biotecnika
Your Bio Resource

NEXT-GEN SEQUENCING & MULTI-OMICS DATA ANALYSIS TRAINING WITH PROJECT WORK

100% PLACEMENT ASSISTANCE

PAPER PUBLICATION ASSISTANCE

(Live Online Sessions)

Duration: 30 Days Training + 2 Months Project Work

Online Internship + Hands-on Project Work

Internship Completion & Project Work Experience Certificate

Toll free 1800-1200-1818 or 080-5099-7000

Detailed Curriculum

Module I: Introduction & Fundamental Concepts

Day 1: Orientation and Introduction to NGS

- Principle & Importance
- Historical context and evolution from Sanger sequencing
- Comparison with traditional sequencing methods

Day 2: NGS Workflow

- Library preparation, sequencing, and data analysis
- Library preparation steps: DNA fragmentation, adapter ligation, amplification
- Quality control measures

Day 3: NGS Platforms

- Overview of platforms: Illumina, Ion Torrent, Pacific Biosciences
- Read lengths, throughput, and applications
- Platform selection criteria

Day 4: Library Preparation Techniques

- Techniques for DNA, RNA, ChIP samples
- Protocols for whole-genome, RNA-seq, ChIP-seq libraries
- Troubleshooting and common challenges

Day 5: Introduction to Linux & Python/R

- Linux command-line basics
- Python/R scripting basics and data handling practice

Module II: Preprocessing, Alignment, Data Formats & Variant Calling

Day 6: Manipulation of Linux & Python/R in NGS Data Analysis

- Manipulation of Linux & Python/R in NGS Data Analysis
- Basic Linux commands and scripting
- Python/R basics for bioinformatics (Bioconductor, variables, loops)

Day 7: Data Formats & QC

- FASTQ, BAM, SAM, BED, VCF
- Phred quality scores, FastQC, MultiQC

Day 8: Adapter Trimming & QC

- Trimming algorithms: Trimmomatic, Cutadapt
- Adapter contamination handling

Day 9: Read Alignment

- BWA, Bowtie2, BWA-MEM
- Alignment to reference genomes (hg19, hg38)

Day 10: Sorting and Indexing

- SAM/BAM format, flags, and sorting/indexing
- Sorting and indexing with SAMtools

Day 11: Variant Calling, Annotation and Filtering

- SNVs, indels, VCF format, annotations (QUAL, DP), filtering

Day 12: Practical on Variant Calling

- Filter VCF with bcftools
- Annotation with VEP, Varsome

Module III: Gene Expression Analysis

Day 13: RNA-Seq Introduction

- Transcript quantification and differential expression

Day 14: RNA-Seq Data Preprocessing

- Practical: Demo on data preprocessing

Day 15: RNA-Seq Alignment

- Practical: Align reads using STAR aligner

Day 16: Count Matrices

- Generate gene-count matrices
- Normalization techniques: TPM, RPKM

Day 17: Practical on Count Matrix Generation

- FeatureCounts

Day 18: Differential Expression Analysis

- DESeq2/edgeR, fold change, p-value adjustment

Day 19: Practical on DEG Identification

- Run DESeq2 on count matrix

Day 20

- Practical on DEG Visualization and Reporting

Module IV: Applications of NGS

Day 21: NGS in Cancer, Genetics and Microbial Genomics

- Applications in oncology, rare diseases, and microbial genomics

Day 22: NGS in Drug Discovery and Clinical Settings

- NGS for Target Identification, Validation & Clinical Trials
- Future Directions of NGS in Drug Discovery & Challenges

Day 23: CRISPR-Cas9 Genome Editing

- Design sgRNAs using online tools
- Visualization of off-targets

Day 24: NGS in Agriculture

- Genomic breeding, disease resistance, microbiome analysis

Module V: Cloud-Based NGS Analysis

Day 25: Galaxy Server Demo

- Introduction to cloud-based NGS analysis
- Practical: RNA-seq walkthrough

Day 26: Single-Cell RNA-Seq Analysis and Demo

- Basics of scRNA-seq, dimensionality reduction (PCA, UMAP)
- Practical: scRNA-seq workflow on Google Colab

Day 27: 16S Metagenomic Analysis

- QIIME2, Kraken2, MetaPhlAn
- Practical demo with sample data

Day 28: Epigenomics Analysis

- Practical: Demo using Google Colab

Module VI: Exploring the Future – Prospects, Challenges, Ethics, Regulations and Career Guidance

Day 29: Future Directions, Challenges and Ethical Considerations

- Emerging trends (e.g., long-read sequencing, spatial transcriptomics)
- Ethics and regulatory frameworks (HIPAA, GDPR, FDA)

Day 30: Career Scope of NGS

- Opportunities in India and abroad
- Career counselling, research and industry prospects

2 MONTHS PROJECT WORK

Participants will work on one or more of the following projects, guided by experts. All projects involve real datasets and will culminate in deliverables for portfolio building.

