

Sr. No	Videos	Description	Duration	Category	Main Category
Segment 1: Bioinformatics Databases					
1	Introduction to NCBI	<ul style="list-style-type: none"> • Basic introduction to NCBI • Functionality and search categories provided by NCBI 	18:01	NCBI	Biological Databases
2	Sequence Retrieval	<ul style="list-style-type: none"> • Biological sequence data storage, retrieval and analysis. • Describes the research methodologies on NCBI. 	16:16	NCBI	Biological Databases
3	Sequence Analysis	<ul style="list-style-type: none"> • Biological sequence data storage, retrieval and analysis. • Retrieval of various sequence related information. 	17:59	NCBI	Biological Databases
4	PubMed Central & ENTREZ	<ul style="list-style-type: none"> • Introduction to PubMed • Retrieval of millions of citations for Biomedical literature from MEDLINE and Life Sciences journals. 	11:06	NCBI	Biological Databases
5	FASTA vs GenBank	<ul style="list-style-type: none"> • Basic difference between the FASTA and Genbank formats. • Main differences of their structures and the information they provide. 	18:26	NCBI	Biological Databases
6	Gene	<ul style="list-style-type: none"> • Describes the use of Gene Database. • Analyze a particular gene, its location, expression and functional information. 	30:21:00	NCBI	Biological Databases
7	GenBank	<ul style="list-style-type: none"> • Description of GenBank database. • Accession of the most up-to-date and comprehensive DNA sequence information within scientific community. 	6:50	NCBI	Biological Databases
8	Assembly & NCBI Genome	<ul style="list-style-type: none"> • Introduction to NCBI Genomes & Assembly databases. • Retrieval and analysis of an entire genome using Genome database. • Procedure to download and retrieve the fully sequenced genome using Assembly database. 	36:14:00	NCBI	Biological Databases
9	Genome Reference Consortium (GRC)	<ul style="list-style-type: none"> • Describes the main purpose of establishing Genome Reference Consortium (GRC). • Discuss about 4 main genome assemblies of Human, Mouse, Zebrafish and Chicken along with their details. 	7:48	NCBI	Biological Databases
10	BioProject	<ul style="list-style-type: none"> • Introduction to BioProject, a sub-database of NCBI. • Retrieval of various information for a particular organism/species from the respective BioProject. 	6:39	NCBI	Biological Databases
11	BioSystems	<ul style="list-style-type: none"> • Briefly introduces the BioSystems database, a sub-database of NCBI. • Describes the procedure of analyzing metabolic pathways of protein interactions. 	4:16	NCBI	Biological Databases
12	BioSample	<ul style="list-style-type: none"> • Introduction to the BioSample database, sub-database National Center for Biotechnology Information. • Describes various features and information provided by BioSample. 	2:56	NCBI	Biological Databases

13	Sequence Read Archive (SRA)	<ul style="list-style-type: none"> • Introduction to Sequence Read Archive (SRA) database. • Describes the procedure of retrieving and downloading the sequence reads for a particular genome in the specific format. 	7:14	NCBI	Biological Databases
14	Introduction to UCSC Genome Browser & SARS-CoV-2 Viral Genome	<ul style="list-style-type: none"> • Detailed introduction to UCSC Genome Browser. • Retrieval and analysis of SARS-CoV-2 genome. 	13:40	UCSC	Biological Databases
15	Retrieve an Entire Genome & Retrieval of SARS-CoV-2 Viral Genome	<ul style="list-style-type: none"> • Explains the procedure to retrieve entire genome of SARS-CoV-2 using UCSC Genome Browser. • Retrieval of an entire genome through two different Operating System, Linux and Windows. 	9:40	UCSC	Biological Databases
16	Table Browser & SARS-CoV-2 Viral Genome	<ul style="list-style-type: none"> • Introduction to UCSC Table Browser Tool. • Retrieval of SARS-CoV-2 genome and its different gene sequence using Table Browser. 	12:15	UCSC	Biological Databases
17	Retrieval of Genomic Data & Annotation of SARS-CoV-2 Viral Genome	<ul style="list-style-type: none"> • Introduction to UCSC Table Browser Tool. • Retrieval and annotation of SARS-CoV-2 genome • Difference between GFF, GFF3 and GTF annotation files. 	5:29	UCSC	Biological Databases
18	Visualization of Genomic Data on the Genome Browser & SARS-CoV-2 Genome	<ul style="list-style-type: none"> • Interactive visualization of SARS-CoV-2 genome using UCSC Genome Browser. • Defines parameters for the visualization of genomic data. 	10:51	UCSC	Biological Databases
19	Introduction to ENSEMBL	<ul style="list-style-type: none"> • Introduction to ENSEMBL Genome Browser and information it provides. • Describes its various features and tools utilized for particular search. 	7:49	ENSEMBL	Biological Databases
20	Retrieval of a Gene-Protein-Chromosomal Region	<ul style="list-style-type: none"> • Procedure to retrieve gene, protein and chromosomal region and their visualization. • Genomic annotation. 	18:01	ENSEMBL	Biological Databases
21	Gene Analysis & Annotation	<ul style="list-style-type: none"> • Procedure for retrieval of a particular gene and analysis of genomic data through ENSEMBL. • Comparative genomics. 	34:40:00	ENSEMBL	Biological Databases
22	Genome Assembly Retrieval and Analysis	<ul style="list-style-type: none"> • Retrieval of genome assembly for a particular vertebrate species. • Provides analysis of genomic data for vertebrates. 	10:23	ENSEMBL	Biological Databases
23	Comparative Genomics Analysis	<ul style="list-style-type: none"> • Retrieval of genome assembly for a particular vertebrate species. • Comparative genomics. • Download the alignment files for CDS, proteins or RNA sequences. 	5:34	ENSEMBL	Biological Databases
24	Database of Short Genetic Variations (dbSNP)	<ul style="list-style-type: none"> • Introduction to Database of Single Nucleotide Polymorphism. • Retrieval of SNP variation information within Human genome. • Provides clinical significance and frequency of the different variations. 	12:16	NCBI	Biological Databases

25	Database of Genomic Structural Variation (dbVar)	<ul style="list-style-type: none"> • Introduction to database of genomic structural variation. • Retrieval of information about the variation of Human genome. 	6:24	NCBI	Biological Databases
26	Variation	<ul style="list-style-type: none"> • Retrieval and analysis of different types of variants through ENSEMBL. • Describes phenotypic relationship between variants. • Provides comprehensive way to access data widely used in genomic analysis. 	24:36:00	ENSEMBL	Biological Databases
27	NCBI BLAST Database Searching	<ul style="list-style-type: none"> • Describes NCBI BLAST searching to find regions of similarity between biological sequences. • Calculates statistical significance. • Compares nucleotide and protein sequences to sequence databases. 	25:36:00	NCBI	Biological Databases
28	BLAST/BLAT	<ul style="list-style-type: none"> • Describes ENSEMBL BLAST/BLAT searching to find regions of similarity between biological sequences. • Calculates statistical significance of matches • Analysis of sequence alignment between query and target sequence. 	15:08	ENSEMBL	Biological Databases
29	HomoloGene (Gene and Protein Families)	<ul style="list-style-type: none"> • Description of Homologene, sub-database of NCBI. • Compares and sequence homologs and mapping back to the DNA sequence. 	6:10	NCBI	Biological Databases
30	RefSeq Database	<ul style="list-style-type: none"> • Introduction to RefSeq database, a sub-database of NCBI. • Provides integrated and well-annotated set of reference sequences. • Non-Redundant Data Storage, Retrieval, Analysis and Visualizing. 	11:15	NCBI	Biological Databases
31	Taxonomy	<ul style="list-style-type: none"> • Provide nomenclature and classification for the source organisms in the sequence databases. • Information about the query's taxonomy ID and provides complete detail of the query's lineage. 	9:56	NCBI	Biological Databases
32	Introduction to UniProt	<ul style="list-style-type: none"> • Introduction to UniProt, its purpose and uses. • Sub-databases hosted by UniProt database. 	9:56	UniProt	Protein Databases & Analysis
33	UniProtKB & Protein Analysis	<ul style="list-style-type: none"> • Introduction to UniProtKB database. • Retrieval and analysis of protein sequences and genomic level information of proteins. 	39:29:00	UniProt	Protein Databases & Analysis
34	Introduction to Protein Data Bank (PDB)	<ul style="list-style-type: none"> • Introduction to Protein Data Bank (PDB). • Describes the repository of experimentally structured biomolecules. 	6:44	PDB	Protein Databases & Analysis
35	Introduction to Molecular Modeling Database (MMDB)	<ul style="list-style-type: none"> • Introduction to Molecular Modeling Database (MMDB). • Retrieval and analysis of a particular dataset from MMDB. • Lists the tools provided by MMDB. 	8:06	NCBI	Protein Databases & Analysis
36	UniProteome & Retrieval of an Entire Proteome	<ul style="list-style-type: none"> • Introduction to UniProteome • Retrieval of an entire proteome • Proteomics data and data annotation 	13:05	UniProt	Protein Databases & Analysis

