Sr. No	Videos	Description	Duration	Catagory	Main Category
	Segment 4: Predictive Bioinformatics				
1	Prodigal	• 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	• 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	• Utilization of GenScan webserver for gene prediction. • Describes the parameters of GenScan. • Analysis of a particluar nucleotide sequence and predicting gene out of it.	10:40	Gene Prediction	Gene Prediction
4	AUGUSTUS	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• Introduction to homology modeling and Molecular Operating Enviroment (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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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	• 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 addict.	19:48	Molecular Docking	Molecular Docking
29	SwissDock Protein Ligand Docking	• 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	• 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	• 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	• Introduction to ClusPro server and its purpose. • Utilization of various features of ClusPro to perform protein-protein doc king. • Describes advanced functionalities offered by ClusPro to select the best docked complex.	21:44	Molecular Docking	Molecular Docking

33	MDockPEP protein peptide docking	• 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	• 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	• 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	• 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