

Michael Akpabey, MS

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Professional Summary

Computational Biologist developing quantitative and machine-learning methods for functional genomics, perturbation biology, and drug discovery, with training in toxicology and translational science. Lead large-scale perturbation and multi-omics analyses that support target prioritization, mechanism-of-action inference, and experimental decision-making, using reproducible Python/R workflows across Nextflow, HPC, and cloud environments.

Skills

Computational Biology: Functional genomics, CRISPRi/perturbation screens, multi-omics integration, enrichment analysis

Quantitative Methods: Statistical modelling, clustering, dimensionality reduction, dose-response modeling, experimental design

ML & AI: scikit-learn, PyTorch, Representation Learning, Graph Neural Networks, Fine-Tuning, Benchmarking, , RAG/LLM, MLOps

Scientific Computing: Python, R, SQL, Bash, Nextflow, Docker, HPC, AWS, Azure, Git/GitHub, RDKit, Scanpy, Shiny, Streamlit

Professional Experience

Broad Institute of MIT and Harvard

June 2024 - Present

Computational Biologist II

- Lead computational development for **PROSPECT**, analyzing **100K+ small-molecule compounds** in pooled *M. tuberculosis* perturbation screens through barcode QC, dose-response modeling, clustering, hit prioritization, and mechanism-of-action inference, prioritizing the **top 1%** high-confidence candidates for experimental follow-up.
- Develop quantitative methods for **target and mechanism-of-action analysis**, including gene-set curation and weighted, null-comparison, and threshold-free ranking approaches to benchmark biological signal against known antibiotic mechanisms.
- Built a **10B+ compound virtual-screening pipeline** for mechanism-of-action inference and candidate prioritization, guiding selection-algorithm design and evaluating alternative strategies for scaffold generalization and biological relevance.
- Developed a deterministic **medicinal-chemistry triage** system integrating structural liabilities, drug-likeness metrics, applicability-aware ADMET predictions, and TB chemical precedent into a reproducible human-review workflow for final compound selection.
- Build provenance-aware biological knowledge systems integrating genomic, metabolic, and pathway evidence, using graph-based approaches to identify gene relationships and support **LLM-assisted hypothesis generation**.
- Partner with experimental scientists across screening QC and assay development, diagnosing contamination, replicate concordance, barcode-count, pool-structure, and dose-response issues to guide **go/no-go** decisions and follow-up experiments.
- Optimized microbial genomics workflows across **15M+** sequences and **11+** taxa, using API-driven retrieval, probabilistic filtering, and parallelization to reduce diagnostic turnaround by **2+ days**.

University of Michigan School of Public Health

Aug 2022 – May 2024

Bioinformatic Research Associate

- Integrated adolescent RNA-seq and cord-blood DNA **methylation** data to identify exposure-associated molecular signatures of prenatal heavy-metal toxicity, linking transcriptomic and epigenetic changes to immune and neurodevelopmental pathways.
- Built automated RNA-seq pipelines spanning FASTQ QC, alignment, and count generation, increasing processing speed by **50%** and improving reproducibility across **250+ pediatric biospecimens**.

Charles River Laboratories Intl.

May 2021 – June 2022

Surgical Research Technician

- Supported **IND-enabling preclinical studies** by performing pharmacokinetic and toxicology assessments in non-human primates, generating high-integrity data for drug candidates across multiple therapeutic areas in compliance with **GLP and FDA** standards.

Projects

Spatial Transcriptomics GCN: Developed a graph convolutional network integrating spatial and gene-expression features from breast tissue to predict metastatic potential, achieving AUROC 0.91.

Education

University of Michigan, Ann Arbor: Master of Science in Bioinformatics; Master of Science in Toxicology, 2022 - 2024

Calvin University: Bachelor of Science in Biological Sciences, 2017 - 2021

Publication

Akpabey, M. *Transcriptomic and Epigenetic Alterations Induced by Pre-natal Heavy Metal Exposures in Pediatric Populations: Assessed at Adolescence (2024)* [DOI: 10.7302/27924](https://doi.org/10.7302/27924). Keywords: Biomarkers, Neurotoxicity, Toxicology, Immunology.