37	UniRef & Retrieve Protein Clusters	<ul style="list-style-type: none"> • Introduction to UniRef • Describes clusters sets from UniParc and UniProtKB • Sequence space at three resolution (UniRef100, UniRef90, UniRef50). 	11:55	UniProt	Protein Databases & Analysis
38	UniParc & Find the Non-Redundant Entries	<ul style="list-style-type: none"> • Introduction to UniParc • Retrieval of non-redundant protein sequences. • Non-redundant protein sequence data and data annotation. 	4:58	UniProt	Protein Databases & Analysis
39	Introduction to InterPro	<ul style="list-style-type: none"> • Protein family classification and analysis using InterPro database. • Proteome analysis of a particular protein. • Protein families domains analysis. 	4:10	InterPro	Protein Databases & Analysis
40	Protein & Protein Domain Analysis	<ul style="list-style-type: none"> • Protein and protein domain analysis through InterPro database. • Protein families domain analysis. 	9:29	InterPro	Protein Databases & Analysis
41	InterPro - Protein Family Classification and Analysis	<ul style="list-style-type: none"> • Introduction to UniProt BLAST searching tool. • Finds functional and evolutionary relationship between sequences. • Search query sequences against the entire UniProt database. 	14:35	InterPro	Protein Databases & Analysis
42	Peptide Search	<ul style="list-style-type: none"> • Introduction to Peptide Search tool hosted by UniProt database. • Search methods of retrieving a particular amino acid sequence. • Retrieving regions of particular protein against the entire database of UniProt. 	3:15	UniProt	Protein Databases & Analysis
43	UniProt Align & Alignment of 2 Proteins	<ul style="list-style-type: none"> • Description of UniProt Align tool hosted by UniProt Database. • Aligning multiple sequences using UniProt Align tool. • Annotation of alignment results. 	3:47	UniProt	Protein Databases & Analysis
44	Accurately Searching for a Protein Structure on PDB & Protein Analysis	<ul style="list-style-type: none"> • Describes different search methods to retrieve query protein molecule on PDB. • Defines parameters and filters to specify the searches. • Accurately searching a protein structure on Protein Data Bank (PDB). 	13:55	PDB	Protein Databases & Analysis
45	Browsing PDB According to Annotation	<ul style="list-style-type: none"> • Retrieval of a protein structure using Biological annotation on PDB. • Describes categories of annotation and their description. 	6:52	PDB	Protein Databases & Analysis
46	Digging Out Categorized & Specific Protein Structures from PDB Archives	<ul style="list-style-type: none"> • Retrieval of detailed information for a particular protein structure through Protein Data Bank (PDB). • Accessing the PDB Archive using multiple sorts of parameters. 	6:23	PDB	Protein Databases & Analysis
47	3D Structure Visualization on PDB	<ul style="list-style-type: none"> • Visualization and analysis of protein structure using visualization tool hosted by PDB. • Defines parameters to interactively visualize the protein. 	10:49	PDB	Protein Databases & Analysis

48	Biological Annotation and Protein Features View & Analysis	<ul style="list-style-type: none"> • Visualization of features of the query protein through Protein Data Bank. • Procedure to look into the visualization and analysis of the protein features. 	8:18	PDB	Protein Databases & Analysis
49	Genomic Discovery of Protein Structure Through Gene	<ul style="list-style-type: none"> • Search the query gene against a genome and discovered the protein structure by utilizing PDB. • Describes correspondence between the 3D structure of the protein and the human genome. 	4:07	PDB	Protein Databases & Analysis
50	Mapping Genomic Position to Protein Sequence and 3D Structure	<ul style="list-style-type: none"> • Description to map a genomic position to a protein sequence and 3D structure. • Defines conditions to map genomic position to protein sequence and structure. 	4:34	PDB	Protein Databases & Analysis
51	Alignment Between Two PDB Sequences & Structures	<ul style="list-style-type: none"> • Alignment of biomolecular structures and sequences through a PDB tool; sequence & structure alignment. • Defines parameters to align two query molecules and its analysis. 	6:07	PDB	Protein Databases & Analysis
52	Ligands	<ul style="list-style-type: none"> • Retrieval of a particular ligand molecule from PDB-Ligand dictionary on Protein Data Bank (PDB). • Defines parameters and filters to specify the Ligand search. • Visualization of ligand molecule in various structure visualization tool. 	5:23	PDB	Protein Databases & Analysis
53	Protein Symmetry	<ul style="list-style-type: none"> • Description of protein symmetry page of Protein Data Bank (PDB). • Visualization and analysis of protein of interest. 	2:34	PDB	Protein Databases & Analysis
54	Introduction to Phytozome	<ul style="list-style-type: none"> • A detailed introduction to Phytozome genome browser. • Describes different features and services provided by Phytozome. • Retrieval of dataset of plant genome through Phytozome. 	9:38	Phytozome	Biological Databases
55	Interpret Plant Genome Records	<ul style="list-style-type: none"> • Retrieval of a particular plant genome dataset through Phytozome database. • Description of information of plant genome provided by Phytozome database. 	9:06	Phytozome	Biological Databases
56	Keyword or BLAST Search in a Plant Genome	<ul style="list-style-type: none"> • Searching efficiently through keyword(s) on Phytozome database. • Describes different parameters to analyze the results. • BLAST search on a particular species in the Phytozome. 	15:58	Phytozome	Biological Databases
57	Visualize a Plant Genome using JBrowse	<ul style="list-style-type: none"> • Visualization of plant genome using Phytozome database. • Description of analysis options. • Plotting VISTA plots for visualization of plant genome. 	17:38	Phytozome	Biological Databases

58	Download an Entire Plant Genome & Proteome	<ul style="list-style-type: none"> Retrieval and downloading a particular genome or proteome using Phytozome database. Describes different ways to retrieve genome through Phytozome. Analysis of dataset files for a particular species and their information. 	26:41:00	Phytozome	Biological Databases
59	Gene Expression Omnibus (GEO) Database	<ul style="list-style-type: none"> Introduction to Gene Expression Omnibus Database hosted by NCBI and it's Goal. Describes the subdatabases and the kind of data they store. 	9:15	NCBI	Biological Databases
60	Gene Expression Omnibus (GEO) Platforms	<ul style="list-style-type: none"> Elaborated introduction to GEO 'Platform' repository. Look through the data it stores and analyze an entry. 	5:42	NCBI	Biological Databases
61	Gene Expression Omnibus (GEO) Samples	<ul style="list-style-type: none"> Elaborated introduction to GEO 'Sample' repository. Look through the data it stores and analyze an entry. 	4:15	NCBI	Biological Databases
62	Gene Expression Omnibus (GEO) Datasets	<ul style="list-style-type: none"> Introduction to Datasets of biologically and statistically comparable GEO Samples and forms. Look through the data it stores and analyze an entry. 	4:44	NCBI	Biological Databases
63	Gene Expression Omnibus (GEO) Series	<ul style="list-style-type: none"> Elaborated introduction to GEO 'Series' repository. Look through the data it stores and analyze an entry's record. 	4:00	NCBI	Biological Databases
64	Regulation	<ul style="list-style-type: none"> A detailed introduction of a subdatabase of ENSEMBL, Regulation. Comprehension of the regulatory elements influencing the query gene. 	4:18	ENSEMBL	Biological Databases
65	UniProt BLAST & Protein Database Searching	<ul style="list-style-type: none"> Searching a query against the entire UniProt database using UniProt BLAST Detailed analysis of local similarity, functional and evolutionary relationship between different sequences 	12:32	UniProt	Protein Databases & Analysis
66	ID Mapping & Making Analysis Easier	<ul style="list-style-type: none"> Introduction to ID Mapping tool provided by UniProt. ID mapping of different types of identifiers and batch search with UniProt IDs. Convert UniProt IDs to another type of database ID utilizing this tool. 	7:17	UniProt	Protein Databases & Analysis
67	PROSITE	<ul style="list-style-type: none"> Introduction to protein domain, families and functional sites database , PROSITE. Analyze various informative sections provided by the documentation page. 	13:46	Protein Families Database	Protein Databases & Analysis
68	Pfam	<ul style="list-style-type: none"> Detailed introduction of a database of curated protein families, Pfam. Analyze a protein and retrieve significant information related to that protein. 	15:55	Protein Families Database	Protein Databases & Analysis
69	STRING	<ul style="list-style-type: none"> Introduction to protein-protein iInteraction database, STRING. Understanding of protein interaction network through analyzing the query protein result and visualization. 	13:16	PPI Database	PPI Database

