Favour N. Esedebe, PhD

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SUMMARY

Applied scientist specialized in developing machine and deep learning approaches to analyze multi-omics datasets in translational cancer research. Experienced in building reusable pipelines and collaborating across interdisciplinary teams to study resistance mechanisms and identify vulnerabilities. Interested in developing computational methods to support disease modeling and precision medicine in hematologic malignancies.

SKILLS AND TECHNIQUES

- **AI/ML**: Supervised & Deep Learning, Transformers, LLMs, Fine-Tuning, RAG, Model Evaluation
- **Languages & Tools**: Python, R, Git, Bash, Jupyter, Snakemake, CI/CD, HPC/Cloud (AWS, GCP)
- **NGS Data**: Transcriptomics (Bulk, Single Cell, Spatial), Functional Genomics, Pathology Images, WGS, Chip-Seq
- **Frameworks & Libraries:** PyTorch, HuggingFace, scikit-learn, Seurat, Bioconductor, Pandas, Plotly

PROFESSIONAL EXPERIENCE

Applied Scientist **Sept 2025 – Present**

Norebase, AI R&D *Remote (US)*

- Designed retrieval and extraction pipelines to automate identification of relevant information from complex biomedical documents, with applications to regulatory and clinical trial data.
- Fine-tuned open-weight language models for regulatory text simplification and deployed inference behind standardized API, with reproducible model loading and configuration.

Research Scientist – Bioinformatics PhD Fellow **Sept 2019 – June 2025**

University of California Los Angeles (UCLA) *Los Angeles, CA*

- Developed R/Python pipelines to analyze bulk, single cell, and spatial transcriptomics across longitudinal and cross-cohort datasets from patient and patient-derived xenografts (PDX) tumors.
- Fine-tuned BioBERT transformer classifiers to identify conserved pathway dysregulation across cancers, improving macro-F1 by ~30 points over baselines.
- Trained ensemble machine learning models (XGBoost, random forest) to detect aggressive subpopulations and derive gene signatures for biomarker discovery.
- Built Snakemake workflows to apply predictions across longitudinal cohorts, validating against functional dependency cell-line data to reveal vulnerabilities associated with therapy resistance.
- Combined H&E histopathology with spatial transcriptomics to identify morphologically distinct tumor regions linked to treatment resistance and enriched in independent bulk cohorts.
- Produced automated data visualizations in collaboration with clinicians, experimental biologists, and immunologists to validate computational outputs with histology and functional assays.

Bioinformatics PhD Intern **Aug 2023 – Dec 2023**

Eli Lilly & Company, Lilly Genetic Medicine (LGM) *Indianapolis, IN*

- Built pipeline to detect off-target effects in therapeutic design from RNA-seq data, reducing manual analysis time.
- Generated visual reports to mark toxic pathways and processes, prioritizing safer candidates in RNA therapeutics.
- Communicated implications to cross-functional groups, translating findings into actionable recommendations.

Data Analyst **Aug 2017 – Aug 2019**

UCLA – Jonsson Comprehensive Cancer Center *Los Angeles, CA*

- Developed predictive and statistical models to uncover cross-disease feature patterns and guide target selection.
- Analyzed public large-scale omics datasets (TCGA, DepMap) and created reusable code libraries that standardized feature extraction and modeling workflows across teams.

EDUCATION

Ph.D., Bioinformatics **June 2025**
UCLA *Los Angeles, CA*

- Dissertation: Computational approaches to investigate chemotherapy resistance in aggressive cancers
- Coursework: Machine Learning for Bioinformatics, Algorithms & Statistical Methods in Computational Biology

B.S., Biochemistry & Molecular Biology, Computer Science **May 2017**
Fisk University *Nashville, TN*

- Achievements: summa cum laude, Phi Beta Kappa
- Coursework: Data Structures and Algorithms, Operating Systems, Computer Architecture, Linear & Matrix Algebra

LEADERSHIP, COMMUNITY ENGAGEMENT, AND PROFESSIONAL SOCIETIES (SELECTED)

- Member, American Medical Informatics Association (AMIA) 2026 – Present
- Member, Toastmasters International 2025 – Present
- Member, International Society for Computational Biology (ISCB) 2024 – Present
- Member, National Society of Black Engineers (NSBE) 2023 – Present
- Associate Member, American Association for Cancer Research (AACR) 2023 – Present
- Leadership & Outreach Team; Mentor, QBio-Edge, UCLA 2021 – Present
- Bioinformatics Mentor & Team Lead, UCLA 2018 – 2025
- Marketing Analyst, Media & Marketing Team, Biotech Connection Los Angeles (BCLA) 2023 – 2024

HONORS AND AWARDS (SELECTED)

- Scientist Mentoring and Diversity (SMDP) Biotech Scholar 2024 – 2025
  - Selected for mentorship program pairing PhD students with biotech industry leaders.
- University of California–Historically Black Colleges and Universities (UC–HBCU) Initiative Fellowship 2019 – 2025
  - Awarded six-year fully funded PhD package, covering tuition, fees, and stipend.

PUBLICATIONS AND PATENT

1. **Esedebe FN***, Singh T*, Liao YJ, Borujerdpur A, Dibernardo GA et al. Small cell neuroendocrine features are enriched in RB-deficient recurrent high-grade serous ovarian carcinomas. *Submitted to Cancer Cell*. 2026.
2. **Esedebe FN**. Computational Approaches to Investigate Adaptive Small Cell Neuroendocrine Features in Recurrent High-Grade Serous Ovarian Carcinomas. PhD Dissertation, UCLA, 2025.
3. Huerta-Yepez S, …, **Esedebe FN** et al. Supercharged NK cells, unlike primary activated NK cells, effectively target ovarian cancer cells irrespective of MHC-class I expression. *BMJ Oncology.* 2025 Apr 5; 4(1): e000618.
4. Varuzhanyan G, Chen CC, Freeland J, He T, Tran W, Song K, Wang L, Cheng D, Xu S, Dibernardo GA, **Esedebe FN** et al. PGC-1α drives small cell neuroendocrine cancer progression toward an ASCL1-expressing subtype with increased mitochondrial capacity. *Proc Natl Acad Sci USA.* 2024 Nov 26; 121(49): e2416882121.
5. Graeber TG, Balanis NG, Sheu KM, Witte ON, **Esedebe FN**, Park JW. Methods for treating small cell neuroendocrine and related cancers. WO Patent 2020243329A1. Published December 3, 2020.
6. Wang L, Smith BA, Balanis NG, ..., Esedebe FN, et al. A genetically defined disease model reveals that urothelial cells can initiate divergent bladder cancer phenotypes. Proc Natl Acad Sci USA. 2020 Jan 7; 117(1): 563-572.
7. Balanis NG*, Sheu KM*, **Esedebe FN**, et al. Pan-cancer convergence to a small-cell neuroendocrine phenotype that shares susceptibilities with hematological malignancies. *Cancer Cell.* 2019 Jul 8; 36(1): 17-34.e7.