ADITHYA S

BIOINFORMATICIAN

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E X P E R I E N C E

PROJECT- TRANSCRIPTOME DATA ANALYSIS TO IDENTIFY THE RELATION BETWEEN ADIPOGENESIS AND ANGIOGENESIS   Present

SELF PROJECT IN VARIANT CALLING

VARIANT CALLING-germline variants in a human WGS paired end reads using GATK Good Practice Workflow

Developed a complete variant calling workflow for identifying genomic variants from NGS data. The pipeline involved raw sequence quality assessment, adapter and low-quality base trimming, alignment of reads to the reference genome (hg38), sorting and indexing of BAM files, and variant detection using GATK. Post-processing included variant filtration and annotation to identify SNPs and INDELs. The project strengthened understanding of data preprocessing, alignment strategies, and variant interpretation in genomics.

DEGREE PROJECT WORK

E D U C A T I O N

M.Sc. Computational Biology ↗   08/2024 - Present

Department of Computational Biology and Bioinformatics, University of Kerala

Specialization: Next-Generation Sequencing (NGS) Data Analytics.Relevant Coursework: Bioinformatics, Genomics, Big Data in Biology, and Machine Learning for Biological Systems.

B.Sc. Biochemistry ↗   06/2021 - 06/2024

Government of College Kariavattom , University of Kerala

S K I L L S

Leadership	PCR
Communication	DNA Isolation
RNA seq analysis	Phytochemical Analysis
Variant interpretation	Clinical Biochemistry
Genome Alignment	Gel Electrophoresis
SPAdes and QUAST	NGS tools
Shell Scripting Using Bash	Variant Calling using GATK
Perl Programming Language	HTML,CSS,JS
Python	R Programing language

L A N G U A G E S

English	Hindi

Tamil

Malayalam