Sr. No	Videos	Description	Duration	Catagory	Main Category
		Segment 5: Bioinformatics Scripting in Linux, Python and R			
1	Introduction to Python and Python Installation	• 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	• 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	• Description of Basic input and output function in Python language. • Example code to print out values and characters. • Getting intput from the user and printing it out.	15:37	Introduction	Python
4	Mathematical Operations	• Description of different operators to perform that perform vaious 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	• 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	• 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	• 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	• 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 thay can be used to keep data unmanipulated.	10:37:00	Iterable Objects	Python

9	Dictionaries	· 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	· 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	· 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)	· 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	· 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	· 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)	· 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)	· 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)	· 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	• 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
		• 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	• 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	• 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	• 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	• Introduction to modules and their uses within Python. • Procedure for installation of modules. • Describes Python script for imporing, creating and testing modules.	16:50	Functions & Modules	Python
24	Error Handling	• 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	• 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 it modules.	10:18	Introduction	BioPython

26	Bio.Seq Create a Seq Object	• 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	• 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	• 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, transcripted and back-transcripted sequences by built-in
		  functions of Bio.Seq.
			8:41	Sequence Analysis	BioPython

29	Bio.Seq Unkown & Mutable Sequences	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• Description of the AlignIO module within BioPython Package. • Information mapping of alignments.	2:33	Alignment Parsing and Analysis	BioPython
46	AlignIO – Format Alignments	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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 Quries for Search Counts	• 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	• Explains Bio.Entrex 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	• Intrduction 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	• Intrduction 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	• Intrduction 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	• Intrduction to Bio.Entrez module. • Searching Taxonomy database of NCBI using Bio.Entrez module of BioPython. • Retrieveing 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	• 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	• 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	• 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	• 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	• Intrduction to Bio.Phylo module. • Convrting a phylogentic tree format into ASCII representation.	2:17	Phylogenetic Analysis	BioPython
71	Bio.Phylo - Visualization and Manipulation of Phylogenetic Trees	• 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	• 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 Explaination	• 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	• 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	• Description of Declaraing variables in R. • Describes mathmatical operators that can be applied on variables.	5:24	Variables & Functions	R
76	Built-in Functions and ARGS	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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 multple values in it.	3:30	Vectors & Data Types	R
86	Integers	• 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	• 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	• Introduction to logicals in R language. • Example code to store the logicals in variables.	2:27	Vectors & Data Types	R
89	Attributes & Names	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• Importing the biological data in R proramming. • 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	• 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	• 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)	• 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)	• 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)	• 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	• 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	• 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	• 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	• 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	• Introduction to NA values in R datasets. • Describes to figure out NA values using built-in funcyions.	2:06	Biological Data Analysis	R
109	Logical Subsetting in Biological Datasets	• Introduction to ligical 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	• 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	• Introduction to for loop in R programminf 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	• 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	• 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	• 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)	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• Description of stat command in linux. • Lisls various options for stat command. • Using stat command to provide various statistical details about input files.	2:43	Finding Files	Linux
135	which	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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)	• Description of Piping character in Linux. • Utilization of piping methodologies for bioinformatics analysis.	6:34	Piping & Redirection	Linux
151	vim	• 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 | • 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 |