1. Variant Calling Pipeline

- Dataset: 1000 Genomes Project
- Tools: FastQC, BWA, GATK, bcftools
- Deliverables: Cleaned BAM file, Filtered VCF, Report

2. RNA-Seq Differential Expression

- Dataset: GEO (e.g., GSE12345)
- Tools: STAR, featureCounts, DESeq2
- Deliverables: Count matrix, Volcano plot, DEGs report

3. ChIP-Seq Peak Calling

- Dataset: ENCODE (CTCF in HeLa)
- Tools: MACS2, IGV
- Deliverables: BED file, IGV snapshot, Summary

4. Single-Cell RNA-Seq Clustering

- Dataset: 10x Genomics PBMC
- Tools: Scanpy (Python), Seurat (R)
- Deliverables: UMAP plot, Marker genes, Interpretation

5. Metagenomic Taxonomic Profiling

- Dataset: Human Microbiome Project
- Tools: Kraken2, Bracken, Krona
- Deliverables: Taxonomic table, Krona chart, Diversity report

6. Functional Annotation of a Novel Genome

- Dataset: Assembled contigs (FASTA, NCBI)
- Tools: Prokka, BLAST, InterProScan
- Deliverables: GFF file, Functional table, Annotation summary

7. miRNA Expression Analysis

- Dataset: GEO (e.g., GSE266440)
- Tools: edgeR, limma, RStudio
- Deliverables: Heatmap, Significant miRNAs, Summary

8. Pathway Enrichment of DEGs

- Dataset: RNA-Seq DEGs or TCGA
- Tools: DAVID, GSEA, Enrichr
- Deliverables: Enrichment tables, Pathway plots, Interpretation

9. Protein-Ligand Docking Simulation

- Dataset: PDB structure, PubChem ligand
- Tools: AutoDock Vina, PyMOL
- Deliverables: Docking poses, Visualizations, Report

10. Comparative Genomics of Bacterial Strains

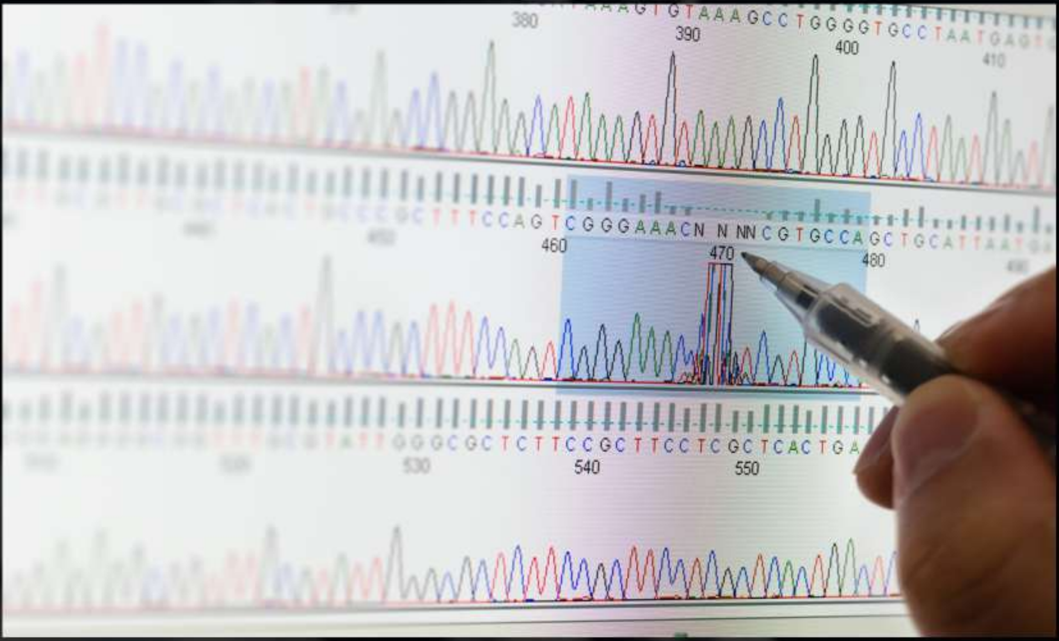
- Dataset: NCBI genomes
- Tools: Roary, MAUVE, OrthoFinder
- Deliverables: Core/accessory genes list, Alignment map, Functional summary

Why Join This Internship?

