


TONY KABILAN OKEKE

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EDUCATION

Drexel University

B.S. and M.S. in Biomedical Engineering (Accelerated Program)

Concentrations: Bioinformatics & Neuroengineering

Minor: Computer Science

Philadelphia, Pennsylvania

Anticipated Graduation: June 2024

Cumulative GPA: 4.00

EXPERIENCE

IVIVT - Non-Clinical Safety - Global Investigative Safety, GSK

April 2023 – Present

Scientific Student Worker

Collegeville, Pennsylvania

- Utilizing *SquidPy*, *Seurat*, and other tools to enhance interpretation of GeoMx and 10X Visium datasets, and provide critical insights into spatial gene expression patterns and their implications in genetic toxicology research.
- Developing and implementing bioinformatics algorithms to analyze genomic datasets from non-clinical safety studies, providing insights into molecular mechanisms leading to potential safety concerns during drug development.
- Collaborated with eSTAR carcinogenicity working group to design a neural network model predicting molecular initiating events related to liver carcinogenicity using rat transcriptomics studies.

IVIVT - Non-Clinical Safety - Global Investigative Safety, GSK

April 2022 – September 2022

Scientific Student Worker

Collegeville, Pennsylvania

- Utilized the *Dash* and *Flask* libraries in python to develop an interactive web application for performing statistical analysis on data generated in high-content imaging toxicology studies. Also utilized *Dask* to parallelize computations on larger data sets to improve efficiency. The web application was then deployed via *RStudio Connect* on the internal HPC.
- Trained the *Noise2Void* deep neural network on HPC to perform noise reduction in microscopy images in order to improve the accuracy of *CellProfiler* pipelines for image segmentation and feature extraction.
- Developed a python package with tools for performing statistical analysis, visualization, and machine learning on high-content imaging data sets.
- Implemented pipelines in *CellProfiler* and *Columbus* to perform feature extraction for high-content images generated via cell painting assays.
- Utilized *Scikit-learn* to implement decision tree, random forest, and support vector machine models for biomarker discovery on high-content imaging datasets.

Invenio Lab, Hospital of the University of Pennsylvania

March 2021 – August 2022

Immunology Research Assistant

Philadelphia, Pennsylvania

- Developed SOPs and conducted assays for the isolation and extraction of DNA, RNA, and protein from human blood and urine samples, as well as the preparation of Next-Generation Sequencing libraries for Reduced Representation Bisulfite Sequencing (RRBS) and gene expression microarrays.
- Utilized *Scikit-learn*, *Pandas* and *NumPy* to apply unsupervised learning algorithms to clinical and multi-omic datasets, and presented results to colleagues using *Seaborn* in *Jupyter* notebooks.
- Developed python and R scripts for analyzing DNA methylation levels in data from Illumina microarrays.
- Developed R scripts for analyzing protein expression and clinical data from electronic medical records.
- Performed differential methylation, KEGG pathway enrichment, and Gene Ontology analysis on microarray results for patients who underwent cardiopulmonary bypass surgeries using *bash* and R scripts.

Zhou Lab, Children's Hospital of Philadelphia

May 2020 – June 2021

Undergraduate Research Intern

Philadelphia, Pennsylvania

- Contributed to the development of R packages for analyzing DNA methylation levels in data from Illumina microarrays.
- Validated R package performance using *GEO* public datasets.

PROJECTS

MEDDIBIA | Python, TensorFlow, Flask, Flutter

March 2023

- Recipient of the Collaborative Team Award at the 2023 Philly CodeFest.
- Developed a machine learning-based solution for diagnosing skin conditions using pre-trained models like VGG16 and EfficientNet, achieving approximately 70% accuracy in image-based classification.
- Employed GPT-3 for symptom identification from user input, and trained a *Random Forest* classifier to predict the corresponding disease with 87% accuracy; GPT-3 was then used to provide informative disease descriptions to users.
- Built a cross-platform app using Flask API for the backend, deployed on Heroku, and developed the frontend with Flutter, ensuring accessibility across multiple devices.

