JAMILLA **AKHUND-ZADE**

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SUMMARY

Staff Bioinformatics Scientist with 9+ years of experience applying **machine learning, biostatistics, and bioinformatics** to multi-omics sequencing data in clinical diagnostics and genomics. Expert in designing and validating **computational pipelines for cfDNA/cfRNA sequencing and metagenomics**. Skilled in **experimental design under regulatory frameworks (CLIA/CAP)**, statistical modeling, and AWS-based workflows. Ph.D. in Molecular and Cellular Biology (Harvard). Passionate about advancing diagnostic products using data-driven insights from multi-omics signatures of disease.

SKILLS

Programming & Data Science: Python, R, Stan
Workflow & Automation: Nextflow, Bash, Docker
Cloud & HPC: AWS (Batch, EC2, S3), Slurm, High-Performance Computing
Statistical Modeling: GLMs, mixed-effects, hierarchical models, Bayesian inference
Machine Learning: Feature extraction, PCA, clustering, classification methods
Bioinformatics: NGS analysis, variant calling, GWAS, metagenomics

EDUCATION

Ph.D.	**Harvard University**	Molecular and Cellular Biology	May 2020
B.A.	**Cornell University**	Biology (Phi Beta Kappa)	May 2014

EXPERIENCE

Staff Bioinformatics Scientist, Assay Development, Karius, Inc. **Mar 2025 – present**

- Designed and optimized bioinformatics pipelines (Python/Nextflow/AWS Batch) for cfDNA/cfRNA sequencing, advancing next-generation infectious disease diagnostics
- Developed statistical methods to estimate true gene expression signals from mixed nucleic acid background
- Developed automated workflows and a Python library for push-button CLIA/CAP analytical validation, improving transparency and reducing turnaround time

Senior Bioinformatics Scientist, Assay Development, Karius, Inc. **Mar 2022 – Mar 2025**

- Led assay development of a novel antimicrobial resistance diagnostic test within a cross-functional team, applying statistical frameworks to guide experimental design and product decisions
- Sole owner of the planning, execution, and analysis of a laboratory-developed test analytical validation for CLIA/CAP
- Designed and optimized bioinformatics pipelines (Python/Nextflow) for cfDNA-based antimicrobial resistance detection

Bioinformatics Scientist, Karius, Inc. **Sep 2020 – Mar 2022**

- Applied machine learning to metagenomic sequencing data to identify disease-specific signatures
- Built computational tools for extracting clinically relevant features from microbial cfDNA
- Conducted retrospective analyses of liquid biopsy test performance, identifying product improvements

Ph.D. Researcher, de Bivort Lab, Harvard University **Aug 2014 – May 2020**

- Designed and implemented custom pipelines (Python, SAMtools, GATK, Picard) for population-level genomics analyses on HPC clusters
- Implemented Bayesian inference models in Stan, including hierarchical models, to quantify components of behavioral individuality