# Tony Kabilan Okeke

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## Education

**Drexel University** **Philadelphia, Pennsylvania**
*Master/Bachelor of Science in Biomedical Engineering* *Anticipated Graduation: June 2024*
*Concentrations: Bioinformatics & Neuroengineering* *Cummulative GPA: 4.00*
*Minor: Computer Science*

## Experience

**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.
- Implemented the *Noise2Void* deep neural network on HPC to perform noise reduction in microscopy images in order to improve the accuracy of an image segmentation and feature extraction pipeline.
- 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*

- 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 *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

**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
**Software:** CellProfiler, Columbus Imaging Software, Microsoft Office, LoggerPro, Simulink, Fusion 360, Ultimaker Cura

## Publications

- *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).
- *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).

## Activities

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