# VIPIN SURENDRA KUMAR

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**Bioinformatician | Bioinformatics Analyst | Genome Analyst**

## PROFESSIONAL SUMMARY

Bioinformatics postgraduate (M.Sc.) with hands-on experience in WGS/WES, RNA-seq, metagenomics and nutrigenomics data analysis. Skilled at building reproducible Nextflow, Python and Bash pipelines in Linux, and at turning complex genomic data into clear insights. Seeking a Bioinformatics Associate role in genomic data analysis, pipeline optimization and statistical genomics.

## PROFESSIONAL EXPERIENCE

**Bioinformatics Analyst-I** Aug 2026 – Present
*Decipher Genomics and Research, Sanand, Gujarat*

- Design, implement and maintain bioinformatics workflows for NGS, nutrigenomics and targeted genotyping applications.
- Develop data models for gene–diet interactions, SNPs and lifestyle-associated risk factors, turning results into actionable health and wellness insights.
- Automate and optimize pipelines with workflow management tools to improve scalability, efficiency and reproducibility.
- Collaborate with molecular scientists, clinicians and data engineers to integrate bioinformatics insights into product solutions.
- Prepare technical documentation, analytical reports and presentations for internal and external stakeholders.

**Bioinformatician Intern** Jan 2026 – Jul 2026
*Decipher Genomics and Research, Sanand, Gujarat*

- Analyzed amplicon (16S/ITS) and shotgun sequencing datasets, including taxonomic profiling and functional analysis.
- Built and optimized pipelines for quality control, read alignment and variant analysis.
- Managed large-scale datasets in Linux/Unix; worked with CEL, FASTA, FASTQ, BAM and VCF formats.
- Assisted in genome annotation and prepared technical reports for research and internal review.

**Research Intern** Dec 2023 – Apr 2024
*Bionome, Bengaluru, Karnataka*

- Performed molecular docking and computational analysis of Plumbago zeylanica compounds targeting dopamine D2 receptors in schizophrenia.

## OPEN-SOURCE TOOL DEVELOPMENT

**V13Shield – Pharmacogenomic Toxicity Screening Tool** | GitHub | Docker Hub

- Built a containerized tool that screens germline VCF files for CPIC-documented pharmacogene variants (DPYD, TPMT, NUDT15, UGT1A1) linked to severe chemotherapy toxicity.
- Developed the variant-matching engine, automated risk classification and interactive HTML reports with graphical visualizations.
- Released under the MIT License on GitHub and Docker Hub, with Docker and Singularity/Apptainer support for reproducible deployment.

## TECHNICAL SKILLS

- **Whole Exome Sequencing:** FASTQ QC, trimming, alignment, duplicate marking, variant calling, filtering and annotation of SNVs/INDELs. Tools: FastQC, Fastp, Trimmomatic, BWA-MEM, SAMtools, Picard, GATK, BCFtools, ANNOVAR, VEP, IGV.
- **RNA-seq:** QC, alignment, quantification, normalization, differential expression. Tools: STAR, HISAT2, featureCounts, StringTie, DESeq2, edgeR, MultiQC.
- **Amplicon Metagenomics (16S/ITS):** denoising, ASV/OTU generation, taxonomy, alpha/beta diversity. Tools: QIIME2, DADA2, VSEARCH, SILVA, Greengenes, UNITE, Krona.
- **Shotgun Metagenomics:** host read removal, taxonomic profiling, functional and pathway analysis, assembly. Tools: KneadData, Kraken2, Bracken, MetaPhlAn, HUMAnN3, MEGAHIT, Bowtie2.
- **PacBio Long-Read:** QC, preprocessing, assembly support, polishing, structural variants. Tools: bam2fastx, NanoPlot, minimap2, SAMtools, StringTie, ASpli.
- **ChIP-seq:** alignment, duplicate removal, peak calling, annotation, visualization. Tools: BWA-MEM2, Picard, MACS2, bedtools, deepTools, IDR, pyGenomeTracks.
- **Workflow and Reproducibility:** Nextflow, Python, Bash, Docker, Singularity, Git, Linux/Unix.
- **Programming and Analysis:** Python (Pandas, NumPy, Keras), R (data analysis, R Markdown, visualization), microarray analysis, microbial identification pipelines.
- **Network and Systems Biology:** STRING, Cytoscape.

## PROJECTS

- In Silico Design of a Multi-Epitope Vaccine for Zaire Ebola Virus (dissertation)
- NGS-Driven Metagenomic Profiling and Unsupervised Learning Reveal Hidden Microbial Structures in the Tomato Rhizosphere (dissertation)

## EDUCATION

**M.Sc. in Bioinformatics** | Garden City University, Bangalore | 2024 – 2026

**B.Sc. in Bioinformatics** | MES M.K. Mackar Pillay College for Advanced Studies, Edathala, Aluva, Kerala | 2021 – 2024

## PRESENTATIONS AND CONFERENCES

- Oral presentation, "In Silico Design of a Multi-Epitope Vaccine for Zaire Ebola Virus": RTIMR 2025, Thiruvalluvar University, Vellore (Aug 2025)
- Oral presentation, same topic: IKS-HORIZONS 2025, Seshadripuram First Grade College (Oct 2025)
- Participant: Biorujivith 2025, International Conference on Cancer Research and Integrative Medicine (ICCRIM), Garden City University (Nov 2025)

## CERTIFICATIONS

- Primer Designing and qPCR for Molecular Expression Profiling and Data Analysis, VIT-TBI
- Design Sprints: A Rapid CADD, Dr. Omics Lab
- Programming in Python, Meta
- Algorithms for DNA Sequencing, Johns Hopkins University
- Machine Learning for All, University of London

## LANGUAGES

English (Professional), Hindi (Conversational), Malayalam (Native), Tamil (Conversational)