



**Dr.Omics** Labs  
The Doctor of your DNA



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# MASTER THE FUTURE OF BIOINFORMATICS

ELEVATE YOUR SKILLS WITH A  
**6 MONTH**  
INDUSTRIAL BIOINFORMATICS  
INTERNSHIP ON  
**NEXT-GENERATION SEQUENCING (NGS)**

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# Your NGS Internship journey starts here:

At Dr.Omics Labs, we're excited to offer you an opportunity to embark on an incredible journey of discovery and innovation in the field of Next-Generation Sequencing (NGS).



## *About Us*

Dr.Omics Labs is a leader in the field of bioinformatics and genomics research. We are committed to pushing the boundaries of scientific knowledge and fostering the next generation of bioinformatics experts.

## **The Internship Experience**

- Our Industrial Bioinformatics Long-term Internship program is designed to provide you with a comprehensive understanding of NGS technologies, data analysis, and their real-world applications.

## **Six Months Internship Program Highlights**

- Six Months Internship Program Highlights
  - 4 months of intensive coursework.
  - 2 months of research-oriented project (Research Paper Publication Guidance).
  - Mentorship from renowned experts.
  - HR sessions for making you industry ready.
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# Coursework Overview

1. Beginners to Advance Bioinformatics  
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  2. Linux & Cloud Computing  
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  3. Python and its Application in NGS Data Analysis Techniques  
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  4. R and introduction to Bioconductor  
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  5. HR Session  
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  6. DNA Sequencing (Variant calling), Annotation  
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  7. RNA Sequencing (Reference and DeNovo Based)  
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  8. Targeted Metagenomics Data analysis  
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  9. Microarray Illumina GSA  
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  10. Research Project on NGS  
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# Module 1: Beginners to Advanced Bioinformatics

- Introduction to Bioinformatics
- NCBI Database Overview
- Genbank Database Practical Exercises
- UCSC Genome Browser Overview
- UCSC Genome Browser Hands-on Exercises
- Pubmed Database Introduction
- Clinvar Database Overview
- KEGG Database Overview and Exercises
- Protein Databases Overview
- Protein Data Bank (PDB) Overview
- Online BLAST Introduction and Exercises
- Standalone BLAST Setup and Initial Exercises
- Standalone BLAST Advanced Exercises
- Multiple Sequence Alignment with ClustalW
- Multiple Sequence Alignment with MEGA



# Module 2: LINUX & Cloud Computing

- Linux overview and significance
- File and directory operations (create, copy, move, delete)
- Text file editing and creation
- Process management (introduction and termination)
- Basic networking and ownership overview
- Conclusion and further resources
- Basics of Cloud technology (AWS)
- Basics of Pipeline Engineering



# Module 3: Python, Biopython and its Application in NGS Data Analysis Techniques

## 3.1) Python Programming

- Introduction to Python language
- Role of Programming in Bioinformatics
- Installation of Python on various platforms
- Installation of IDE
- Print function
- Comments
- User input
- Command line arguments
- Data types
- Variables and rules to create a variable
- In-built functions of python
- Slicing and indexing in String
- String and data formatting
- Control statements (if -else, If -elif-else, for loop, etc)
- Python data structure (List, Set, Tuple, etc)
- Methods of data structures
- Function introduction & its requirement
- Exception Handling, File Handling & Pandas Library



### 3.2) Biopython

- Introduction to Biopython
- Installation of Biopython
- Conversion of a string into a biological sequence
- Obtaining complement, reverse complement, transcribe, reverse transcribe, and translation from a sequence
- Finding GC content from a sequence
- SeqIO object:
- Reading various biological file formats such as Fasta and GenBank
- Analysis of fasta sequences
- Finding GC content of a fasta file containing multiple sequences and storing the data in a file
- Converting a GenBank file into fasta format
- Accessing NCBI's Entrez databases: Entrez Guidelines (EInfo, ESearch, etc)



# Module 4: R and Introduction to Bioconductor

## 4.1) R Programming

- Introduction to the R language
- Importance of R in Bioinformatics
- Installation of R
- Installation of IDE (R studio)
- Print, cut, and paste functions
- Comments
- Variables
- Data types
- Functions of math
- Operators
- Installation of packages
- String formatting
- Learning Control Statements (if -else, while loop, break, etc.)
- R Data Structures (Lists, Vectors, Arrays, etc)
- File Handling & User-Defined Functions





## 4.2) Introduction to Bioconductor

- Bioconductor package installation
- Sequence analysis
- Basics of seqinr package
- Import and export FASTA sequences
- Reverse complement
- GC content
- Retrieving genbank and fasta files from NCBI
- Statistical study for Analysis (z-test, t-test, etc)
- Plot generation for data visualization (box plot, PCA plot, Heatmap, Volcano Plot)



