

# LOGAN HALLEE

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## EDUCATION

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- PhD** University of Delaware, Bioinformatics Data Science Expected May 2026  
Dissertation: TBD  
Committee: TBD  
GPA - 4.00
- BS** University of Delaware, Quantitative Biology May 2022  
Minored in Biochemistry  
GPA - 3.77
- AAS** Delaware Technical Community College, Biological Sciences May 2020  
Graduated Magna Cum Laude  
GPA - 3.72

## HONORS AND AWARDS

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- Unidel Distinguished Graduate Scholars Fellowship** 2022 - 2027  
Highly competitive award offered to doctoral students by the University of Delaware. Used to recruit exceptional doctoral students and provide them with intellectual and professional experiences that foster the development of disciplinary and community leaders.
- William Clark Prize** 2022  
In recognition of unusual talent and ability in mathematics among the graduating math seniors.
- Math and Physics Department Outstanding Performance Award** 2020  
Selected out of Delaware Technical Community College class of 2020.
- President's Award** 2020  
Awarded to a student-athlete on the basis of merit, academics, and athletic performance.
- Athletic Director's Award** 2020  
Awarded to a student-athlete on the basis of merit, academics, and athletic performance.
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## RESEARCH EXPERIENCE

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**University of Delaware**, Newark DE

July 2022 - Present

**Center for Bioinformatics & Computational Biology**

**Predocutorial Researcher**, Gleghorn Lab

Title: TBD

- Exploring computer vision architectures to streamline the processing of Z-stacked biomedical images into 3D meshes for solving complex pharmacokinetic ODE models.
- Extensive data manipulation, Attention UNET models, 2D interpolation, 3D interpolation, and polygon meshing.
- Producing data, figures, and sections of R01 grant proposals.
- Applying bioinformatics, co-attentive neural networks, and molecular quantum mechanics to develop in silico enzyme kinetic models.
- Embedding and tokenizing, BERTology, hyperparameter tuning.

**University of Delaware - Mathematical Sciences**, Newark DE

August 2021 - Present

**Research Project**, Dr. Dominique Guillot

Title: Estimating the Graphical Structure of Climate Fields

- Exploring if recent advances in graph signal processing can improve climate reconstructions, detect geophysical structures from datasets, and compare to state-of-the-art reconstruction methods.
- Advanced linear algebra, extensive lasso and elastic net regression models.

**Wolfram Research**, Champaign IL

December 2022 - January 2023

**Wolfram Winter School**, Stephen Wolfram, James Boyd, Eric Parfitt

Title: Tetris for Proteins – Shape Based Molecular Chemistry in the Wolfram Language

- We propose a new system from the Wolfram Language: Tetris for Proteins. By constructing combinatorial graphs of random pseudo-molecules, we enable a preliminary shape-based interaction for molecular chemistry.
- Random generation of topological structures.
- Computational methods for approximating efficient packing of random structures.
- Multiway graphs to visualize structure-based chemistry of pseudo-molecules.

**University of Delaware - Biological Sciences**, Newark DE

June 2021 - June 2022

**Undergraduate Researcher**, Lam Lab

Title: Expanding the Domain-Based HSP90 Interactome for Various Applications in Cardiac Diseases

- Attempting to help elucidate the multiplex interaction environment of the ubiquitous HSP90 chaperone complex.
- Published literature reviews with graduate students about HSP90 and gamma-secretase as targets for cardiac diseases.
- Project design, developed lab site-directed mutagenesis protocol, implemented python code to optimize ligation procedures, and designed recombinant plasmids and proteins.
- Conducted site-directed mutagenesis, ligated mutated sequences into protein expression vectors, protein purification, gel electrophoresis, western blots, qPCR, and animal cell culture.
- Differentiated induced pluripotent stem cells into cardiomyocytes, tissue engineering.

- Use of common molecular biology equipment and basic mass spectroscopy knowledge.
- Produced imaging data, conducted RNAseq and proteomic analysis for R01 grant proposal figures.

## **PUBLICATIONS**

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### ***Journal Publications***

Roberts, R.J.; Hallee, L.; Lam, C.K. “The Potential of Hsp90 in Targeting Pathological Pathways in Cardiac Diseases,” *J. Pers. Med.* **2021**, 11, 1373.

