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# Intermediate Bioinformatics & NGS Analysis Program

## Program Overview

Hands-on training in next-generation sequencing (NGS) analysis, RNA-Seq workflows, Python and R for bioinformatics, and reproducible computational workflows. Designed for learners with foundational bioinformatics or programming background.

## TARGET AUDIENCE

Learners who have completed a beginner bioinformatics course or have equivalent experience in Linux and basic scripting. Ideal for MSc and PhD students, research assistants, and laboratory scientists seeking practical computational skills.

## LEARNING OUTCOMES

- Process and quality-control next-generation sequencing data
- Perform end-to-end RNA-Seq differential expression analysis
- Use Python (Pandas, Biopython) for genomics data manipulation
- Visualize genomic data using R and ggplot2
- Build automated, reproducible bioinformatics pipelines
- Apply Snakemake for workflow management

## CURRICULUM BREAKDOWN (8 WEEKS)

Period	Topic	Key Content
Weeks 1-2	<b>Next-Generation Sequencing</b>	Sequencing technologies. QC with FastQC & MultiQC. Adapter trimming. Read filtering.
Weeks 3-4	<b>RNA-Seq Analysis</b>	Alignment concepts. STAR / HISAT2. Expression quantification. Count matrices. Differential expression overview.
Weeks 5-6	<b>Python for Bioinformatics</b>	Pandas. FASTA/VCF parsing. Data visualization (matplotlib/seaborn). Biological data structures.
Week 7	<b>R for Genomics</b>	ggplot2. Statistical analysis. DESeq2 workflow. Gene expression visualization.
Week 8	<b>Workflow Automation</b>	Snakemake concepts. Reproducibility principles. Pipeline structuring. Git version control.

## TOOLS & TECHNOLOGIES

FastQC	MultiQC	STAR
HISAT2	Python 3	R / RStudio
Snakemake	Git	Conda
DESeq2	Pandas	Biopython

## FINAL PROJECT

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### Capstone Project

A full RNA-Seq workflow project from raw FASTQ files through alignment, quantification, differential expression analysis, and biological interpretation, documented in a reproducible Snakemake pipeline.

## CERTIFICATION

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### CERTIFICATION

A Certificate of Completion is awarded upon successful submission of the final RNA-Seq project. Recognizes competency in NGS data analysis, Python/R scripting, and workflow automation.

## CONTACT & ENROLLMENT

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