Nneka Ede

Nne1st@aol.com - (409)828-0610
7550 Coral Creek, Beaumont, Tx, 77707

PERSONAL STATEMENT

I am a senior computer science major at Prairie View A&M University. I am a highly motivated individual and a self-learner who is interested in Big Data, Computational Biology, Bioinformatics, and Machine Learning for Biological Data. I am seeking to Further my knowledge software engineering, computational biology, and programming for scientific data.

EDUCATION

Bachelor of Science: Computer Science - September 2015- May 2019
GPA:4.0
Prairie View A&M University – Prairie View, Tx

WORK EXPERIENCE

Summer Intern – June 2018 – August 2018
Harvard Medical School Dept. of Biomedical Informatics, Avillach Lab - https://dbmi.hms.harvard.edu/
Boston, Massachusetts

Explore Sex and Population Influence in Protein Expression in Lymphoblastoid Cells from 1000 Genome Project

Responsibilities:

- Use a scalable variant store (stores genomic data): HAIL
- Deployed HAIL on a google cloud cluster
- Manipulated clinical and genomic data from 1k genome project and produced a PCA of 84.4 million variants in the 1000 genome project
- Reanalyzed the principle results from a nature paper which uses 1000 genome project using HAIL, including linear regression and a Proteome Wide Association Study.
- Conducted a new analysis exploring protein level differences in sex including a Genome Wide Association Study (GWAS) and cis- Protein Quantitative Trait Loci (cis-pQTL) Analysis.

Research Intern – September 2017 – May 2018
Prairie View A&M University Department of Electrical Engineering and Center for Computational Systems Biology, Kim Lab - www.pvamu.edu/ccsb/
Prairie View, Texas

Create algorithms to determine Gene Commanding Height and Gene Master Regulators in cancer cells and normal cells.

Responsibilities:

- Programmed in Python for data analysis.
- Calculate the Gene Commanding Height based on a correlation map based on the gene expression levels and the expression control
- Connect to KEGG API to search the KEGG database resource for gene pathways, then sort all genes based on which pathway they are in.
- Determine weighted pathway regulation for each pathway based on fold-change and average gene commanding height

Summer Intern – June 2017 – August 2017
Harvard Medical School Department of Systems Biology, Klein Lab - https://sysbio.med.harvard.edu/
Boston, Massachusetts

Analyse cell commitment as cell differentiation from Hematopoietic Stem Cells to Terminal Granulocytes using high dimensional single cell RNA sequenced data of Kit+Sca1+ cells Hematopoietic Stem cells.

Responsibilities:

- Program in Python for data analysis.
- Map known stages of Granulopoiesis onto a KNN Plot of Hematopoietic progenitor cells in murine bone marrow.
- Filter through very noisy data using various statistical techniques and perform dimensionality reduction.
- Identify dynamic gene expression patterns as cells commit to Granulopoiesis using various clustering algorithms. Then describe major changes in gene expression throughout differentiation.
- Developed web based interactive interface to further explore Granulopoiesis and neutrophil progenitor cells
- Compare the development of granulocytes to the development of erythrocytes. In many instances the same genes are induced throughout both blood cell development.

C++ Supplemental Instructor – September 2016 – May 2017
Roy G Perry College of Engineering - www.pvamu.edu
Prairie View, Texas

Responsibilities:

- Hold 2 C++ classes per week
- Attend C++ courses and lab every week to aid students with their weekly lab work and projects
- Conduct one on one tutoring for students who need further assistance

Summer CE2I Camp Counsellor – July 2016 – August 2017
Roy G Perry College of Engineering - www.pvamu.edu
Prairie View, Texas

Responsibilities:

- Guided incoming freshman on the path to becoming a success engineering student.
- Direct daily functions for summer camp dedicated to creating engaging educational and recreational opportunities for the incoming students.
- Tutoring students in Computer Science, Algebra/Trig, Chemistry, Intro to Engineering, and Physics

SKILLS

Fluent
- C++
- Python (including: numpy, scipy, matplotlib, bokeh)
- Javascript (including: json, d3)
- HTML/ CSS/ Bootstrap

Familiar
- R
- Assembly Language
- Swift
- Java
- Terminal / Powershell
- Gscloud
- Variant Store (HAIL)

Other

- Linear Algebra
- Probability and Statistics
- Data Analytics / Machine Learning

PERSONAL INTERESTS

I decided to major in computer science because I realized how significantly the medical field is being affected by technology. I want to merge this power with a medical degree to impact the lives of those whom I cross paths with, and to push the bounds of the medical field in every aspect. The same algorithms that I have learned in computer science to process large amounts of data can be used to collect biological data and solve medical issues. Therein computers are so powerful. Computer algorithms can be utilized to pinpoint where seizures are coming from, can identify cancerous genes in a sea of data, can model the spread of diseases, and can aid doctors predicate the best treatment for each patient. Every patient is unique and their disease may progress in different ways. Thus, individualized care could revolutionize medicine. It would allow physicians to formulate a combination of prescriptive medicine tailored for everyone. Individualized care is especial important when it comes to cancer. Cancer has various genetic mutations. Building large databases of genomes will help to pinpoint person mutation and prescribe treatment and medication based on person's specific mutation.

REFERENCES

References are available on request.