- Real-World Skill Development: Learn to analyze DNA/RNA sequencing data using industry-relevant tools and workflows
- Hands-On Projects: Work on real datasets with deliverables to showcase in your resume or academic portfolio
- Expert Mentorship: Sessions led by experienced trainers and bioinformatics professionals
- Career Guidance: Learn how to position your NGS skills for research and high-paying biotech roles
- Flexible Learning: Access session recordings and complete your project work at your own pace
- Recognized Certification: Get certified with Internship + Project Work credentials to boost your academic or career profile

Key Benefits

- 30+ hours of live instruction with recordings
- 10 optional mini-project tracks with datasets and tools
- Certification for internship + guided project work
- Access to open-source and cloud platforms
- Doubt-clearing support and guidance
- Resume-building assets including visual reports and project files



Career Prospects After Completing the Internship

With the rapid adoption of next-generation sequencing (NGS) technologies across research, clinical diagnostics, agriculture, and pharmaceutical sectors, skilled professionals in NGS and multi-omics data analysis are in high demand. Completing this internship equips you with the technical knowledge and practical experience needed to qualify for diverse and high-impact roles.

Top Job Roles You Can Target

- NGS Data Analyst
- Bioinformatics Scientist / Analyst
- Genomics Research Associate
- Computational Biologist
- Transcriptomics Data Scientist
- Cancer Genomics Researcher
- Clinical Genomics Analyst
- Molecular Biology Data Specialist
- NGS Application Scientist (Industry/Diagnostics)
- Single-Cell Bioinformatician
- Microbiome Data Analyst
- **Agrigenomics Researcher**

Top Companies Hiring in India

MEDGENOME

strand
New Generation Healthcare

NIBMG

SciGenom

Genotypic
genomics simplified

mapmygenome.in™
Know Yourself

TATA MD

xcelris™
WE MAKE DNA SPEAK

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& INTEGRATIVE BIOLOGY
Genomics Knowledge Partner

Top Global Employers

illumina®

10x GENOMICS

ThermoFisher SCIENTIFIC

BROAD INSTITUTE

QIAGEN

Pfizer

Stanford University

NOVARTIS

AstraZeneca

Oxford NANOPORE Technologies

Genentech
A Member of the Roche Group

Massachusetts Institute of Technology

NIH
National Institutes of Health

VE RI TAS
HARVARD UNIVERSITY

Industries Hiring NGS Professionals

- Biotechnology & Pharmaceutical R&D
-
- Hospitals & Clinical Diagnostic Labs
- Precision Medicine & Oncology Research Centers
- Agricultural Genomics Firms
- Microbiome & Metagenomics Startups
- Academic Research Institutes
- Genomic Software & Bioinformatics Service Providers

Course Instructors

Dr. Nilofer K Shaikh

With a strong background in big data analysis using computational approaches in cancer omics data, Ms. Nilofer K Shaikh brings a wealth of experience from MIT ADT University. Her expertise spans cancer research, drug design, molecular dynamics simulation, data mining, and various omics technologies. Proficient in Python, R, and computational methodologies, she has a deep understanding of genomics, metabolomics, proteomics, transcriptomics, pharmacogenomics, and AI for cancer treatment. Her skillset also includes machine learning, MySQL database management, and natural language processing (NLP

Course Instructors

Dr. Elamathi

Dr. Elamathi Natarajan is a dedicated bioinformatician with a robust background in computational biology, data analysis, and genomics. Holding a Doctorate in Bioinformatics from Dr. A.P.J Abdul Kalam Technical University and an MBA in Information Systems Management, she has made significant contributions to the field through both research and teaching. she has served as an Assistant Professor and Head of Department (HOD) In-Charge at Kalinga University, Raipur, where she excelled in lecturing, research, and departmental management. At Biotecnika Info Labs Pvt Ltd, Bangalore, she played a key role in academic support, enhancing student success through coaching and program development.

Elamathi's expertise includes developing bioinformatics pipelines, conducting quality assessments, and applying machine learning algorithms to genomics data. Recognized for her work, including a Senior Research Fellowship from the Indian Council of Medical Research (ICMR), she continues to drive innovation in bioinformatics and is seeking a new challenge to further advance scientific discoveries.

Course Instructors

Mr. Prodyot Banerjee

Prodyot Banerjee is a seasoned professional in Computer-Aided Drug Designing, Bioinformatics Analysis, and Genomics, boasting rich experience from institutions like CSIR-IGIB, CSIR-CLRI, IIT Madras, and Delhi Technological University.