Sr. No	Videos	Description	Duration	Category	Main Category
Segment 2: Understanding Bioinformatics					
1	FASTA (Sequence Format)	<ul style="list-style-type: none"> • Understanding of FASTA format, its syntax and extensions of FASTA. • Analyzing a particular sequence in FASTA format. 	6:13	Sequence File Format	Bioinformatics File Formats
2	GenBank (Sequence Annotation Format)	<ul style="list-style-type: none"> • Description of Genbank format and its syntax. • Organizes and stores the sequence and its annotation together. 	7:08	Sequence File Format	Bioinformatics File Formats
3	BAM	<ul style="list-style-type: none"> • Introduction to Binary Alignment Map (BAM). • Description of format and extension of BAM and its practical uses. 	9:06	Sequence File Format	Bioinformatics File Formats
4	SAM	<ul style="list-style-type: none"> • Introduction to Sequence Alignment Map (SAM). • Description of format and extension of SAM, its constitutes and practical uses. 	9:06	Sequence File Format	Bioinformatics File Formats
5	Gene File Format/Gene Transfer Format	<ul style="list-style-type: none"> • Introduction to Gene Feature Format/Gene Transfer Format. • Analyzing features of biological data through GFF/GTF. 	11:06	Sequence File Format	Bioinformatics File Formats
6	BED (Gene Structure Format)	<ul style="list-style-type: none"> • Introduction to BED file and its syntax. • Annotation of biological data through BED file. 	4:26	Sequence File Format	Bioinformatics File Formats
7	PHYLIP (Alignment Format)	<ul style="list-style-type: none"> • Introduction to PHYLIP alignment format and its syntax. • Describes the rules for representing sequences and uses of PHYLIP format. 	4:34	Sequence File Format	Bioinformatics File Formats
8	MEGA (Alignment Format)	<ul style="list-style-type: none"> • Introduction to MEGA file format, a multiple sequence alignment format and its syntax. • Rules for representing sequences within MEGA format and its uses. • Exporting an alignment file from the MEGA tool in the MEGA format. 	5:32	Sequence Alignment File Format	Bioinformatics File Formats
9	CLUSTAL (Alignment Format)	<ul style="list-style-type: none"> • Introduction to Clustal Omega alignment format and its syntax. • Describes the rules for representing sequences and uses of Clustal alignment format. 	5:07	Sequence Alignment File Format	Bioinformatics File Formats
10	STOCKHOLM (Alignment Format)	<ul style="list-style-type: none"> • Introduction to STOCKHOLM alignment format and its syntax. • Describes the rules for representing sequences and uses of STOCKHOLM alignment format. 	3:10	Sequence Alignment File Format	Bioinformatics File Formats

11	SANGER/SOLEXA FASTQ (Sequence Quality Format)	<ul style="list-style-type: none">• Introduction to Sanger/Solexa FASTQ format, its quality scores, variants and file extension.• Describes how it stores both the biological sequence and its corresponding quality scores.	18:01	Sequence Alignment File Format	Bioinformatics File Formats
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Sr. No	Videos	Description	Duration	Category	Main Category
Segment 3: Sequence and Biological Data Analysis					
1	Clustal Omega	<ul style="list-style-type: none"> • Introduction to Clustal Omega, a multiple sequence alignment tool. • Procedure to align multiple sequence using Clustal Omega. • Interpretation of the output final alignment. 	19:18	Multiple Sequence Alignment	Sequence Alignment & Analysis
2	MUSCLE	<ul style="list-style-type: none"> • Introduction to MUSCLE tool. • Procedure to align multiple sequences and interpretation of final output alignments. 	21:07	Multiple Sequence Alignment	Sequence Alignment & Analysis
3	TCoffee	<ul style="list-style-type: none"> • Introduction to T-Coffee, a multiple sequence alignment tool and its characteristics. • Analyzing multiple sequence alignment (MSA) on T-Coffee. • Interpretation of alignment results and generating phylogenetic tree on MEGA. 	8:37	Multiple Sequence Alignment	Sequence Alignment & Analysis
4	Mafft	<ul style="list-style-type: none"> • Introduction to Mafft, multiple sequence alignment program. • Analyzing fastest multiple sequence alignment (MSA) on Mafft. • Provides various commands to install, and utilize the MAFFT tool on Linux OS 	8:22	Multiple Sequence Alignment	Sequence Alignment & Analysis
5	Jalview	<ul style="list-style-type: none"> • Introduction to Jalview tool. • Analysis and visualization of MSA through Jalview. • Generating phylogenetic tree an PCA using Jalview. 	13:42	Multiple Sequence Alignment	Sequence Alignment & Analysis
6	NEEDLE	<ul style="list-style-type: none"> • Introduction to EMBOSS Needle, a pairwise alignment tool. • Procedure to perform and analyse global alignment and track the optimum sequence. 	20:02	Pairwise Sequence Alignment	Sequence Alignment & Analysis
7	WATER	<ul style="list-style-type: none"> • Introduction to EMBOSS Needle, a pairwise alignment tool. • Procedure to perform and analyse local alignment and how Needleman-Wunsch algorithm works. 	9:10	Pairwise Sequence Alignment	Sequence Alignment & Analysis
8	SignalP	<ul style="list-style-type: none"> • Introduction of SignalP tool. • Predicton of signal peptide from protein sequence. 	7:57	Protein Analysis	Protein Databases & Analysis

9	TargetP	<ul style="list-style-type: none"> • Introduction to TargetP server. • Prediction and detailed analysis of Mitochondrial transfer peptide through TargetP. 	9:21	Protein Analysis	Protein Databases & Analysis
10	Aln2Plot	<ul style="list-style-type: none"> • Introduction to Aln2Plot tool. • Generates graphical plots of hydrophobicity and side chain volumes for two or more query proteins using the Aln2Plot tool. 	2:30	Protein Analysis	Protein Databases & Analysis
11	DeepCoil	<ul style="list-style-type: none"> • Introduction to a web based tool, DeepCoil. • Prediction of the coiled coil domain regions within a query protein sequence. 	3:22	Protein Analysis	Protein Databases & Analysis
12	HHrepID	<ul style="list-style-type: none"> • Introduction to HHrepID, a web-based tool for the prediction of secondary structures of the protein. • Find repetitive regions within a query protein sequence using the HHrepID tool. 	5:15	Protein Analysis	Protein Databases & Analysis
13	MARCOIL	<ul style="list-style-type: none"> • Introduction to Marcoil, an HMM for the recognition of proteins with a CCD. • Analysis and prediction of potential coiled-coil domains in protein sequences. 	4:05	Protein Analysis	Protein Databases & Analysis
14	REPPER	<ul style="list-style-type: none"> • Introduction to REPPER to analyses regions with short gapless REPeats in protein sequences. • Analysis of output that is complemented by coiled coil prediction (COILS) and optionally by secondary structure prediction (PSIPRED). 	2:25	Protein Analysis	Protein Databases & Analysis
15	HMMER	<ul style="list-style-type: none"> • Introduction of HMMER; hidden Markov model based database for protein profiling. • Retrieve the sequence homologs of the query protein using the HMM profile method and it's elaborated analysis. 	13:16	Motif & Domain Analysis	Protein Databases & Analysis
16	SMART: Finding Domains in Proteins	<ul style="list-style-type: none"> • Introduction of SMART; Simple Modular Architecture Research Tool for the identification and analysis of protein domains. • Detection of protein domains from the multiple sequence alignments of proteins. 	6:44	Motif & Domain Analysis	Protein Databases & Analysis
17	ScanProsite	<ul style="list-style-type: none"> • Establishment of ScanProsite, an improved version of the web-based tool provided by PROSITE. • Scan proteins for matches against the PROSITE collection of motifs as well as against your own patterns. 	7:36	Motif & Domain Analysis	Protein Databases & Analysis

18	MEGA	<ul style="list-style-type: none"> • Introduction to Phylogenetics and MEGA software for phylogenetic analysis. • Multiple sequence analysis through MEGA software. • Generating phylogenetic trees with different methods through MEGA. 	21:20	Phylogenetic Analysis & tools	Phylogenetic Analysis
19	FigTree	<ul style="list-style-type: none"> • Introduction to FigTree and its purposes. • Generating a publication quality figure out of phylogenetic tree data. • Defines parameters to make tree visually interactive and well anotated. 	21:26	Phylogenetic Analysis & tools	Phylogenetic Analysis
20	iTOL	<ul style="list-style-type: none"> • Introduction to iTOL, a phylogenetic tree viewer tool. • Creating a high resolution picture out of phylogenetic tree data using iTOL • Editing phylogenetic tree and making it visually interactive. 	13:42	Phylogenetic Analysis & tools	Phylogenetic Analysis

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Segment 4: Predictive Bioinformatics					
1	Prodigal	<ul style="list-style-type: none"> Utilization of Prodigal software for gene prediction. Describes the properties, modes and parameters of Prodigal. Analysis of a particular genome and predicted genes out of it utilizing prodigal software. 	25:46:00	Gene Prediction	Gene Prediction
2	GeneMark	<ul style="list-style-type: none"> Utilization of GeneMark tool for gene prediction. Describes GeneMark family of programs. Gene prediction analysis using GeneMark.hmm. 	16:51	Gene Prediction	Gene Prediction
3	GenScan	<ul style="list-style-type: none"> Utilization of GenScan webserver for gene prediction. Describes the parameters of GenScan. Analysis of a particular nucleotide sequence and predicting gene out of it. 	10:40	Gene Prediction	Gene Prediction
4	AUGUSTUS	<ul style="list-style-type: none"> Utilization of AUGUSTUS tool for gene prediction and annotation. Describes the parameters for utilizing the AUGUSTUS. Analysis of the result provided by AUGUSTUS and step-by-step procedure to find a novel gene. 	17:27	Gene Prediction	Gene Prediction
5	Ali2D	<ul style="list-style-type: none"> Use of Ali2D tool for secondary structure prediction. Detailed analysis of the secondary structure prediction results. 	4:09	Secondary Structure Prediction	Secondary Structure Prediction
6	Quick2D	<ul style="list-style-type: none"> Use of Quick2D tool for secondary structure prediction. Detailed analysis and information retrieval of the secondary structure features like alpha-helices, extended beta-sheets, transmembrane helices and disorder regions of the query protein. 	4:33	Secondary Structure Prediction	Secondary Structure Prediction
7	Jpred	<ul style="list-style-type: none"> Use of Jpred server for secondary structure prediction. A detailed analysis of secondary structure features' information of the query protein sequence. 	4:54	Secondary Structure Prediction	Secondary Structure Prediction

