

| Serial | Name | Durations | Category | Main Category |
|--------|---|-----------|--|--|
| 1 | In-Depth Introduction to Bioinformatics Freelancing | | Introduction to Bioinformatics Freelancing | Introduction to Bioinformatics Freelancing |
| 2 | In-Depth Guide on FIVERR | | Top Platforms for Freelancing | Top Platforms for Freelancing |
| 3 | In-Depth Guide on Upwork | | Top Platforms for Freelancing | Top Platforms for Freelancing |
| 4 | What Kind of Services Can You Sell as a Bioinformatician? | | How to Set Up Your Bioinformatics Services | How to Set Up Your Bioinformatics Services |
| 5 | What Exactly Do You Need to Learn to Provide Your Services? | | How to Set Up Your Bioinformatics Services | How to Set Up Your Bioinformatics Services |
| 6 | How to Connect With Clients and Accept Their Projects? | | How to Set Up Your Bioinformatics Services | How to Set Up Your Bioinformatics Services |
| 7 | Case Study 1: Mutagenesis of Proteins Using PyMol | | Case Studies | Case Studies |
| 8 | Case Study: Scripting for Biological Analysis | | Case Studies | Case Studies |
| 9 | Case Study 3: Functional Bioinformatics Analysis | | Case Studies | Case Studies |
| 10 | Introduction to National Center of Biotechnology Information (NCBI) | 18:01 | NCBI | Bioinformatics Databases |
| 11 | Sequence Analysis | 17:59 | NCBI | Bioinformatics Databases |
| 12 | Sequence Retrieval from NCBI | 16:16 | NCBI | Bioinformatics Databases |
| 13 | PubMed Central & ENTREZ | 11:06 | NCBI | Bioinformatics Databases |
| 14 | FASTA (Sequence Format) | 6:13 | Sequence Format | Bioinformatics File Formats |
| 15 | GenBank: Nucleotide Database on NCBI | 6:50 | NCBI | Bioinformatics Databases |
| 16 | GenBank (Sequence Annotation Format) | 7:08 | Sequence Format | Bioinformatics File Formats |
| 17 | FASTA vs. GenBank | 18:26 | NCBI | Bioinformatics Databases |
| 18 | Gene Database: A Comprehensive Gene Database | 30:21:00 | NCBI | Bioinformatics Databases |
| 19 | NCBI Genomes & NCBI Assembly: Retrieval of Genomes | 36:14:00 | NCBI | Bioinformatics Databases |
| 20 | FASTQ Format | 18:01 | Sequence Format | Bioinformatics File Formats |
| 21 | Gene File Format/Gene Transfer Format | 11:06 | Sequence Format | Bioinformatics File Formats |
| 22 | BED (Gene Structure Format) | 4:26 | Sequence Format | Bioinformatics File Formats |
| 23 | SAM | 9:06 | Sequence Format | Bioinformatics File Formats |
| 24 | BAM | 9:06 | Sequence Format | Bioinformatics File Formats |
| 25 | RefSeq Database: Retrieval of Single Reference Sequences | 11:15 | NCBI | Bioinformatics Databases |
| 26 | BLAST Database Searching | 25:36:00 | NCBI | Bioinformatics Databases |
| 27 | Introduction to Molecular Modeling Database (MMDB) | 8:06 | NCBI | Bioinformatics Databases |
| 28 | Database of Short Genetic Variations (dbSNP) | 12:16 | NCBI | Bioinformatics Databases |
| 29 | HomoloGene: Discovery of Gene and Protein Families | 6:10 | NCBI | Bioinformatics Databases |
| 30 | Taxonomy | 9:56 | NCBI | Bioinformatics Databases |
| 31 | Introduction to UCSC Genome Browser & SARS-CoV-2 Viral Genome | 13:40 | UCSC | Bioinformatics Databases |
| 32 | Retrieve an Entire Genome & Retrieval of SARS-CoV-2 Viral Genome | 9:40 | UCSC | Bioinformatics Databases |

