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Beginner Bioinformatics Training Program

Program Overview	This program introduces learners to the foundations of bioinformatics, computational biology, Linux, and biological sequence data analysis. No prior programming experience required.

TARGET AUDIENCE

Undergraduate and postgraduate students, laboratory scientists, medical professionals, and researchers with little or no programming background who wish to enter the field of bioinformatics.

LEARNING OUTCOMES

- Understand core bioinformatics concepts and workflows
- Navigate and use Linux command line tools confidently
- Understand and work with FASTA and FASTQ biological file formats
- Handle biological sequence data for downstream analysis
- Set up and manage reproducible Conda environments
- Apply reproducibility principles to bioinformatics research

WEEKLY CURRICULUM

Period	Topic	Key Content
Week 1	**Introduction to Bioinformatics**	What is bioinformatics? Applications in genomics and medicine. Omics overview. Sequencing technologies.
Week 2	**Linux Command Line Fundamentals**	Linux navigation. File management. grep, cat, pipes, redirects. Working with large datasets.
Week 3	**Biological File Formats**	FASTA. FASTQ. GFF/GTF. Sequence quality scores. Data interpretation.
Week 4	**Data Handling & Environment Setup**	Conda environment setup. Python basics. Reading biological files. Reproducible research principles.

TOOLS & TECHNOLOGIES

Linux / Bash	Conda	Python (basics)
NCBI Databases	FASTA/FASTQ tools	Vim / Nano

FINAL PROJECT

Capstone Project	A structured sequence exploration project involving biological data handling, quality inspection of FASTQ files, and documentation of the analysis workflow in a reproducible format.

CERTIFICATION

CERTIFICATION	A Certificate of Completion is awarded to all participants who successfully attend the program sessions and submit the final project. Suitable for academic portfolios and LinkedIn profiles.

CONTACT & ENROLLMENT

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