Session	Topic	Main Contents	Instructor
1	Essentials of Linux	Linux file system navigation, command-line basics, working with text files, installing software using conda/mamba.	Mahdi Anvari
2	Bash Scripting	Writing and running scripts, using variables, loops, and conditionals to automate analysis pipelines.	Mahdi Anvari
3	Basic Biological Data Formats	Understanding FASTA, FASTQ, GTF/GFF, VCF formats and using tools like samtools, bcftools, and bedtools.	Dr Mehrmohammadi
4	NGS Variant Calling	Quality control (FastQC/fastp), read mapping (BWA/Bowtie2), post-processing (SAMtools), and variant calling (bcftools/GATK-lite).	Dr Mehrmohammadi
5	Epigenomics	Analyzing DNA methylation (Bismark), ChIP/ATAC-seq peak calling (MACS2), and visualizing peaks in IGV.	Mahdi Anvari
6	RNA-seq (bulk)	Mapping reads (HISAT2/STAR), counting (featureCounts), differential expression analysis (DESeq2), and visualization.	Mahdi Anvari
7	scRNA-seq	Preprocessing and clustering single-cell data using Scanpy, performing dimensionality reduction and marker gene detection.	Mahdi Anvari
8	Proteomics	Processing and analyzing proteomics data using MaxQuant and Perseus, performing normalization, clustering, and enrichment analysis.	Mahdi Anvari