

# Chirag Khandelwal

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## SUMMARY

Bioinformatics engineer skilled in **developing cloud-native, reproducible pipelines** for genomics and transcriptomics. Proficient in AWS (S3, EC2, Lambda, HealthOmics), Docker/Kubernetes, Nextflow/Snakemake, and CI/CD. Experienced in **NGS variant calling (GATK, SAMtools, bcftools)** and large-scale data integration (Ensembl, UCSC Genome Browser). Strong collaborator applying software engineering best practices to accelerate clinical and research insights.

## EDUCATION

**M.S., Biological Data Science**, Arizona State University — **GPA: 3.6/4.0** May 2025

**B.S., Pharmaceutical Sciences**, Vishwakarma Institute of Technology — **CGPA: 8.1/10** May 2023

## PROFESSIONAL / RESEARCH EXPERIENCE

**Research Assistant (NIH-funded)** — *Maley Lab, ASU* Aug 2025 – Present

- Developed **Dockerized Nextflow pipelines** on Slurm for WGS/WGBS; implemented **CI/CD (GitHub Actions)** to auto-test and deploy updates, cutting reruns by **40%**.
- Optimized **CHESS.cpp tumor simulation** workflows; built a **Flask + RShiny web app** for interactive parameter tuning and visualization to speed collaborator iteration.
- Applied **Bayesian/phylogenetic models** (BEAST, PISCA) to estimate stem-cell turnover and mutation rates; outputs supported NIH grant proposals.
- Standardized variant workflows using **GATK, SAMtools, bcftools, VEP/ANNOVAR**; validated against **Ensembl** and **UCSC Genome Browser** references.

**Translational Research Fellow** — *Arizona State University* Jan 2024 – Present

- Built **de novo genome assembly/annotation** pipelines (PacBio/ONT) on HPC/AWS orchestrated with **Nextflow + Docker**.
- Automated **Hi-C** analysis using **HiC-Pro, HiC Genome Assembler**, and **RepeatMasker/RepeatModeler** to characterize chromosome structure.
- Developed reproducible **scRNA-seq/bulk RNA-seq** workflows (QC, normalization, clustering, DE) in R/Python; applied RF/SVM to detect immune activation.
- Produced publication-ready **network visualizations** (Cytoscape/igraph); integrated outputs with **MSigDB, Ensembl, UCSC** for interpretation.

**Bioinformatics Intern (NGS/Clinical)** — *Ruby Hall Clinic* May 2023 – Jul 2023

- Designed clinical pipelines (FASTQ->BAM->VCF) using **BWA, GATK, and SAMtools**; benchmarked CNV tools to improve reporting confidence.
- Enhanced QC and reporting with **MultiQC**; improved reliability of variant calls used in oncology decisions.

## PROJECTS

**Single-Cell RNA-Seq Analysis of Rheumatoid Arthritis** Nov 2024 – May 2025

- Created reproducible **Scanpy** workflow with doublet detection (SOLO/scrublet), **scVI/Harmony** integration, clustering/annotation, and **fgsea/clusterProfiler**.
- Identified immune cell-type shifts linked to disease progression; findings shared with collaborators for biomarker discovery.

## TECHNICAL SKILLS

- Programming:** Python, R, C/C++, Bash, SQL
- Workflows/Infra:** Nextflow, Snakemake, Docker, Kubernetes, Git/GitHub, **CI/CD**, Slurm, **AWS** (S3, EC2, Lambda, HealthOmics)
- Variant & Repertoire:** GATK (Mutect2/HaplotypeCaller), **SAMtools**, bcftools, VCFtools, **VEP/ANNOVAR**; BCR/TCR (MiXCR, TRUST4, scirpy/scRepertoire)
- Epigenetics:** bismark, methylKit, bsseq; DMR calling and integration with expression
- Data QC & Visualization:** FastQC/MultiQC; ggplot2/tidyverse, matplotlib; Cytoscape/igraph; PCA/UMAP/t-SNE; references: **Ensembl, UCSC, MSigDB**

## PUBLICATIONS

Khandelwal C. *Natural Remedies for Onychomycosis: A Review*. **J Nat Remedies** 23(4), Oct 2023.

In progress: *Trophic levels explain the inverse association between genetic variation and neoplasia in mammals*.