8	MODELLER	<ul style="list-style-type: none"> • Introduction to Modeller tool and its uses. • Procedure to predict a protein structure through Modeller. • Evaluation method of MODELLER to find out the most optimal and good protein structure predicted. 	36:13:00	3D Structure Prediction	3D Structure Prediction
9	ROBETTA	<ul style="list-style-type: none"> • Introduction to Robetta, a protein structure prediction tool. • Procedure to predict and analyse protein structure. • Prediction of protein structure for a query sequence using ab-initio techniques. 	14:39	3D Structure Prediction	3D Structure Prediction
10	M4T	<ul style="list-style-type: none"> • Introduction to M4T, a protein structure prediction tool. • Procedure to predict the protein structure from a Target protein sequence, using the M4T server. 	9:26	3D Structure Prediction	3D Structure Prediction
11	SwissModel	<ul style="list-style-type: none"> • Introduction to homology modeling and SwissModel, a homology modeling server. • Prediction of protein structure for a target sequence using SwissModel. • Defines parameters for a good protein structure and analysis of resulting protein. 	12:52	3D Structure Prediction	3D Structure Prediction
12	PEPFOLD 3 peptide structure modeling	<ul style="list-style-type: none"> • Introduction to PEPFOLD_3 server and its purpose. • Generating 3D models of a peptide using the query sequence. • Defines parameters and analysis of results. 	13:14	3D Structure Prediction	3D Structure Prediction
13	HHPRED	<ul style="list-style-type: none"> • Basic description of HHPred tool and its purpose. • Procedure to predict the protein structure from target sequence through HHPred tool. • Selecting a particular template structure for homology modeling of target protein using HHPred tool. 	14:09	3D Structure Prediction	3D Structure Prediction
14	IntFOLD	<ul style="list-style-type: none"> • Introduction to IntFOLD and its purpose. • Procedure to predict the protein structure from target protein sequence, using the IntFOLD server. • Interpretation of results. 	8:41	3D Structure Prediction	3D Structure Prediction

15	Homology Modeling Using MOE	<ul style="list-style-type: none"> • Introduction to homology modeling and Molecular Operating Environment (MOE) tool. • Generating a homology 3D model of a target protein using MOE. • Analysis of results and how to align the two structures of the protein using the MOE tool. 	12:34	3D Structure Prediction	3D Structure Prediction
16	PROSA	<ul style="list-style-type: none"> • Introduction to ProSA server. • Procedure to evaluate protein model predicted using different methods. • Analysis of three different structures of the protein predicted from three different tools for their comparative analysis. 	10:05	3D Structure Evaluation	3D Structure Evaluation
17	SAVES	<ul style="list-style-type: none"> • Introduction to SAVES tool and its purpose. • Procedure to evaluate a predicted protein model using Saves server. • Analysis of Ramachandran plot generated by the SAVES server for the predicted query protein structure. 	5:31	3D Structure Evaluation	3D Structure Evaluation
18	WhatCheck	<ul style="list-style-type: none"> • Introduction to WhatCheck, a protein model evaluation tool. • Utilization of WhatCeck tool for protein model evaluation. • Analysis and implication of results for protein structure evaluation. 	8:40	3D Structure Evaluation	3D Structure Evaluation
19	ERRAT	<ul style="list-style-type: none"> • Introduction to ERRAT, a protein model evaluation tool. • Procedure to evaluate experimentally determined protein model. • Analysis and interpretation of results to evaluate the best model. 	6:44	3D Structure Evaluation	3D Structure Evaluation
20	Verify3D	<ul style="list-style-type: none"> • Introduction to Verify3D, a protein model evaluation tool. • Procedure to evaluate a protein model using the web server of Verify3D. • Interpretation and analysis of the results provided by Verify3D 	8:31	3D Structure Evaluation	3D Structure Evaluation
21	RAMPAGE	<ul style="list-style-type: none"> • Introduction to RAMPAGE, a protein model evaluation tool. • Procedure to evaluate protein model based on Ramachandran plotting by RAMPAGE. • Interpretation of Ramachandran plotting to select the best model. 	3:29	3D Structure Evaluation	3D Structure Evaluation

22	ProCheck	<ul style="list-style-type: none"> • Introduction to ProCheck, a protein model evaluation tool. • Utilization of ProCheck to check quality of protein model based on certain parameters. • Interpretation of results to select the best model. 	12:36	3D Structure Evaluation	3D Structure Evaluation
23	Chimera	<ul style="list-style-type: none"> • Introduction to UCSC Chimera and its uses. • Visualization and analysis of a protein 3D model using Chimera. • Comparing and analysis of more than one protein structure for research purposes. 	25:23:00	3D Structure Visualization	3D Structure Visualization
24	PyMol	<ul style="list-style-type: none"> • Introduction to PyMol. • Defines parameters to visualize and analyze the protein 3D model. • Commands used in PyMol to visualize and manipulate protein 3D model. 	40:48:00	3D Structure Visualization	3D Structure Visualization
25	Molecular Docking of Protein Ligand using MOE	<ul style="list-style-type: none"> • Introduction to Molecular Operating Environment (MOE) and molecular docking. • Preparation of the receptor for docking. • Searching active site residues in receptor and ligand preparation. • Docking of receptor and ligand molecules and analysis of the docked complex. 	9:23	Molecular Docking	Molecular Docking
26	Protein-Protein Docking Using MOE	<ul style="list-style-type: none"> • Basic description of Molecular Operating Environment (MOE) software and protein-protein docking. • Procedure to dock a ligand protein against a receptor protein (protein-protein docking) using the MOE software. • Defines parameters to select the best docking conformation for a specific drug candidate. 	11:38	Molecular Docking	Molecular Docking
27	Structure Based Drug Desinging Using MOE	<ul style="list-style-type: none"> • Introduction to MOE software and structure based drug designing. • Procedure to design a drug based on knowledge of 3D structure of biological target. • Defines parameters and modifications to make the ligand molecule an effective drug candidate. 	16:19	Molecular Docking	Molecular Docking

28	Docking a Library of Compounds using MOE	<ul style="list-style-type: none"> • Introduction to Molecular Operating Environment (MOE) software and its uses. • Procedure of docking a library of compounds against a particular protein of interest using MOE software. • Defines parameters to analyse the best docking conformation to indicate the stable adduct. 	19:48	Molecular Docking	Molecular Docking
29	SwissDock Protein Ligand Docking	<ul style="list-style-type: none"> • Introduction to SwissDock server and its purpose. • Procedure to dock a ligand compound against a receptor molecule (Protein-Ligand Docking). • Defines parameters to be selected for docking process. • Creating ligand and receptor files in the required formats. 	19:16	Molecular Docking	Molecular Docking
30	ZDock Protein-Protein/ Ligand Docking	<ul style="list-style-type: none"> • Introduction to ZDOCK server and its purpose. • Procedure to dock a receptor protein molecule against the ligand protein molecule (Protein-Protein docking) using the ZDOCK server. • Procedure to dock a protein molecule against its multimers using the M-ZDOCK program and analysis of results. 	19:35	Molecular Docking	Molecular Docking
31	PatchDock Protein-Protein Docking	<ul style="list-style-type: none"> • Introduction to PatchDock server and its purpose. • Procedure to dock a receptor protein molecule against the ligand protein molecule (Protein-Protein docking) using the PatchDock server. • Analysis of results and the best complexes refined by FireDock server. 	17:39	Molecular Docking	Molecular Docking
32	ClusPro Protein-Protein Docking	<ul style="list-style-type: none"> • Introduction to ClusPro server and its purpose. • Utilization of various features of ClusPro to perform protein-protein docking. • Describes advanced functionalities offered by ClusPro to select the best docked complex. 	21:44	Molecular Docking	Molecular Docking

33	MDockPEP protein peptide docking	<ul style="list-style-type: none"> • Introduction to MDockPEP server and its uses. • Procedure to dock a receptor protein molecule against the ligand peptide molecule (Protein-Peptide docking) using the MDockPeP server. • Description to prepare the receptor file for docking process and analysis of the results. 	10:06	Molecular Docking	Molecular Docking
34	PDBepisa Docking Complex Evaluation	<ul style="list-style-type: none"> • Introduction to PDBePISA server and its purpose. • Evaluation of protein-protein and protein-ligand docked complex through PDBePISA server. • Defines parameters for an optimal docking complex model. 	23:27	Docking Complex Evaluation	Docking Complex Evaluation
35	PDBsum Docking Complex Evaluation	<ul style="list-style-type: none"> • Introduction to PDBsum server and its uses. • Procedure to evaluate protein-protein and protein-ligand docking complex using PDBsum server. • Analysis and interpretation of evaluation results. 	18:49	Docking Complex Evaluation	Docking Complex Evaluation
36	SwissADME	<ul style="list-style-type: none"> • Introduction to SwissADME server and its purpose. • Evaluation of pharmacokinetics, drug-likeness and medicinal chemistry friendliness of small molecules or ligands. • Defines parameters for an optimal docking complex model. 	15:31	Docking Complex Evaluation	Docking Complex Evaluation