Sen, S.; Hallee, L.; Lam, C.K. “The Potential of Gamma Secretase as a Therapeutic Target for Cardiac Diseases,” *J. Pers. Med.* **2021**, 11, 1294.

### ***Journal Papers in Review***

Hallee, L.; Khomtchouk, B.B. “Machine Learning Classifiers Predict Key Genomic and Evolutionary Traits Across the Kingdoms of Life,” Submitted to: Scientific Reports.

### ***Preprints***

Hallee, L (2022): Exploring Phylogenetic Classification and Further Applications of Codon Usage Frequencies. BioRxiv. Preprint.  
<https://doi.org/10.1101/2022.07.20.500846>

## **SKILLS**

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**Mathematical / Statistical Analysis:** Background in applied mathematics and applied multivariate statistics: Perturbation theory, bifurcation analysis, growth models, ODE systems, MANOVA, PCA, CCA, LDA, penalized regression, etc.

**Data Science:** Data manipulation and augmentation. Use of many common machine learning techniques: Random forests, SVM, KNN, naive bayes, ensembles, neural networks, transformers, etc.

**Bioinformatic Analysis:** Familiar with common bioinformatic pipelines, experience with RNAseq, differential expression analysis, enrichment analysis, proteomic analysis, multiple sequence alignment, dendrogram generation, annotating genomes, and biological network analysis.

**Molecular Biology:** Formal bio-technician training: courseload rich in hands-on lab work. Basic experience with organic chemistry and biochemistry techniques.

**Programming:** Main workflow in python. Experience with numpy, pandas, scikit-learn, tensorflow, and PyTorch among other packages. Also familiar with R, Mathematica, LaTeX, Matlab, and C++.

**Applications:** Wolfram One, Snapgene, JMP, Biorender, Cytoscape, PyMol, MEGA-X, ApE, STRING, DAVID, and Microsoft Office.

**Operating Systems:** Windows, Mac, Linux.

## **INDEPENDENT PROJECTS**

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### **Phylogenetic Classification using Codon Usage Frequencies**

Improving upon the phylogenetic classification in literature based on codon usage frequencies. Rigorous optimization of hyperparameters for an artificial neural network and ensemble system. Both models performed with unprecedented accuracy, precision, and recall. - For BINF610 at the University of Delaware.

### **Exploring Open Reading Frame Identification with Codon Usage Frequencies**

Designed pipeline to reject possible open reading frames or deem plausible by comparing the frame codon frequencies to their respective organism reference. Ranked codon frequencies by variance in kingdom classification for a multinomial chi-square goodness of fit test. - For MATH637 at the University of Delaware.

### **DNA Type and Kingdom Classification Using Machine Learning**

Using codon usage frequencies in organisms to quickly classify the kingdom and DNA type of a DNA sample. Compared k-nearest neighbors, support vector machines, artificial neural networks, and naive bayes models. - For STAT613 at the University of Delaware.

### **Genomic Variant Analysis in MCM6 for Lactose Intolerance**

Analyzing patient data to look at genetic variants associated with lactose intolerance. - For BINF694 at the University of Delaware.

### **Sarcomere and Muscle Filament Proteins are Highly Expressed in the Heart when Compared to Smooth Muscle Tissue**

This project analyzes specific hallmarks of heart tissue (MYL7, NPPA, TNNT2, TNNT1, MYBPC3, MYL4, MYH6, ACTC1) and their RNA expression levels vs. smooth muscle tissue. - For BINF694 at the University of Delaware.

### **The Pharmacokinetics of Luminespib**

Collaboration with Blake Silver and Xu Yang.

Here we evaluated the pharmacokinetics of the HSP90 inhibitor Luminespib with various ordinary differential equation compartment-based models. - For MATH512 at the University of Delaware.

### **Applying Operations to FASTA and FASTQ File Types**

Building python classes for efficient augmentation and data extraction from FASTA and FASTQ files. - For BINF690 at the University of Delaware.

**PROFESSIONAL AFFILIATIONS**

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Sigma Xi Honor Society, 2021 – Present  
Associate Membership

Phi Theta Kappa Honor Society, 2019 - Present  
Full Membership

**LANGUAGES**

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**English:** Native Language