncology lab investigating peripheral T-cell lymphomas (PTCLs)
 - o Validated read-through transcripts (NT5C1B-RDH14, P3R3URF-PIK3R3) in short- and long-read datasets; reported TPM per sample
 - o Analyzed isoform prevalence for 4 high-interest genes across PTCL samples using IsoSeq cluster data
 - o Queried 3 public PTCL RNA-seq datasets to validate expression of 13 target genes; generated TPM matrices to support manuscript prevalence claims

BridgeBio Gene Therapy, Raleigh, NC **2021 - 2024**

Senior Associate Scientist ~ Computational Genetics **May 2023 - Sept. 2024**

Key provider of computational genetics support to gene therapy affiliates

- Identified small molecule targets to increase AAV yields by developing custom plasmid GTF creation workflow using Python OOP, leveraging GitHub, AWS EC2

- Optimized production efficiency by identifying critical molecular pathways for small molecule intervention screening
 - Applied Nextflow nf-core/rnaseq and nf-core/differential abundance pipeline analyses of AAV9 transfection methods across Seqera platform and local environments
- Key contributor in effort to significantly reduce costs via Nextflow nf-core/rnaseq analysis, revealing cellular pathway for transfection reagent intervention to 2x AAV5 optimization
- Identified low target gene expression in AAV9-treated mouse brain tissue through comprehensive RNA sequencing and gene ontology
 - Used Jupyter Notebook, generating targeted recommendations for subsequent investigation
- With published datasets, validated target, providing strategic recommendations for follow-up through iPSC CRISPR KO screening before advocating to investment committee
- Engineered R Shiny dashboard, consolidating data from cell culture passaging, production bioreactors, analytical assays
 - Empowered project teams to accelerate AAV experimental design and optimize particle production with real-time, integrated data visualization for strategic decision-making
- Recognized for supporting senior leadership drug pipeline strategy, scientific market analysis, by compiling OMIM, Ensembl, GlobalData data into comprehensive indication for AAV therapy

BridgeBio Gene Therapy, Raleigh, NC (con't)

2021 - 2024

Senior Associate Scientist

Jan. 2023 – Sept. 2024

Responsible for experimental design, implementation of AAV gene therapy process optimization

- Key contributor in increasing scalable AAV5 ddPCR yields 4x, maintaining percent full target for downstream purification
- Praised by management for authoring scale agnostic CMC/TDO Upstream process description for AAV9 gene therapy product for technical transfer
- Enabled high-throughput screening, efficient DoE experimental design by setting up a new AMBR15 with experimental protocols
 - Accurately replicated 2L and 200L bioreactor conditions, creating custom triple transfection scripts, enabling systematic AAV5/9 yield optimization for production scales

Scientific Associate II

Apr. 2021 – Jan. 2023

Focused on 2L scale up of AAV gene therapy products

- Expert resource for 2L bioreactors assisting leading to promotion to Senior Associate Scientist
- Reduced gene therapy costs 5x using endonuclease screening experimentation
- Achieved AAV9 product manufacturability and profitability within a year by identifying a transfection reagent to resolve inconsistent AAV9 capsid generation across production scales

Seqirus, Holly Springs, NC

2019 – 2021

Scientific Associate I

Oct. 2019 – Mar. 2021

Supporting influenza strain screening for bi-annual manufacturing campaign

- Used DOE and JMP for AMBR liquid handler scale down model screening for 2,000L bioreactor
- Managed SOP and Good Documentation Practices for pre pandemic influenza campaign support

EDUCATION | CERTIFICATIONS

MS Bioinformatics, Northeastern University, Boston, MA

MS Physiology, North Carolina State University, Raleigh, NC

BS Biological Sciences, North Carolina State University, Raleigh, NC

Biotechnology Certificate, North Carolina State University, Raleigh, NC