



# Foundations of Bioinformatics and Computational Biology Training Program

Gain expertise in bioinformatics fundamentals, computational biology, and omics data interpretation through real-world practical sessions.

## Foundations of Bioinformatics & Computational Biology

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### Session 1

**Fee: Rs 4500** [Apply Now](#)

### Unix, Data Formats & Reproducibility

Linux shell essentials: grep, awk, sed pipelines

[GNU](#) [coreutils](#) [grep](#) [awk](#) [sed](#) [bash](#) [tmux](#)

File integrity: checksum & metadata management

[sha256sum](#) [md5sum](#) [exiftool](#) [rsync](#)

Core bioinformatics formats: FASTA, FASTQ, GFF3, BED, VCF

[Theory](#)

Programmatic data retrieval from NCBI/EBI/UniProt

**NCBI EDirect** **Entrez (Biopython)** **wget** **curl**

Environment isolation using Conda

**Conda** **Mamba** **Micromamba**

Jupyter reproducible notebook setup

**JupyterLab** **nbconvert** **Papermill** **Python**

### **Session 2**

**Fee: Rs 6000** Apply Now

## Algorithms: Similarity, Alignment & Scoring

Needleman–Wunsch vs Smith–Waterman alignment comparison

**Theory**

PAM/BLOSUM matrix handling and interpretation

**Theory**

Local BLAST setup & custom database building

**NCBI BLAST+** **makeblastdb** **DIAMOND**

Multiple sequence alignment (Clustal Omega, MUSCLE)

**Clustal Omega** **MUSCLE** **MAFFT**

Format conversions and consensus generation

**seqkit** **seqtk** **EMBOSS seqret** **EMBOSS cons**

Automated batch alignment reporting

**Biopython** **pandas** **matplotlib**

### **Session 3**

**Fee: Rs 8000** Apply Now

## Gene Structures & Functional Annotation

ORF detection and annotation using Prodigal

**Prodigal** **EMBOSS** **getorf**

Functional domain mapping with InterProScan

**InterProScan** **HMMER3** **Pfam**

Annotation transfer and evidence scoring

**DIAMOND** **BLAST+** **Prokka** **eggNOG-mapper**

Parsing and formatting GFF3/BED files

**bedtools** **gffread** **BCBio.GFF**

Quality checks for codon usage & frameshifts

**EMBOSS** **cusp** **CodonW** **FrameDP**

Preparing summary annotation reports

**pandas** **JupyterLab** **R** **Markdown/Quarto**

#### **Session 4**

**Fee: Rs 10000** Apply Now

### Mini Capstone: End-to-End Pipeline

Designing complete analysis workflow

**Theory**

Data import, QC, alignment & annotation automation

**Snakemake** **FastQC** **MultiQC** **BLAST+** **Prodigal**

Snakemake pipeline setup for reproducibility

**Snakemake** **Git** **Conda/Mamba**

Containerization with Docker

**Docker** **CE** **Podman** **Apptainer/Singularity**

Final report preparation and defense

**Quarto** **JupyterLab** **pandas**