Charlotte, United States
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JULIAN AILERU

COMPUTATIONAL BIOLOGIST

EDUCATION

BS Biology | MS Bioinformatics
UNIVERSITY OF NORTH CAROLINA AT CHARLOTTE
GPA 4.0

TECHNICAL SKILLS

Programming Languages

Python, R, Shell Scripting to support high performance computing tasks, SQL for Relational Database Management

Github – https://github.com/JulianAileru

Foundational Concepts

- Machine Learning, Computational Pipeline Development, Data Structures and Algorithms, Object-Oriented Programming, Database Design and Implementation, High-Performance Computing Environment (Linux/Unix)
- Statistical Analysis, Sequence Analysis, Next-Generation Sequencing, RNAseq Analysis, Whole-genome Assembly, Transcriptome Assembly, Genomics, and Molecular Biology Techniques (PCR,Western Blot)

EMPLOYMENT HISTORY

DEC 2023 – PRESENT

Graduate Research Assistant , UNC Charlotte (Irina Nesmelova Lab) , Charlotte, NC

- Proteomics project to properly characterize and model chemotactic cytokine protein family (Chemokines) quaternary structures based on protein structure and sequence information.
- Generates new dataset for the chemokine subfamily containing structural and sequence-derived physiochemical features.
- Utilizing data programmatically retrieved from various databases such as NCBI and Uniprot in addition to generating new structural alignment data using structural bioinformatics software (Cath-tools, SSAP, DSSP,MUSTANG).
- Applying Supervised Machine Learning techniques to appropriately classify interacting/noninteracting Chemokines based on derived features.
- Utilizes high performance computing cluster to run computational modeling software such as AlphaFold2 and MULTICOM3 and sequence alignment programs such as EMBOSS and clustal-omega.
- Utilizes Molecular Visualization Software (PyMOL) for accessing and manipulating PDB files and protein structures.
- Utilizes several python libraries (pandas,numpy,sklearn,matplotlib,subprocess,os, etc.) and bioinformatic software for sequence alignment, data-preprocessing, and machine learning applications.
- Presents progress in weekly lab meetings

DEC 2023 – PRESENT

Graduate Research Assistant , UNC Charlotte (Jun-Tao Guo Lab), Charlotte,NC

- Proteomics project to study hydrogen bond interactions in protein-DNA complexes
- Leads in the development and implementation of a computational pipeline for studying hydrogen bond interactions in protein-DNA complexes with an end goal of performing a comparative analysis of the hydrogen bond network of ssDNA-protein and dsDNA-protein complexes
- Utilizes advanced python programming for data preprocessing and pipeline development.
- Conducts downstream analysis of processed data using a number of different structural bioinformatics software for hydrogen bond annotation and energy calculations.
- Presents progress in weekly lab meetings

JAN 2023 – JAN 2024

Graduate Research Assistant , UNC Charlotte (Elizabeth Cooper Lab), Charlotte

- Utilizes bioinformatic methods to investigate the selective pressures on gene duplications in Wyeomyia Smithii (Pitcher Plant Mosquito)
- Calculates the non-synonymous / synonymous mutation rate (Ka/Ks) of gene duplicates using KaKsCalculator3.0
- Employs Python libraries (pandas, os, Biopython, etc.) to parse data from OrthoFinder, InterProScan, and KaKsCalculator 3.0.
- Utilizes Computational modeling software to understand the effects of different selective pressures on protein structure.
- Conducts Gene Ontology Analysis in R to identify enriched functional categories within gene duplicates
- Performed statistical analysis of enriched functional categories of genes in gene families undergoing expansion.
- Provides supplemental material and other contributions to an in-progress publication surrounding the Wyeomyia Smithii Genome.
- Presented Poster at Annual Bioinformatics Graduate Research Symposium

JAN 2022 – MAY 2022

Microbiologist, Cosette Pharmaceuticals, Lincolnton

- Performed Antimicrobial Testing daily for drugs such as Nystatin, Gentamicin, and Neomycin through extraction of antimicrobial components from their delivery methods, plating against different bacteria (S. Epidermidis and S. Cerevisiae) and measuring efficacy using the TRINITY V3 Antibiotic Zone Reader and Statistical Analysis.
- Adhered to SOPs to perform assays and recorded results in compliance with Good Documentation Practices (GDP).
- Extracted bacteria from culture and prepared them for plating for the entire lab.