




# NHI X LUU


Silver Spring, MD 20906

 About Me

 NHI LUU

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 nluu1

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## EDUCATION

### UMBC at the Universities at Shady Grove

B.S., Applied Biotech (TLST) - Bioinformatics; GPA: 4.0

B.S./M.P.S. in Data Science: Introduction to Data Science

Rockville, MD

Expected: Fall 2023

### University at Maryland - College Park

Microbiology - Credits: 32

College Park, MD

Jan 2018 - May 2019

### Montgomery College

A.S., Life Sciences; GPA: 3.83

Rockville, MD

Dec 2017

## TECHNICAL SKILLS & KNOWLEDGE AREAS

- **Programming Language:** Python, R, Bash/Shell, HTML/CSS, Latex
- **Bioinformatics Softwares/Tools:** Edirect API/SRA-toolkit, BLAST/NCBI, fastqc/trimmomatic, BWA, Samtools/BCFtools, Mummer4, SnpEff, GATK, BV-BRC CLI, ClustalX2, Jalview, ImageJ
- **Related softwares:** R-Shiny, AWS Services (EC2, S3, RDS, Nextflow, Appflow), Docker, Scikit-Learn, Cloud Computing/HPC in Ubuntu/Redhat, Databases (MongoDB, SQL), REST APIs, GitHub
- **Laboratory/Instrumentation:** NGS/WGS Sequencing (DNA extraction, PCR, Gel electrophoresis), Cell culture, Immunostaining, Spectrophotometry (Nanodrop), HPLC

## RESEARCH EXPERIENCE

### Universities at Shady Grove

#### ExtremeBiome Research - Bioinformatics Pipeline

Rockville, MD

08/2022- Present

- Merck Fellowship: Designed and developed a user-friendly Genome browser using R/R-Shiny, incorporating an automated back-end annotation workflow to analyze NCBI genomes and generate comparative genome visualizations (Circos)
- Pending research publication: Experimental Neutral Theory of Evolution on Genetics Adaptations and Mutation Rates of Ionizing Radiation Resistance in *Halobacterium salinarum*
- Led the processing of annotated VCF files, generating statistical charts, facilitating insightful data visualization and analysis in support of the research manuscript
- Develop genomics tools and automate variant calling workflow on Illumina/PacBio NGS data (*OmicsVM-configure*: <https://doi.org/10.5281/zenodo.7641805>)

### Student Projects - Data Analysis

04/2022- Present

- Develop small projects and final project workshop for the TLST Bioinformatics course, with an emphasis on NGS annotation pipeline to analyze and interpret genomic data with cutting-edge bioinformatics tools and methodologies
- Construct phylogenetic trees and analyze bacterial taxonomy based on different molecular markers using NCBI/BLAST and alignment tools (ClustalX2, Jalview, iTOL)

## WORK EXPERIENCE

### Adaptive Phage Therapeutics, Inc.

Gaithersburg, MD

#### Genomic Products Development Intern

04/2023- 08/2023

- Created a user-friendly R-Shiny dashboard for seamless communication and task tracking of bioinformatics pipelines across five departments by integrating SharePoint files with AWS services
- Enhanced phage genome accuracy and quality for FDA-regulated analysis by integrating BV-BRC databases and Mummer4 annotation into existing Docker and Nextflow scripts on AWS
- Acquired 20-hour training on phage and bacterial genome sequencing monitored by the APT Genomics Team, utilizing industry-standard DNA sequencing technologies (Qbit, Illumina RNA-Seq)

### Phage Hunting Intern

08/2022- 04/2023

- Utilized aseptic microbiology techniques to enrich, isolate, and purify targeted phages against multi-drug resistant bacterial strains, providing critical support for on-demand clinical trial patients
- Demonstrated meticulous adherence to cGMP and GDP standards in a BSL-2 laboratory, ensuring safe and efficient utilization of lab procedures, instruments, and tools