- Develop a R pipeline for preprocessing RNA-Seq datasets and performing differential expression analysis on data sets from GEO and DEE2.
- Developed neural network for predicting Gene Ontology enrichment in differential expression analysis data from RNA-Seq experiments.
- Trained an autoencoder model to reconstruct log fold-change values from RNA-Seq datasets, and used the latent space representation as input to a neural network for predicting GO terms.
- Utilized *Tensorboard* and *Keras Tuner* to monitor model performance and tune hyperparameters.

CaBiD, Cancer Biomarker Discovery Tool | Python, Flask, Qt

September 2022

- Developed a web application and GUI to investigate variations in gene expression across various cancer types.
- Preprocessed and curated datasets from GEO (Gene Expression Omnibus) and CuMiDa (Curated Microarray Database) in a SQLite database.
- Identified key differences in gene expression between healthy controls and tumoral samples across various cancer types.

ELISA Analysis Tool | R, Shiny

September 2021

- Processed Optical Density values from microplate readers using *tidyverse* packages.
- Developed R script for fitting OD values for ELISA standards to a 5-Parameter logistic regression model to estimate unknown sample concentrations.
- Built interactive web-application for ELISA curve fitting using the *RShiny* framework.

TECHNICAL SKILLS

Programming Languages: Python, R, Bash, C++, MATLAB, SQL, AWK, Git, PHP**Frameworks and Libraries:** TensorFlow, Keras, PyTorch, Scikit-learn, Flask, FastAPI, Shiny, Dash**Bioinformatics Tools:** Seurat, SquidPy, CellProfiler, Columbus**Wet Lab Skills:** PCR, qPCR, ELISA, Western Blot, DNA/RNA/Protein Extraction, NGS Library Preparation**PUBLICATIONS**

- Unbiased Analysis of Temporal Changes in Immune Serum Markers in Acute COVID-19 Infection With Emphasis on Organ Failure, Anti-Viral Treatment, and Demographic Characteristics. *Frontiers in Immunology* 12:650465 (2021).
- Longitudinal urinary biomarkers of immunological activation in COVID-19 patients without clinically apparent kidney disease versus acute and chronic failure. *Scientific Reports* 11, 19675 (2021).
- Dynamic Changes in Central and Peripheral Neuro-Injury vs. Neuroprotective Serum Markers in COVID-19 Are Modulated by Different Types of Anti-Viral Treatments but Do Not Affect the Incidence of Late and Early Strokes *Biomedicine* 9, no. 12 (November 2021): 1791.
- A disturbed balance between blood complement protective factors (FH, ApoE) and common pathway effectors (C5a, TCC) in acute COVID-19 and during convalesce *Scientific Reports* 12, no. 1 (August 2022).
- Persistent Depletion of Neuroprotective Factors Accompanies Neuroinflammatory, Neurodegenerative, and Vascular Remodeling Spectra in Serum Three Months after Non-Emergent Cardiac Surgery *Biomedicine* 10, no. 10 (September 2022): 2364.

CONFERENCE ABSTRACTS

- 174: LONGITUDINAL CHANGES OF NEURO-SPECIFIC SERUM PROTEINS IN COVID-19 PATIENTS Society of Critical Care Medicine 51st Critical Care Congress, April 2022.
- 181: PATTERNS OF URINARY BIOMARKERS OF IMMUNOLOGIC ACTIVATION AND SEPSIS IN PATIENTS WITH COVID-19 Society of Critical Care Medicine 51st Critical Care Congress, April 2022.

AWARDS AND HONORS

- HESI GTTC Professional Development Award, Spring 2023
- Philly Codefest 2023 - Collaborative Team Award

SERVICE AND LEADERSHIP

- Project Manager, *Drexel Computational Design*, May 2023 – Present
- Vice President, *Drexel Computational Design*, March 2021 – May 2023
- Member, *Tau Beta Pi*, December 2021 – Present
- Member, *Drexel Society of Artificial Intelligence*, September 2022 – Present