

| Lecture Title | Category |
|---|----------------------------------|
| In-depth Introduction to RNA-Seq Data Analysis, Linux Computing and R | In-Depth Introduction to RNA-Seq |
| Introduction to Linux for Bioinformatics | In-Depth Introduction to RNA-Seq |
| Introduction to ArrayExpress - Getting Started With MicroArray Analysis | In-Depth Introduction to RNA-Seq |
| BioProject | Genomic Databases for Raw Data |
| BioSystems | Genomic Databases for Raw Data |
| BioSample | Genomic Databases for Raw Data |
| Introduction to Gene Expression Omnibus Database | Genomic Databases for Raw Data |
| Gene Expression Omnibus - Platforms | Genomic Databases for Raw Data |
| Gene Expression Omnibus - Samples | Genomic Databases for Raw Data |
| Gene Expression Omnibus - Series | Genomic Databases for Raw Data |
| Gene Expression Omnibus - Datasets | Genomic Databases for Raw Data |
| Gene Expression Omnibus - Profiles - How to Search for Gene Expression Profiles | Genomic Databases for Raw Data |
| NCBI Genomes & NCBI Assembly | Genomic Databases for Raw Data |
| Genome Reference Consortium | Genomic Databases for Raw Data |
| BioProject | Genomic Databases for Raw Data |
| BioSystems | Genomic Databases for Raw Data |
| BioSample | Genomic Databases for Raw Data |
| Introducton to Phytosome | Genomic Databases for Raw Data |
| Download an Entire Plant Genome & Proteome | Genomic Databases for Raw Data |
| Introduction to UCSC Genome Browser | Genomic Databases for Raw Data |
| How to retrieve an entire genome & Retrieval of SARS-CoV-2 Viral Genome | Genomic Databases for Raw Data |
| Introduction to ENSEMBL | Genomic Databases for Raw Data |
| Genome Assembly Retrieval and Analysis | Genomic Databases for Raw Data |
| BED | File Formats |
| GTF/GFF | File Formats |

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| SAM | File Formats |
| FASTQ | File Formats |
| How to Retrieve Raw Reads for RNA-Seq Data Analysis | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Retrieval of Data Required for this Course | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| In-depth Theory: Quality Control | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: Preprocess Raw Reads Using FASTQC, FASTP, Trimmomatic & Cutadapt | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| In-depth Theory: Mapping & Transcriptome Assembly | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: Mapping Preprocessed Reads Against a Reference Genome Using HISAT2, TOPHAT2, BOWTIE2, STAR | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: <i>De novo Transcriptome</i> Assembly Using StringTie | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Mapping Visualization & Evaluation | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| In-depth Theory: Gene Quantification, Expression Estimation & Differential Gene Expression | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| In-depth Theory: DeSeq2, Ballgown, edgeR | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: Differential Gene Expression Analysis Using Ballgown, edgeR, DESEQ2 in R | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Theory: Functional Enrichment Analysis of the DEGs | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: Gene Ontology Analysis | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: Pathways Analysis Using KEGG, PANTHER, Reactome | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Practical: Protein-Protein Interaction Using STRING | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |
| Conclusion of the Results | RNA-Seq Data Analysis Pipeline (Theoretical & Practical) |