Sr. No	Videos	Description	Duration	Category	Main Category
Segment 5: Bioinformatics Scripting in Linux, Python and R					
1	Introduction to Python and Python Installation	<ul style="list-style-type: none"> • A detailed introduction to Python language and its Installation. • Advantages of Python over other programming languages. • Uses of Python in Bioinformatics. 	8:25	Introduction	Python
2	Why Python in Bioinformatics & Code editor selection	<ul style="list-style-type: none"> • Importance of Python in Bioinformatics. • Description of different code editors and their importance like Atom, PyCharm and Visual Studio Code. • Advantages of Visual Studio Code as a code editor. 	9:16	Introduction	Python
3	Basic Input and output	<ul style="list-style-type: none"> • Description of Basic input and output function in Python language. • Example code to print out values and characters. • Getting input from the user and printing it out. 	15:37	Introduction	Python
4	Mathematical Operations	<ul style="list-style-type: none"> • Description of different operators to perform that perform various operations in Python. • Description of different ways to perform operations in Python shell and script mode. • Description of methods to perform the operations on variables in script mode. 	7:20	Introduction	Python
5	Comments	<ul style="list-style-type: none"> • Introduction to comments and its use. • Description of importance of comments in a Python script. • Example code to make comments in Python script. 	5:42	Introduction	Python
6	Strings	<ul style="list-style-type: none"> • Introduction to Strings within Python language. • Utilization of Strings with different built-in functions in Python. • Describes the built-in functions that are helpful in Bioinformatics. 	21:51	Iterable Objects	Python
7	Lists	<ul style="list-style-type: none"> • Introduction to lists in Python language. • Creating and modifying lists within Python code. • Using list with Python's built-in functions. 	28:47:00	Iterable Objects	Python
8	Tuples	<ul style="list-style-type: none"> • Description of lists and how they can be called with built-in functions. • Example code for accessing and concatenating lists. • Description Tuples within Python code and how they can be used to keep data unmanipulated. 	10:37:00	Iterable Objects	Python

9	Dictionaries	<ul style="list-style-type: none"> • Introduction to Dictionaries and their importance in Python. • Describes the syntax of declaring a dictionary. • Describes different built-in functions to access the data in a dictionary. 	10:57	Iterable Objects	Python
10	Sets	<ul style="list-style-type: none"> • Introduction to sets and thier use to analyze Bioinformatics data. • Example code of using sets with Python's built-in functions. • Describes various purposes of sets. 	7:35	Iterable Objects	Python
11	If-Else	<ul style="list-style-type: none"> • Introduction to if-else statement and its syntax. • Example code of how if-else statement is executed. • Describes importance of if-else statement to perform various tasks in Bioinformatics. 	9:19	Control Flow	Python
12	For Loop and Calculation of Mol. Weight of Protein)	<ul style="list-style-type: none"> • Introduction to For loop within Python. • Describes use and importance of For loop in Python. • Example code to calculate molecular weight of a protein using For loop. 	10:56	Control Flow	Python
13	While Loop and Code Generation	<ul style="list-style-type: none"> • Introduction to While loop within Python and its importance. • Example code to get the codons from a DNA sequence using while loop. • Describes usage of break statement in loops. 	9:37	Control Flow	Python
14	Estimation of Net Charge and Protein	<ul style="list-style-type: none"> • Example code to estimate the net charge of protein using Python script. • Calculation of net charge of protein using For loop in Python script. 	4:36	Biological Data Analysis	Python
15	Reading Normal and Bioinformatics Files (FASTA)	<ul style="list-style-type: none"> • Describe Python's built-in functions for reading files. • Define Python's file reading methods. • Describes script to read data from files by providing relative path and absolute path. 	13:45	File Handling	Python
16	Writing Normal and Bioinformatics Files (FASTA)	<ul style="list-style-type: none"> • Describe Python's built-in functions for writing files. • Define Python's file writing methods. • Describes script to write data; to open and create files. 	7:17	File Handling	Python
17	CSV (A special kind of file in Bioinformatics)	<ul style="list-style-type: none"> • Introduction to CSV file and its importance. • Describes the structure of CSV file. • Describes script to read a particular CSV file. 	8:41	File Handling	Python

18	File Handling OS Module	<ul style="list-style-type: none"> • Introduction to Python's built-in OS module. • Describes functions included in OS module utilized within code. • Describes script to access the functions of os module. 	31:47:00	File Handling	Python
19	Consolidate (Merge) Multiple DNA or Protein Sequences into one FASTA file	<ul style="list-style-type: none"> • Describes how Python modules utilized to save multiple sequences files into one FASTA file. • Describes Python script to consolidate multiple DNA or Protein sequences into one FASTA file. 	9:24	File Handling	Python
20	Estimating Net Charge of several Proteins at once	<ul style="list-style-type: none"> • Describes the use of Python script to calculate net charge of protein. • Calculation of net charge of thousands of proteins using built-in functions. • Describes the use of nested loop to count the sequences. 	7:13	Biological Data Analysis	Python
21	With: A secure way to open Files	<ul style="list-style-type: none"> • Introduction to 'With' statement and its syntax within Python. • Creating files using 'With' statement and its advantages over other conventional ways. • Describes Python script to create file with and without using 'With' statement. 	8:50	Functions & Modules	Python
22	Functions	<ul style="list-style-type: none"> • Introduction to functions, its syntax and its types with Python. • Describes script to create functions and using them to analyze data. • Describes different ways of returning values from the functions into the main program. 	26:41:00	Functions & Modules	Python
23	Modules	<ul style="list-style-type: none"> • Introduction to modules and their uses within Python. • Procedure for installation of modules. • Describes Python script for importing, creating and testing modules. 	16:50	Functions & Modules	Python
24	Error Handling	<ul style="list-style-type: none"> • Introduction to error handling in Python. • Describes different keywords for error handling. • Describes Python script using error handling keywords to handle possible errors. 	15:31	Error Handling	Python
25	Introduction to BioPython & Installation	<ul style="list-style-type: none"> • A detailed introduction to BioPython package and its purpose. • Describes the installation of BioPython package. • Describes various tasks that can be performed using BioPython and its modules. 	10:18	Introduction	BioPython

26	Bio.Seq Create a Seq Object	<ul style="list-style-type: none"> • Introduction to Bio.Seq module of BioPython. • Importing Seq objects module from Bio.Seq module. • Utilization of Seq() function in program. 	7:38	Sequence Analysis	BioPython
27	Bio.Seq Seq Object Behaves Like a String	<ul style="list-style-type: none"> • Introduction to Bio.Seq module of BioPython. • Describes Seq object behaves like the string data type in Python. • Describes manipulations applied on Seq objects in BioPython. 	9:54	Sequence Analysis	BioPython
28	Bio.Seq Central Dogma in Play Through Python	<ul style="list-style-type: none"> • Introduction to Bio.Seq module of BioPython. • Utilization of Bio.Seq module to generate small Python script. • Converting a particular sequence into its complementary, non complementary, transcribed and back-transcribed sequences by built-in functions of Bio.Seq. 	8:41	Sequence Analysis	BioPython
29	Bio.Seq Unkown & Mutable Sequences	<ul style="list-style-type: none"> • Introduction to Bio.Seq module of BioPython. • Importing UnknownSeq and MutableSeq objects from the Bio.Seq class. • Utilization of MutableSeq() and UnknownSeq() functions in a BioPython script to perform different tasks. 	6:53	Sequence Analysis	BioPython
30	Bio.Alphabet Understanding the Alphabets of Biology	<ul style="list-style-type: none"> • Introduction to Bio.Alphabet module of BioPython. • Utilization of Bio.Alphabet class to figure the alphabets that underlie within the sequences of interest. 	7:37	Sequence Analysis	BioPython
31	Bio.Alphabet IUPAC and Types of Sequence Representations	<ul style="list-style-type: none"> • Introduction to BioAlphabet IUPAC module. • Describes types of sequence representation. • Describes functionality provided by IUPAC. 	10:34	Sequence Analysis	BioPython
32	Bio.Alphabet Concatenation of Multiple Seq Records Using Generic Alphabets	<ul style="list-style-type: none"> • Intriduction to BioAlphabet class of BioPython. • Utilization of generic_alphabets in BioAlphabet. • Concatenation of multiple seq records into single object. 	9:47	Sequence Analysis	BioPython
33	SeqRecord Creating Seq Records	<ul style="list-style-type: none"> • Introduction to SeqRecord module of Bio.SeqRecord class of BioPython. • Creating sequence records that resonate the sequence records of GenBank, FASTA, EMBL(EBI), etc. 	12:27	Sequence Analysis	BioPython
34	SeqRecords & FASTA	<ul style="list-style-type: none"> • Description of SeqRecord module in BioPython. • Utilization of SeqRecord to demonstrate the representation of the fasta file within the BioPython. 	4:35	Sequence Analysis	BioPython
35	SeqRecords & GenBank	<ul style="list-style-type: none"> • Description of SeqRecord module in the BioPython. • Utilization of SeqRecord to demonstrate the representation of the GenBank file within the BioPython. 	3:28	Sequence Analysis	BioPython