## Module 5: DNA Seq (Variant calling), Annotation

- Introduction and installation of tools
- Data retrieval & quality check of reads
- Mapping of reads using reference Genome
- Understanding Mapping Output
- Variant detection
- Visualization of variation
- Annotation and variant effect prediction
- Determining effect of coding non-synonymous mutation on protein function ability



# Module 6: RNA Sequencing (Reference and DeNovo based)

## 6.1 Reference based

- Introduction to RNA Seq
- Necessary Tools installation
- Learn how Data Retrieval is done
- Quality Check of reads using FASTQC, FastP
- Trimming and cleaning of data using Cutadapt
- Understanding mapping of reads on reference genome and file formats (SAM, BAM) with Hisat2
- Visualization techniques
- Gene Expression Quantification & Analyzation
- Pathway & Gene ontology enrichment analysis using StringTie, DESeq2
- Pathway Network analysis using KEGG

## 6.2 DeNovo based

- Generation of transcriptomic assembly
- Statistical study of assembly
- Mapping and abundance calculation
- Visualization of mapped reads using Cytoscape
- Generate the count matrices for differential expression analysis



## Module 7: Targeted Metagenome analysis

- Data Downloading (NCBI SRA/EBI SRA)
- Quality control using Fastqc
- Trimming (cutadapt/Fastp/Trimmomatic)
- Demultiplexing
- Data Importing
- Quality Check by DADA2
- Phylogenetic Diversity Analysis (Alpha and Beta Diversity)
- Taxonomy Analysis
- Krona Plot
- Phylogenetic Tree Construction using MEGA



# Module 8: Microarray Illumina GSA

- Understanding Microarray & its techniques
- Chip designing in Microarray
- Using R for Microarray Data Analysis
- Quality control & Normalization
- Differential Expressional Studies (Up-Regulated & Down-Regulated)
- Gene Ontology Pathway & Enrichment Analysis
- Pathway Network analysis (stringDB(PPI) & Cytoscape)
- Pathway Network Analysis (KEGG Mapper tool for DEG genes)
- Learn Different plots (Heatmap, volcano plot etc) using R





## *Program Structure*

- Duration: 6 months
- Course work: 4 months
- Project work: 2 months
- Research Paper Publication of top 5 Students

## From Theory to Practice: Bridging the Gap in Genomic Research

- **Comprehensive NGS Training:** Understand NGS fundamentals, data generation, and quality control.
  - **Bioinformatics Tools and Resources:** Master NGS analysis tools and explore essential genomic databases.
  - **Real-world Projects:** Engage in genome assembly, variant calling, and functional annotation projects.
  - **Professional Development:** Enhance your resume and gain mentorship from experienced professionals
  - **HR Session:** Gain invaluable HR expertise through interactive sessions.
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# Frequently Asked Questions

**Q: Are these courses suitable for those new to the field without prior experience?**

A: Yes, our courses are designed to cater to beginners with no prior experience in the field. We provide foundational content suitable for all skill levels.

**Q: Will I receive a certification upon completing the course?**

A: Absolutely, a digital certificate will be awarded upon course completion. You'll receive this certificate via email.

**Q: Do the courses include practical projects and research opportunities?**

A: Certainly, our courses incorporate practical projects and research opportunities to ensure hands-on learning and the practical application of acquired knowledge.

**Q: Can I access class recordings if I miss a class?**

A: Yes, class recordings are available. We'll send you the recording link via email if you miss a class, typically on the day following the live session.

**Q: Can I continue to access course materials and resources after finishing the course?**

A: Absolutely, you'll retain access to course materials and resources even after completing the course. These materials will be shared with you via email or WhatsApp.

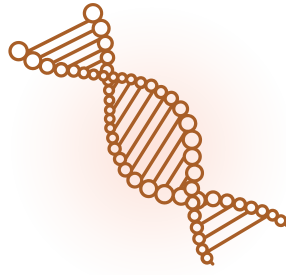
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## Terms and Conditions

- **Maintaining Discipline during the Tenure.**
  - **It is mandatory to maintain 85% attendance for all students.**
  - **Students must maintain an average 'A2' grade throughout their training period.**
  - **Project completion is a must for research.**
  - **Publication Students must participate actively in the Project group**
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NEED MORE INSIGHT & SUPPORT?

CONTACT US!

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*Thank you!*



**Dr.Omics Labs**  
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OUR CERTIFICATIONS & GRANTS

