SANDRA OLUOCH

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Scientific Data Engineer

4+ years of experience delivering computer vision, deep learning, and machine learning insights to large datasets of 3D stem cell images. Contributed to developing advanced algorithms and scalable solutions that enhance biomedical image analysis. Previous work experience in immunology, malaria and cancer research. Passionate about open science, multidisciplinary collaboration and utilizing artificial intelligence to improve scientific understanding.

EDUCATION

UNIVERSITY OF WASHINGTON, BIOENGINEERING, Seattle, WA · June 2020

Master of Applied Bioengineering, Concentration in Computational Biology

UNIVERSITY OF ROCHESTER, BIOMEDICAL ENGINEERING, Rochester, NY · May 2016

Bachelor of Science in Biomedical Engineering,

Concentration in Cell and Tissue Engineering, Minor in Chemical Engineering

WORK EXPERIENCE

Allen Institute for Cell Science, Seattle, WA · Oct 2020 – June 2025

SCIENTIFIC DATA ENGINEER II

Provided support in the design and implementation of machine learning algorithms and computer vision solutions for image analysis to better understand cell-cell dynamics. The work encompassed algorithm development, open-source tool creation, large-scale data pipeline management, and the use of high-performance GPUs within a collaborative scientific environment.

- *MACHINE LEARNING AND DATA ANALYSIS*
  - **Computer Vision:** Designed and implemented advanced machine learning algorithms and computer vision techniques to extract key biological features from 3D stem cell images, improving accuracy and efficiency of image analysis.
  - **Open-Source Development Tool ([Allen Cell and Structure Segmenter](#)):** an open source, Python-based image segmentation tool that has supported over 50 researchers, diagnosticians, and PhD candidates in data analysis using our premade image segmentation workflows.
  - **Data Preprocessing and Feature Engineering:** Experience with cleaning and preparing large-scale imaging datasets and optimizing feature extraction methods to improve model accuracy.

- *DEEP LEARNING AND MULTI-SCALE MODEL DEPLOYMENT*
  - **Deep Learning Pipeline Optimization ([EMT Image Analysis Pipeline](#)):** Generated over 30 TB worth of image data (13,300 Z-stacks) using a scaled-up high-throughput computational pipeline that uses deep learning models to create predictions on raw image data to better understand the role the Epithelial-to-Mesenchymal Transition (EMT) plays in cell colonies.
  - **High-Performance Computing and Model Optimization:** Diagnosed and resolved bottlenecks in large-scale model training, optimizing multi-GPU computational workflows and scheduling software such as Slurm to ensure smooth execution of high-performance machine learning jobs, improving model convergence efficiency for complex biomedical datasets.
  - **Cloud Computing and Scalable Infrastructure:** Experience with training models and running inference using AWS and ML Flow to track metrics

- *SCIENTIFIC CONTRIBUTIONS AND COLLABORATION*
  - **Cross-Disciplinary Collaboration:** Worked with biologists, engineers, and data scientists to integrate computational methods into biological research, fostering interdisciplinary innovation.
  - **[Publications:](#)** Contributed to research papers, translating findings into actionable insights for the scientific community.

Institute for System Biology, Seattle, WA · Jun 2020 – Oct 2020

MACHINE LEARNING INTERN

Designed and implemented supervised and unsupervised machine learning algorithms to predict gut microbiome responses to intervention within the **[Arivale Wellness Study](#)**, enhancing the understanding of microbiome dynamics.

- *MACHINE LEARNING*
  - **Data Preprocessing:** Conducted end-to-end analysis of project data, including quality control, data tidying, hypothesis testing, and graphical presentation of 127 calculated polygenic scores, optimizing feature extraction methods for improved model accuracy.
  - **Supervised and Unsupervised Methods:** Applied various machine learning techniques such as regression, decision trees, K-means clustering, K-nearest neighbors, PCA, and K-means clustering to model testing, regression, classification, and clustering tasks, improving predictive performance.

Bristol Myers Squibb, Seattle, WA   Dec 2018 – Jun 2019
RESEARCH ASSOCIATE
Part of the Clinical Product Characterization team developing and testing Celgene CAR-T Cell therapies, JCAR017 and JCARH125.

- *IMMUNOLOGY*
  - **Immune Receptor Biology and Data Analysis:** Proficient at advanced molecular biology/immuno-histochemistry including real-time PCR, DNA/RNA/protein extraction and isolation and immunofluorescent assays (IFA)
  - **scRNAseq Data:** Perform multiparameter flow cytometry assays for multiple teams in Process Development.
  - Execution and analysis of molecular and cell-based assays via DIVA and FlowJo

Fred Hutch Cancer Center, Seattle, WA   Sep 2017 – Nov 2018
RESEARCH TECHNICIAN
Part of a team studying pancreatic ductal adenocarcinoma (PDA) using genetically engineered mouse models to better understand the mechanism and pathogenesis of the disease

Center for Infectious Disease Research, Seattle, WA   Aug 2016 – Sep 2017
RESEARCH TECHNICIAN
Assigned to clinical research trial for the development of a potential malaria vaccine using the genetically attenuated parasite Plasmodium falciparum

RELEVANT SKILLS

- **Programming:** Python, Git, Linux, Jupyter, Slurm
- **ML/DL Frameworks:** PyTorch, CUDA, Scikit-learn, Dask, OpenCV, Pandas, Matplotlib, Numpy, MONAI, Hydra
- **Data Tools**: Napari, ImageJ, Zen, Cellpose, Omnipose
- **Cloud & DevOps:** AWS, Docker

PREPRINTS AND PUBLICATIONS

1. C. Hookway, A. Borenzstejn, L.Harris, **S. Oluoch**, *et al.,* A Human Induced Pluripotent Stem (hiPS) Cell Model for the Holistic Study of Epithelial to Mesenchymal Transitions (EMTs), Under Review [Middle author]

2. S. Mishra, **S. Oluoch**, B. Morris, A. Khan, *et al.,* Enhancing Microscopy Image Analysis with Streamlined Deep-Learning-Based 3D Segmentation, Biophysical Journal, February 2025 [Second author]

3. J. Dixon, C. Frick, C. Leveille, **S. Oluoch,** *et al.,* Colony Context and Size-Dependent Compensation Mechanisms Give Rise to Variations in Nuclear Growth Trajectories, Cell Systems, May 2025 [Middle author]

4. M. Viana, J. Chen, T. Knijnenburg, S. Rafelski, **S. Oluoch**, et al., Integrated Intracellular Organization and its Variation in Human iPS Cells, Nature, January 2023 [Middle author]

PROFESSIONAL ORGANIZATIONS

- National Society of Black Engineers (NSBE)
- American Women in Science (AWIS)