36	SeqRecord Formatting Records	<ul style="list-style-type: none"> • Introduction to SeqRecord module in BioPython. • Utilization of formatting features of the SeqRecord. 	3:47	Sequence Analysis	BioPython
37	SeqRecord Comparison & Reading Multiple FASTA Files from Directory	<ul style="list-style-type: none"> • Introduction of the SeqRecord module in BioPython. • Checking redundancy of files using SeqRecord class. • Importing modules and subclasses to make the code efficient. 	5:47	Sequence Analysis	BioPython
38	SeqIO Reading a Sequence File	<ul style="list-style-type: none"> • Introduction to SeqIO module of BioPython package. • Description of SeqIO.read() function of SeqIO module. • Reading a FASTA file and a GenBank file utilizing the SeqIO.read() function. 	10:32	Sequence Data Parsing	BioPython
39	SeqIO Parsing a Sequence File	<ul style="list-style-type: none"> • Introduction to SeqIO module of BioPython. • Description of SeqIO.parse() function of SeqIO module. • Converting a single file containing multiple sequences into an iterator list of records. 	7:16	Sequence Data Parsing	BioPython
40	SeqIO Extracting Annotations and Pattern-wise Sequence Data Extraction	<ul style="list-style-type: none"> • Description of SeqIO module of BioPython. • Creating FASTA file of the annotations, IDs, Descriptions and other details for a particular organism from the GenBank file. 	10:35	Sequence Data Extraction	BioPython
41	SeqIO Parsing a Compressed Sequence File & Creating a Dictionary of Sequences	<ul style="list-style-type: none"> • Description of SeqIO module in BioPython. • Parsing a compressed sequence file. • Creating a dictionary of sequences. 	6:10	Sequence Data Parsing	BioPython
42	SeqIO - Write Sequences and SeqRecords Into Files	<ul style="list-style-type: none"> • Description of SeqIO module of the BioPython. • Creating new sequence files in any format using the SeqIO module. • Writing multiple sequences in a single file and multiple sequences in separate files. 	11:42	Sequence Data Parsing	BioPython
43	AlignIO - Reading and Parsing a Multiple Sequence Alignment File	<ul style="list-style-type: none"> • Introduction to AlignIO module in BioPython. • Reading and parsing multiple sequence alignment file. 	8:19	Alignment Parsing and Analysis	BioPython
44	AlignIO - Writing Alignments and Multiple Sequence Alignment Records	<ul style="list-style-type: none"> • Introduction to AlignIO module of BioPython. • Writing alignments and multiple sequence alignment records. 	5:28	Alignment Parsing and Analysis	BioPython
45	AlignIO - Information Mapping of Alignments	<ul style="list-style-type: none"> • Description of the AlignIO module within BioPython Package. • Information mapping of alignments. 	2:33	Alignment Parsing and Analysis	BioPython
46	AlignIO - Format Alignments	<ul style="list-style-type: none"> • Description of the AlignIO module in the BioPython package. • Utilization of AlignIO.read() function to read a file into a particular format. • Converting the input format into other formats at the run time. 	3:55	Alignment Parsing and Analysis	BioPython

47	AlignIO - Conversion of Alignment Formats	<ul style="list-style-type: none"> • Introduction to AlignIO module of the BioPython. • Converting file of a particular format into different formats of multiple sequence alignments. 	4:01	Alignment Parsing and Analysis	BioPython
48	AlignIO - Slicing Alignments	<ul style="list-style-type: none"> • Description of AlignIO module of BioPython package. • Reading a multiple sequence alignment file in a particular format. • Truncating a specific regions from the entire alignment. 	6:05	Alignment Parsing and Analysis	BioPython
49	AlignIO - Manipulating Alignments	<ul style="list-style-type: none"> • Describes the AlignIO module of BioPython package. • Reading a Multiple Sequence Alignment file of a particular format. • Manipulating the truncated alignments and the entire alignment. 	2:57	Alignment Parsing and Analysis	BioPython
50	AlignIO - ClustalW Python Wrapper - Align Multiple Sequences	<ul style="list-style-type: none"> • Describes the AlignIO module of the BioPython package. • Utilization of the ClustalW command-line software within BioPython. • Generating a guide tree of the aligned sequences using the Phylo module. 	7:47	Alignment Parsing and Analysis	BioPython
51	AlignIO - Pairwise2 - Align Two Sequences	<ul style="list-style-type: none"> • Describes AlignIO module within BioPython. • Performs pairwise sequence alignment on two sequences using the pairwise2 function. • Converting the alignment files into SeqRecords and the SeqRecords into separate files. 	7:31	Alignment Parsing and Analysis	BioPython
52	Bio.Blast - Querying NCBI BLAST Through Python	<ul style="list-style-type: none"> • Introduction to Bio.Blast module of BioPython package. • Querying NCBI BLAST tool using via Python using the Bio.Blast module of the BioPython packages. 	11:41	BLAST Database Searching	BioPython
53	Bio.Blast - Parsing BLAST Results	<ul style="list-style-type: none"> • Introduction to Bio.Blast module of BioPython package. • Parsing the BLAST results in Python using the Bio.Blast module to create a separate file of the results. 	14:51	Parsing BLAST results	BioPython
54	Bio.Entrez - Accessing ENTREZ Using Python	<ul style="list-style-type: none"> • Introduction to Bio.Entrez module of BioPython package. • Retrieving the information about all the databases of NCBI. • Performs a particular search within a single database utilizing the Entrez module. 	9:32	Biological Data Retrieval	BioPython
55	Bio.Entrez - Use ESearch to Search the Entrez Databases	<ul style="list-style-type: none"> • Description of Bio.Entrez module of BioPython. • Searching for a particular query in various databases of Entrez NCBI using the Entrez.esearch function 	8:20	Biological Data Retrieval	BioPython

56	Bio.Entrez - Use ESummary to Get Summary of Your Accessions	<ul style="list-style-type: none"> • Description of the Bio.Entrez module of BioPython. • Retrieval of information related to a particular query from a particular database using esummary function. 	8:59	Biological Data Retrieval	BioPython
57	Bio.Entrez - Use EFetch to Download Complete Records	<ul style="list-style-type: none"> • Elaborates Bio.Entrez module of BioPython. • Retrieval a particular query in various databases of Entrez NCBI using the Entrez.efetch() function. • Parsing the fetched information into a separate file using the SeqIO.read() function. 	13:56	Biological Data Retrieval	BioPython
58	Bio.Entrez - Use ELink to Search for Database Links of Records	<ul style="list-style-type: none"> • Describes Bio.Entrez module. • Utilization of the elink() function of Bio.Entrez module. • Retrieval of linked datasets related to a particular NCBI accession ID. 	3:41	Biological Data Retrieval	BioPython
59	Bio.Entrez - Use EGQuery to Do Global Queries for Search Counts	<ul style="list-style-type: none"> • Description of Bio.Entrez module. • Retrieving the count for a particular query/keyword against all databases of Entrez using the egquery() function. • Retrieving the count against a particular database by looping over the results. 	7:24	Biological Data Retrieval	BioPython
60	Bio.Entrez - Use ESpell to Get Correct Spellings for Your Search Terms	<ul style="list-style-type: none"> • Explains Bio.Entrez module and its functions. • Spelling correction in the query keywords using the Entrez.espell() function. 	5:21	Biological Data Retrieval	BioPython
61	Bio.Entrez - Download GenBank and Entrez Records	<ul style="list-style-type: none"> • Introduction to Bio.Entrez module. • Downloading multiple sequences from the GenBank database into a single file using some patches of code. 	14:17	Biological Data Retrieval	BioPython
63	Bio.Phylo - Writing Out Phylogenetic Data	<ul style="list-style-type: none"> • Introduction to Bio.Phylo module. • Writing the phylogenetic data in any phylogenetic tree format. • Writing multiple phylogenetic tree files into one single file. 	4:04	Phylogenetic Analysis	BioPython
64	Bio.Phylo - Calculating Distance Matrix Between Sequences for Phylogenetic Analysis	<ul style="list-style-type: none"> • Introduction to Bio.Phylo module. • Writing the phylogenetic data in any phylogenetic tree format. • Writing multiple phylogenetic tree files into one single file. 	4:18	Phylogenetic Analysis	BioPython
65	Bio.Entrez - Taxonomy Database Searching	<ul style="list-style-type: none"> • Introduction to Bio.Entrez module. • Searching Taxonomy database of NCBI using Bio.Entrez module of BioPython. • Retrieving the data about the lineage of an organism from the Taxonomy database of NCBI. 	7:05	Biological Data Retrieval	BioPython
66	Bio.Entrez - Download PubMed Articles	<ul style="list-style-type: none"> • Introduction to Bio.Entrez module. • Downloading research articles and literature from the PubMed database using some patches of code. 	8:28	Biological Data Retrieval	BioPython

