

# Atharva Tikhe

+44 735-380-3171 | a.tikhe2@newcastle.ac.uk | linkedin

## BACKGROUND

Bioinformatics engineer with proven experience in modernising and developing robust, large-scale bioinformatics pipelines. Highly skilled in Python, with direct experience in migrating a proprietary variant annotation pipeline from Perl to Python, enhancing performance and maintainability. Proficient in workflow development with Nextflow, containerisation with Docker, and CI/CD practices. Strong background in human genetics, genomics, and processing various NGS data types (WGS, WES). Completing second masters in bioinformatics in Sept 2026 from Newcastle University

## EDUCATION

<b>MSc. in Bioinformatics</b> Newcastle University	Newcastle upon Tyne, UK Sep 2025 – Sep 2026
<b>Int. MTech. in Bioengineering (University Gold medalist - Rank 1)</b> MIT-ADT University	Pune, IN Aug 2019 – Jun 2024

## EXPERIENCE

<b>Teaching Resource Content Creation Intern</b> <i>School of Medicine, Newcastle University</i>	Nov 2025 - Present Newcastle, UK
• Assist in generation of visual assets for CPD courses within the school of medicine	
• Manage Canvas pages and APIs for the course content	
<b>Bioinformatics Engineer</b> <i>MedGenome Labs Inc.</i>	May 2024 – Aug 2025 Bangalore, IN
• Optimised internal proprietary variant annotation pipeline by migrating perl codebase to python.	
• In-charge of design, development and deployment of 1X-PRS (phasing, imputation, PRS-GWAS) pipeline in nextflow. The pipeline reduced sample processing time by 81%.	
• Orchestration of various internal pipelines using nextflow on PBS-Torque and AWS Batch.	
• Designed, wrote and deployed a web-app for internal primer design/QC protocols which achieved primer screening outcomes 2X faster.	
• Validation and normalization of on-board DRAGEN results from Illumina NovaSeq sequencer.	
• In-charge of design, development and deployment of 3 core pipelines reducing per sample processing times by 2X on average.	
• Wrote an optimization plugin for nextflow in Java/Groovy to smartly cleanup work folders reducing storage by 300GB per GWAS sample.	
<b>Bioinformatics Intern</b> <i>GreenArray Genomic Research &amp; Solutions</i>	Jan 2024 – May 2024 Pune, IN
• Dissertation: Nextflow pipeline for clinical variant calling of WES data.	
• In-charge of development and deployment of 16S rRNA metagenomics pipeline with automated reporting which sped up report-to-customer times by 1.5X	
• Carried out research on assemblers and binners thereby improving species level analysis of vaginal 16S rRNA samples implicated in early-pregnancy related complications.	
<b>Bioinformatics Intern</b> <i>Evolvus Biotech PVT. LTD.</i>	Jun 2021 – Dec 2021 Pune, IN
• Analysed large-scale data for customers.	
• Assisted in crucial customer data pre-processing and data delivery.	

## TECHNICAL SKILLS

**Programming Languages:** Python, Bash, R, Rust, Perl (for migration)

**Bioinformatics Workflow Managers:** Nextflow, snakemake

**Tools & Platforms:** Docker, Git, CI/CD (Jenkins, GitHub Actions), AWS (Batch, EC2, RDS), HPC (PBS/Torque), Linux

**Bioinformatic analyses/tools:** WGS/WES analysis, Variant Annotation, GATK suite, GLIMPSE2, PLINK2, RNASeq, sentieon/DRAGEN

**Web Development:** HTML/CSS/JS, SvelteKit, Flask, FastAPI