With an M.Tech in Bioinformatics from Delhi Technological University, Prodyot has excelled in research and development roles, presenting his work at prestigious venues like IIT Kharagpur. His research is published in esteemed journals such as IEEE and Frontiers in Pharmacology, with more underway.

Prodyot's GATE 2019 qualification from IIT Madras underscores his dedication to both academic excellence and professional growth. With a proven track record and relentless pursuit of knowledge, he is a valuable asset in bioinformatics, genomics, and computer-aided drug design endeavors.

Course Instructors

Dr. Snigdha Tiwari

Ms. Snigdha Tiwari, a highly accomplished Senior Research Fellow from IIT Roorkee, with over five years of experience in Computational Biology, Bioinformatics, and Telemedicine System Design.

Ms. Snigdha has made significant contributions at the intersection of basic and applied research, particularly in protein-protein and protein-ligand interactions, molecular docking and simulation studies, and healthcare/clinical data management.

ne of the highlights of her work includes leading the development of the UTSARJAN App, a digital health platform designed for pediatric nephrotic syndrome data collection & clinical research in collaboration with AIIMS Delhi.

Ms. Snigdha has recently completed her PhD work (submitted thesis) in Computational Biology at the Translational Bioinformatics Lab, Ms. Sngdha brings a rich academic foundation with a background in Chemistry and Bioinformatics, alongside a passion for interdisciplinary research and advancing biotechnology/healthcare through innovation and collaboration. She currently serves as an A

Course Instructors

Ms Shubhi Singh

Ms. Shubhi Singh is a dedicated researcher and educator having completed her Ph.D. in Biotechnology from SRM Institute of Science and Technology, bringing a strong interdisciplinary background in both computational and experimental research.

She is proficient in molecular docking, ADMET prediction, protein–ligand interaction analysis, and bioinformatics workflows for target identification and drug design. Her expertise includes integrating in silico modeling with wet-lab techniques such as qPCR-based gene expression profiling, microbial culture under stress conditions, and biofilm inhibition assays.

Ms. Singh is also experienced in academic teaching and laboratory supervision, fostering scientific skills and critical thinking among students. She is dedicated to advancing research in antimicrobial resistance and therapeutic development through innovative, data-driven approaches.

Course Instructors

Dr. Neeraj Kumar

Dr. Neeraj Kumar is a computational biologist and bioinformatician with expertise in AI-driven drug discovery, cheminformatics, and structural bioinformatics. He holds a Ph.D. in Bioinformatics from CSIR-IHBT and AcSIR, India, specializing in machine learning (ML) and deep learning (DL) for virtual screening, drug repositioning, and lead optimization.

His postdoctoral research at Pennsylvania State University focused on developing computational algorithms for immunoglobulin analysis. He has extensive experience in ML/DL frameworks (TensorFlow, PyTorch), cheminformatics tools (RDKit, OpenBabel), and molecular modeling platforms (AlphaFold, Rosetta, GROMACS). He has contributed primarily to AI-guided virtual screening pipeline development, HIV drug discovery, and structural bioinformatics projects.

His research work has been published in esteemed journals including Journal of Cheminformatics, Medicinal Research Reviews, and Computers in Biology and Medicine, with more publications in progress. He has qualified UGC-NET, GPAT, NIPER-JEE, and GATE.

Course Instructors

Dr. Bhupender

Dr Bhupender Singh is currently working as a Scientist/Trainer at Biotecnika info Labs. He holds a PhD degree specialising in Bioinformatics from Lovely Professional University. During his PhD, he grew as a dynamic researcher with experience as Teaching Assistant and has published his thesis work on Machine Learning and in-silico Drug Discovery in peer-reviewed journals.

With extensive experience at CSIR-Institute of Microbial Technology (IMTECH) as a Project Scientist and Senior Project Associate, he has proven his skills in ML/AI, Cheminformatics, in-silico Drug Discovery, Protein-sequence and Structural Analysis, Database development, supervision and organisation of the Biological-sampling events, gamification of scientific concepts for awareness of children and others. Apart from this, he has also taken scientific administrative roles at Lovely Professional University contributing to PhD thesis submission processes and Plagiarism verification.

Dr Bhupender has published in several peer-reviewed journals and has more than 700 citations. He has active collaborations with reputed National and International Scientists, Academicians, and Researchers. Further, he is also serving as a Reviewer in peer-reviewed scientific journals of Bioinformatics and Computational Biology for more than four years.
Dr Bhupender has joined Biotecnika with an objective to share his learning and experience among growing professionals.

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