67	Bio.PDB - Parsing Protein Structure Files	<ul style="list-style-type: none"> • Intrduction to Bio.PDB module. • Parsing a pdb structure file in BioPython and extracting precise and specific amount of information about a particular keyword. 	11:59	Parsing a PDB Structure file	BioPython
68	Bio.Phylo - Reading Phylogenetic Trees	<ul style="list-style-type: none"> • Intrduction to Bio.Phylo module. • Reading phylogenetic tree files in any format in BioPython. 	6:28	Phylogenetic Analysis	BioPython
69	Bio.Phylo - Converting Phylogenetic Tree Data Formats	<ul style="list-style-type: none"> • Intrduction to Bio.Phylo module. • Converting one phylogenetic tree format into another tree format using various functions of Bio.Phylo module of BioPython 	3:28	Phylogenetic Analysis	BioPython
70	Bio.Phylo - Printing Out Phylogenetic Tree in ASCII	<ul style="list-style-type: none"> • Intrduction to Bio.Phylo module. • Convrtng a phylogentic tree format into ASCII representation. 	2:17	Phylogenetic Analysis	BioPython
71	Bio.Phylo - Visualization and Manipulation of Phylogenetic Trees	<ul style="list-style-type: none"> • Intrduction to Bio.Phylo module. • Visualizing and manipulating a phylogenetic tree using various built-in functions of Bio. Phylo module. 	9:36	Phylogenetic Analysis	BioPython
72	Introduction to R in Bioinformatics & R Installation	<ul style="list-style-type: none"> • A detailed introduction to R language and importance of R language in Bioinformatics. • Describes the procedure of installation of R. 	9:47	Introduction	R
73	The R Studio Interface Explanation	<ul style="list-style-type: none"> • Introduction to R studio and basic description of R studio interface. • Describes windows and tabs of R studio in details. 	6:23	Introduction	R
74	Comments	<ul style="list-style-type: none"> • Introduction to comments in R language. • Describes purpose and advantages of adding comments in R language. • Describes different ways to add comments in R script. 	4:16	Introduction	R
75	Variable Declaration & Objects	<ul style="list-style-type: none"> • Description of Declaraing variables in R. • Describes mathematical operators that can be applied on variables. 	5:24	Variables & Functions	R
76	Built-in Functions and ARGS	<ul style="list-style-type: none"> • Introduction to built-in functions in R. • Describes syntax to write the functions in R. • Example code for using different built-in functions of R. 	4:31	Variables & Functions	R
77	Sample & Replacement	<ul style="list-style-type: none"> • Description of Sample and replacement in R. • Describes built-in function of R for sample and replacement. • Example code to sample out values randomly and getting independent values by using 'replace' parameter. 	9:09	Variables & Functions	R
78	Write Your Own Functions & Arguments	<ul style="list-style-type: none"> • Introduction to user-defined functions and its purpose. • Describes the syntax to write a function in R. • Example code to write the functions in R. 	5:39	Variables & Functions	R
79	Scripts	<ul style="list-style-type: none"> • Introduction to sripts in R and its importance. • Procedure to create a script in R. • Example code to write a script and describes how it run. 	7:36	Variables & Functions	R

80	Packages	<ul style="list-style-type: none"> • Introduction to Packages and their purpose in R language. • Accessing packages from Cran R-project website. • Retrieving information related to a particular package in R repository. 	4:00	Packages	R
81	install packages	<ul style="list-style-type: none"> • Procedure to access the packages within R language. • Discuss different methods to install packages such as comman-line, or through CRAN repository. 	5:25	Packages	R
82	library & Initialize Packages	<ul style="list-style-type: none"> • Description of Libraries in R langiage. • Procedure to initialize packages. • Discuss methods to initialize packages such as command-line or through package tab. 	2:27	Packages	R
83	Getting Help with Help Pages	<ul style="list-style-type: none"> • Description of getting help with help pages in R. • Describes syntax for particular function for getting help. • Describes functions with help commands for their functionality. 	3:42	Packages	R
84	Atomic Vectors	<ul style="list-style-type: none"> • Introduction to atomic vectors in R language. • Example code for creating atomic vectors. • Uses of atomic vectors in R language. 	2:42	Vectors & Data Types	R
85	Doubles	<ul style="list-style-type: none"> • Introduction to doubles in R language. • Describes double atomic vectors and initializing numeric values in R. • Example code to declare the atomic vectors and store multiple values in it. 	3:30	Vectors & Data Types	R
86	Integers	<ul style="list-style-type: none"> • Introduction to integers in R language. • Declaring integers in RStudio. • Finding datatype of an already existing integers. 	3:23	Vectors & Data Types	R
87	Characters	<ul style="list-style-type: none"> • Introduction to character datatype in R language. • Describes the use of character datatype in R. • Utilization of variables and storing them into single and multiple character values. 	4:43	Vectors & Data Types	R
88	Logicals	<ul style="list-style-type: none"> • Introduction to logicals in R language. • Example code to store the logicals in variables. 	2:27	Vectors & Data Types	R
89	Attributes & Names	<ul style="list-style-type: none"> • Description of attributes and names in R language. • Describes the use of attributes and names function in R. • Describes script to use these functions. 	4:46	Vectors & Data Types	R

90	Dim & Dimensions	<ul style="list-style-type: none"> • Introduction to Dim, a built-in function in R programming. • Creating data in a dimension and changing atomic vector's data into multi-dimensional data. • Importance of dim() function in Bioinformatics. 	5:46	Vectors & Data Types	R
91	Matrix & Matrices	<ul style="list-style-type: none"> • Introduction to Matrices in R language. • Purpose of matrix(), a built-in function in R programming. • Describes matrix initiation, customization of matrix rows and columns matrix layout. 	4:42	Vectors & Data Types	R
92	Arrays	<ul style="list-style-type: none"> • Introduction to arrays datatype in R programming language. • Different way of creating dimensions and multi-dimensions. • Describes kind of function to use for creating dimensional data depends upon the kind of analysis one is working on. 	3:42	Vectors & Data Types	R
93	Class	<ul style="list-style-type: none"> • Introduction classes in R programming language. • Use of built-in function class() in R programming. • Describe how classes in R represents data's classification. 	3:12	Vectors & Data Types	R
94	Factors	<ul style="list-style-type: none"> • Introduction to factors in R programming. • Importance of built-in function factor() in R language. • Describes script to categorize data using factor() function in R. 	6:40	Vectors & Data Types	R
95	Coercion	<ul style="list-style-type: none"> • Introduction to coercion in R language. • Describes to coerce integer data type to character data type using built-in functions in R. • Describes script to coerce one data type to another to make the function work properly. 	4:27	Vectors & Data Types	R
96	Lists	<ul style="list-style-type: none"> • Introduction to List data type in R language. • Describes how to work with lists in R programming. • Describes script for creating and retrieving lists in R programming. 	6:41	Vectors & Data Types	R
97	Data Frames	<ul style="list-style-type: none"> • Introduction to data frames in R programming language. • Describes characteristics of data frames. • Creating 2-D table of required data using built-in functions of data frame. 	6:30	Biological Data Analysis	R
98	Loading Biological Data	<ul style="list-style-type: none"> • Importing the biological data in R programming. • Different ways to import loading biological data. • Better visualization of data sets by loading data into R environment. 	7:55	Biological Data Analysis	R

99	Saving Biological Data	<ul style="list-style-type: none"> • Describes to save CSV file from R using built-in functions of R. • Getting working directive of the file. • Changing working directive of R files. 	5:26	Biological Data Analysis	R
100	R Notiation & Selecting Values from Biological Dataset	<ul style="list-style-type: none"> • Introduction to R Notation system. • Describes methods for selecting values from biological datasets. • Basic method to introspect data and use it for different analysis. 	4:09	Biological Data Analysis	R
101	Positive Integers for Subsetting Biological Dataset (DataFrame)	<ul style="list-style-type: none"> • Introduction to positive interger for extracting data from dataset in R. • Describes different ways to extract values and save them in new data frame. 	5:25	Biological Data Analysis	R
102	Negative Integers for Subsetting Biological Dataset (DataFrame)	<ul style="list-style-type: none"> • Introduction to negative integers for extracting data from dataset. • Describes different ways to extract values and save them in new data frame. 	5:28	Biological Data Analysis	R
103	Zero Notation for Subsetting Biological Dataset (DataFrame)	<ul style="list-style-type: none"> • Introdcution to zero notation for extracting values from datasets in R. • Describes different ways to extract data utilizing zero notation. 	1:09	Biological Data Analysis	R
104	Blank Spaces for Biological Data Subsetting	<ul style="list-style-type: none"> • Introduction to R notation system and blank spaces to extract data from datasets. • Describes script to extract data from datasets using blank spaces. • Advantages of blank spaces notation in R. 	3:20	Biological Data Analysis	R
105	Dollar Signs for Biological Data Subsetting	<ul style="list-style-type: none"> • Introduction to R notation system and dollar signs notation. • Describes script to extract data from data frames using dollar signs. 	2:58	Biological Data Analysis	R
106	Modifying Values in Existing DataFrames/Datasets	<ul style="list-style-type: none"> • Introduction to R notation system. • Describes script to modify values and creating new values using R notation system. 	7:06	Biological Data Analysis	R
107	NA Values in Biological Datasets	<ul style="list-style-type: none"> • Introduction to NA values in R datasets. • Finding NA values in R datasets. • Describes script to insert NA values in datasets using stats operations. 	5:24	Biological Data Analysis	R
108	Figuring Out NA Values in Biological Datasets	<ul style="list-style-type: none"> • Introductio to NA values in R datasets. • Describes to figure out NA values using built-in funcnyions. 	2:06	Biological Data Analysis	R
109	Logical Subsetting in Biological Datasets	<ul style="list-style-type: none"> • Introduction to logical subsetting in R language and its uses. • Describes various logical operators and their syntax. • Describes script for logical subsetting and its importance in analyzing data in Bioinformatics. 	9:45	Biological Data Analysis	R

