# TONY KABILAN OKEKE

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## EDUCATION

**Drexel University**                                                                **Philadelphia, Pennsylvania**
*B.S. and M.S. in Biomedical Engineering (Accelerated Program)*        *Anticipated Graduation: June 2024*
*Concentrations: Bioinformatics & Neuroengineering*                              *Cummulative GPA: 4.00*
*Minor: Computer Science*

## 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 Phily 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.

**MLGO, Deep Learning for GO Terms** | *Python, TensorFlow*                                       **September 2022**

- 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

- Laudanski, Krzysztof, et al. "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 (2021): 650465.
- Laudanski, Krzysztof, et al. "Longitudinal urinary biomarkers of immunological activation in covid-19 patients without clinically apparent kidney disease versus acute and chronic failure." Scientific Reports 11.1 (2021): 19675.
- Laudanski, Krzysztof, et al. "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." Biomedicines 9.12 (2021): 1791.
- Laudanski, Krzysztof, et al. "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 12.1 (2022): 13658.
- Laudanski, Krzysztof, et al. "Persistent Depletion of Neuroprotective Factors Accompanies Neuroinflammatory, Neurodegenerative, and Vascular Remodeling Spectra in Serum Three Months after Non-Emergent Cardiac Surgery." Biomedicines 10.10 (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