Muhammad Ekramah

Bioinformatics Graduate | Genomics and Computational Biology

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Portfolio: itsekramah.github.io | **GitHub:** github.com/itsEkramah

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Profile

Bioinformatics graduate from Quaid-i-Azam University with a background in genomics, biostatistics and computational biology. My academic work has included machine learning for antimicrobial-resistance prediction, RNA-seq analysis and biological software development. During my research internship at the National Institutes of Health, I also worked with antimicrobial-resistance surveillance data. These experiences strengthened my interest in using computational methods to study biological questions. I hope to develop stronger statistical and computational skills through postgraduate study and apply them to genomic and biomedical data.

Education

Bachelor of Science in Bioinformatics *Sep 2022 – Sep 2026*

National Centre for Bioinformatics, Quaid-i-Azam University, Islamabad, Pakistan

CGPA: 3.40/4.00

Relevant coursework: Probability and Biostatistics; Bioinformatics Computing; Genomics; Functional Genomics; Systems Biology; Artificial Intelligence; Data Structures and Algorithms; Modelling and Simulation; Database Management Systems.

Higher Secondary School Certificate (Pre-Medical) *Mar 2020 - Jul 2022*

Federal Board of Intermediate and Secondary Education (FBISE), Islamabad, Pakistan

Selected Academic Projects

Antimicrobial-resistance prediction in *Neisseria gonorrhoeae* GitHub Repository

Bioinformatics Computing II | 2025–2026

- Worked with genomic unitigs and 3,786 metadata records, matching labelled isolates to antibiotic-specific features for azithromycin and ciprofloxacin resistance prediction.
- Compared logistic regression and random forest against a prevalence baseline. Used five-fold cross-validation grouped by identical genomic profiles, with variance filtering and chi-square feature selection within training folds.
- Examined class imbalance, bootstrap confidence intervals and geographic differences in model performance. Logistic regression achieved internal balanced accuracy of 0.949 for azithromycin and 0.969 for ciprofloxacin.
- Used BLAST to examine selected unitigs, including alignments to regions associated with *penA* and *gyrA*. The supplied unitigs had already been GWAS-filtered, so the predictive results still require independent validation.

RNA-seq analysis of Notch2 knockout neural stem cells GitHub Repository

Genomics project | 2025–2026

- Analysed the public GSE116773 dataset to compare Notch2 conditional-knockout and wild-type mouse hippocampal neural stem cells. Combined 24 technical count files into six biological RNA preparations, three per condition.
- Used PyDESeq2, negative-binomial modelling and Benjamini–Hochberg correction. Identified 121 genes at FDR < 0.05 among 21,531 retained genes (77 higher and 44 lower in knockout samples).
- Explored sample differences using PCA, sample-distance plots and gene-expression plots. WT3 differed from the other samples, an important consideration given the small number of biological replicates.

Selected Academic Projects (continued)

PathoScope AI: viral genomics and transcriptomics prototype GitHub Repository | Video demo

Functional Genomics team project | Mar–Aug 2026

- Worked with a team on a web-based prototype using FastAPI, PostgreSQL and a Next.js interface. My contributions focused on workflow execution, FASTQ integration, PubMed retrieval and report generation.
- Worked on sequential pipeline steps, job-status tracking, database connectivity and literature retrieval using NCBI E-Utilities. The team integrated read-processing tools including FastQC, fastp and SPAdes.
- The prototype also includes ORF scanning, protein annotation tools and an exploratory gene-expression module. Some fallback functions use simulated results; the software is not a validated diagnostic pipeline.

Experience

Research Intern *Jul–Aug 2025*
National Institutes of Health (NIH), Islamabad, Pakistan

- Used R and the `AMR` package to analyse antimicrobial-resistance surveillance data, including wastewater data, and summarise susceptibility patterns.
- Gained exposure to PCR-based diagnostics, Oxford Nanopore MinION sequencing and bulk RNA-seq workflows.

Python Developer Intern *Jul–Sep 2024*
Digital Empowerment Network | Remote

- Worked on Python backend services and REST APIs using FastAPI and PostgreSQL.
- Automated data cleaning and processing with Pandas and NumPy, and developed visualisation utilities for GitHub Classroom analytics as part of a team.

Technical Skills

Programming	Python (Biopython, Pandas, NumPy, scikit-learn), R, Bash, SQL
Statistics and data	Classification; grouped cross-validation; feature selection; bootstrap intervals; PCA; differential-expression analysis; multiple-testing correction
Bioinformatics	Genomic unitigs; bulk RNA-seq; BLAST; PyDESeq2; DESeq2; FastQC; fastp; HISAT2; featureCounts
Software	Git/GitHub; Jupyter; FastAPI; PostgreSQL; Linux
Data resources	NCBI GEO/SRA; PubMed; Ensembl; UniProt and Pfam (team-project use)
Wet-lab exposure	DNA extraction; PCR-based diagnostics; Oxford Nanopore MinION sequencing; molecular biology laboratory workflows

Languages

Urdu	Native
English	Academic and professional working proficiency; IELTS Academic scheduled for 30 November 2026
German	Beginner (A1; no formal certification)

Research Interests

My interests include computational genomics, transcriptomics, antimicrobial resistance and biomedical data analysis. I am particularly interested in applying statistical and machine learning methods to biological datasets, understanding disease-related molecular changes and evaluating whether computational findings remain reliable across independent datasets.