110	if else Statements	<ul style="list-style-type: none"> • Introduction to if-else statements in R. • Describes the syntax of if-else statement. • Describes script to utilize these conditional statements in R programming. 	4:15	Control Flow	R
111	for Loops & Biological Data Binding	<ul style="list-style-type: none"> • Introduction to for loop in R programming language. • Describes the syntax of for loop and its uses. • Describes script to bind multiple CSV files into a single data frame utilizing for loop. 	16:30	Control Flow	R
112	while Loops & Reading Multiple Biological Datasets	<ul style="list-style-type: none"> • Introduction to while loop in R programming language. • Describes the syntax of while loop and its uses. • Describes script to read multiple files using the while loop and how it can be utilized to analyse data in Bioinformatics. 	16:16	Control Flow	R
113	Introduction to ggplot2 for Biological Datasets	<ul style="list-style-type: none"> • A detailed introduction to ggplot2 package in R programming. • Describes different ways to install ggplot2 package. • Describes how ggplot2 can be utilized for the visualization to represent the particular dataset 	10:46	Data Visualization: ggplot2	R
114	ggplot2: Key components	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R. • Describes different components and functions of ggplot2 package. • Describes the type of graphics to map against a particular dataset. 	8:25	Data Visualization: ggplot2	R
115	ggplot2: Human Mitochondrial Proteome & Aesthetics (Size, Shape, Color)	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Describes mapping of Biological datasets utilizing ggplot2 package. • Using mitochondrial proteome dataset to visualize data utilizing different functions and components of ggplot2 library. 	26:02:00	Data Visualization: ggplot2	R
116	ggplot2: Facetting of Human Genome	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Describes facetting of biological dataset using ggplot2 library. • Describes facetting functions and applying these functions to facet datasets. • Analyzing results of facetting for a particular dataset. 	22:25	Data Visualization: ggplot2	R
117	ggplot2: Smooth Out the Biological Data	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Describes smoothing out the biological data in ggplot2 package. • Describes parameters to smooth out the dataset. 	8:43	Data Visualization: ggplot2	R

118	ggplot2: Frequency Plots for Human Mitochondrial Information Frequency Mining	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Describes the frequency polygons in ggplot2 package. • Describes the utilization of geom_freqpoly() function to visualize biological dataset. 	6:12	Data Visualization: ggplot2	R
119	ggplot2: Bar Charts Human Mitochondrial Knowledge Mining	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Describes the use of bar charts in ggplot2 library. • Describes to utilize the geom_bar() function to visualize the biological dataset. 	10:43	Data Visualization: ggplot2	R
120	ggplot2: Boxplots for Human Mitochondrial Proteome	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Creating different boxplots to visualize the biological dataset. 	7:55	Data Visualization: ggplot2	R
121	ggplot2 :Histograms for Human Mitochondrial Pattern Finding	<ul style="list-style-type: none"> • Introduction to ggplot2 library in R programming. • Describes histograms in ggplot2 library or R. • Utilization of geom_histogram() function to visualize biological dataset. 	6:02	Data Visualization: ggplot2	R
122	ggplot2: Labels	<ul style="list-style-type: none"> • Description of ggplot2 package in R. • Visualize data utilizing different functions and components of ggplot2 library. • Changing labels and Finalizing visualizations. 	8:41	Data Visualization: ggplot2	R
123	ggplot2: Plot Phylogenetic Trees through ggtree	<ul style="list-style-type: none"> • Introduction to ggtree package in R. • Generating phylogenetic tree using ggtree library. • Descibes different functions, formats and parameters for generating phylogenetic tree. 	5:41	Data Visualization: ggplot2	R
124	Introduction to Linux for Bioinformatics	<ul style="list-style-type: none"> • Introduction to Unix and linux operating systems. • Difference between Linux and other operating systems. • Advantages and uses of Linux operating systems in Bioinformatics. 	22:31	Introduction	Linux
125	cd	<ul style="list-style-type: none"> • Description of cd command in Linux. • Lists various option for cd command. • Utilization of cd command to change the directive of various files on Linux. 	5:03	Managing Files and Directories	Linux
126	cp	<ul style="list-style-type: none"> • Description of cp command in Linux. • Lists various option for cp command. • Utilization of cp command to copy files and file contents on Linux. 	3:43	Managing Files and Directories	Linux
127	ls	<ul style="list-style-type: none"> • Description of ls command in Linux. • Lists various option for ls command. • Utilization of ls command for listing files and directories on Linux. 	6:45	Managing Files and Directories	Linux

128	mkdir	<ul style="list-style-type: none"> • Description of mkdir command in Linux. • Lists various option for mkdir command. • Utilization of mkdir command to make directories on Linux. 	8:12	Managing Files and Directories	Linux
129	mv	<ul style="list-style-type: none"> • Description of mv command in Linux. • Lists various option for mv command. • Utilization of mv command moving files quickly on Linux. 	5:10	Managing Files and Directories	Linux
130	rm	<ul style="list-style-type: none"> • Description of rm command in Linux. • Lists various option for rm command. • Utilization of rm command to remove files on Linux. 	1:23	Managing Files and Directories	Linux
131	pwd	<ul style="list-style-type: none"> • Description of pwd command in Linux. • Lists various option for pwd command. • Utilization of pwd command to print working directory on Linux. 	1:26	Managing Files and Directories	Linux
132	touch	<ul style="list-style-type: none"> • Description of touch command in Linux. • Lists various option for touch command. • Utilization of touch command for modifying file statistics and creating files on Linux. 	7:03	Managing Files and Directories	Linux
133	find	<ul style="list-style-type: none"> • Description of find command in Linux. • Lists various option for find command. • Utilization of find command for finding user created files on Linux. 	3:38	Finding Files	Linux
134	stat	<ul style="list-style-type: none"> • Description of stat command in linux. • Lists various options for stat command. • Using stat command to provide various statistical details about input files. 	2:43	Finding Files	Linux
135	which	<ul style="list-style-type: none"> • Description of which command in Linux. • Lists various option for which command. • Utilization of which command to find the installed programs on Linux. 	3:43	Finding Files	Linux
136	cat	<ul style="list-style-type: none"> • Description of cat command in Linux. • Lists various option for cat command. • Utilization of cat command for visualization and inspection of text data on Linux. 	3:55	Processing Files	Linux
137	cut	<ul style="list-style-type: none"> • Description of cut command in Linux. • Lists various option for cut command. • Utilization of cut command for cutting out the sections from each line of files and writing the results as standard output. 	5:48	Processing Files	Linux
138	diff	<ul style="list-style-type: none"> • Description of diff command in linux. • Lists different options for diff command. • Using diff command to find out differences between different files. 	2:34	Processing Files	Linux
139	grep	<ul style="list-style-type: none"> • Description of grep command in linux. • Lists different options for grep command. • Using grep command to find uncharacterized protein in human genome. 	8:55	Processing Files	Linux

140	sort	<ul style="list-style-type: none"> • Description of sort command in linux. • Lists different options for sort command. • Using sort command to sort datasets in tab delimited and other bioinformatics files. 	4:22	Processing Files	Linux
141	uniq	<ul style="list-style-type: none"> • Description of uniq command in linux. • Lists different options for uniq command. • Using uniq command to filter out the repeated lines in a file. In simple words. 	10:32	Processing Files	Linux
142	wc	<ul style="list-style-type: none"> • Description of wc command in linux. • Lists different options for wc command. • Using wc command to count number of words, chacters or lines within a file. 	2:45	Processing Files	Linux
143	gunzip	<ul style="list-style-type: none"> • Description of gunzip command in Linux. • Lists various option for gunzip command. • Utilization of gunzip command to extract compressed content of file on Linux. 	2:14	Archiving & Compressing Files	Linux
144	gzip	<ul style="list-style-type: none"> • Description of gzip command in Linux. • Lists various option for gzip command. • Utilization of gzip command to compress and archive files efficiently on Linux. 	6:05	Archiving & Compressing Files	Linux
145	tar	<ul style="list-style-type: none"> • Description of tar command in linux. • Lisis different options for tar command. • Using tar command to create archives of genome data. 	4:18	Archiving & Compressing Files	Linux
146	wget	<ul style="list-style-type: none"> • Description of wget command in linux. • Lists different options for wget command. • Uding wget command to retrieve genome assemblies. 	6:48	Displaying Dates & Time	Linux
147	Column	<ul style="list-style-type: none"> • Description of column command in linux. • Lists different options for column command. • Using column command to retrieve specific columns from tab delimited or comma delimited files. 	4:38	Processing Files	Linux
148	head	<ul style="list-style-type: none"> • Description of head command in Linux. • Lists various option for head command. • Utilization of head command to read specified number of lines from top in files on Linux. 	3:49	Processing Files	Linux
149	tail	<ul style="list-style-type: none"> • Description of tail command in Linux. • Lists various option for tail command. • Utilization of tail command to read specified number of lines from botton in files on Linux. 	2:22	Processing Files	Linux
150	(Piping)	<ul style="list-style-type: none"> • Description of Piping character in Linux. • Utilization of piping methodologies for bioinformatics analysis. 	6:34	Piping & Redirection	Linux
151	vim	<ul style="list-style-type: none"> • Description of vim command in Linux. • Lists various option for vim command. • Utilization of vim command to create and edit text files. 	5:58	Text Editor	Linux

152	curl	<ul style="list-style-type: none">• Description of curl command in Linux.• Lists various option for curl command.• Utilization of curl command for retrieval of Bioinformatics files.	2:25	Displaying Dates & Time	Linux
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