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| 33 | Retrieval of Genomic Data & Annotation of SARS-CoV-2 Viral Genome | 5:29 | UCSC | Bioinformatics Databases |
| 34 | Table Browser & SARS-CoV-2 Viral Genome | 12:15 | UCSC | Bioinformatics Databases |
| 35 | Visualization of Genomic Data on the Genome Browser & SARS-CoV-2 Genome | 10:51 | UCSC | Bioinformatics Databases |
| 36 | Introduction to UniProt | 9:56 | UniProt | Protein Databases & Analysis |
| 37 | UniProtKB & Protein Analysis | 39:29:00 | UniProt | Protein Databases & Analysis |
| 38 | UniProteome & Retrieval of an Entire Proteome | 13:05 | UniProt | Protein Databases & Analysis |
| 39 | UniProt BLAST - Database Searching | 12:32 | UniProt | Bioinformatics Databases |
| 40 | ID Mapping & Making Analysis Easier | 7:17 | UniProt | Protein Databases & Analysis |
| 41 | UniProt Peptide Search - Find Regions Within UniProt Database | 3:15 | UniProt | Bioinformatics Databases |
| 42 | Introduction to Protein Data Bank (PDB) | 6:44 | PDB | Protein Databases & Analysis |
| 43 | Accurately Searching for a Protein Structure on PDB & Protein Analysis | 13:55 | PDB | Protein Databases & Analysis |
| 44 | Biological Annotation and Protein Features View & Analysis | 8:18 | PDB | Protein Databases & Analysis |
| 45 | Browsing PDB According to Annotation | 6:52 | PDB | Protein Databases & Analysis |
| 46 | Digging Out Categorized & Specific Protein Structures from PDB Archives | 6:23 | PDB | Protein Databases & Analysis |
| 47 | Alignment Between Two PDB Sequences & Structures | 6:07 | PDB | Protein Databases & Analysis |
| 48 | 3D Structure Visualization on PDB | 10:49 | PDB | Protein Databases & Analysis |
| 49 | Mapping Genomic Position to Protein Sequence and 3D Structure | 4:34 | PDB | Protein Databases & Analysis |
| 50 | Genomic Discovery of Protein Structure Through Gene | 4:07 | PDB | Protein Databases & Analysis |
| 51 | PDB - Protein Symmetry | 2:34 | PDB | Protein Databases & Analysis |
| 52 | Introduction to ENSEMBL | 7:49 | ENSEMBL | Bioinformatics Databases |
| 53 | Retrieval of a Gene-Protein-Chromosomal Region | 18:01 | ENSEMBL | Bioinformatics Databases |
| 54 | Genome Assembly Retrieval and Analysis | 10:23 | ENSEMBL | Bioinformatics Databases |
| 55 | Gene Analysis & Annotation | 34:40:00 | ENSEMBL | Bioinformatics Databases |
| 56 | Variation Analysis | 24:36:00 | ENSEMBL | Bioinformatics Databases |
| 57 | ENSEMBL BLAST/BLAT | 15:08 | ENSEMBL | Bioinformatics Databases |
| 58 | Regulation - Understand the Influence of Regulatory Elements on Genes | 4:18 | ENSEMBL | Bioinformatics Databases |
| 59 | Comparative Genomics Analysis | 5:34 | ENSEMBL | Bioinformatics Databases |
| 60 | Introduction to InterPro | 4:10 | InterPro | Protein Databases & Analysis |
| 61 | InterPro - Protein Family Classification and Analysis | 14:35 | InterPro | Protein Databases & Analysis |
| 62 | InterPro - Protein & Protein Domain Analysis | 9:29 | InterPro | Protein Databases & Analysis |
| 63 | Introduction to Phytozome | 9:38 | Phytozome | Bioinformatics Databases |
| 64 | Interpret Plant Genome Records | 9:06 | Phytozome | Bioinformatics Databases |
| 65 | Download an Entire Plant Genome & Proteome | 26:41:00 | Phytozome | Bioinformatics Databases |
| 66 | Keyword or BLAST Search in a Plant Genome | 15:58 | Phytozome | Bioinformatics Databases |

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| 67 | Visualize a Plant Genome Using JBrowse | 17:38 | Phytozome | Bioinformatics Databases |
| 68 | UniProt Align - Pairwise & Multiple Sequence Alignment and Annotation | 3:47 | UniProt | Bioinformatics Databases |
| 69 | EMBOSS NEEDLE: Global Alignment of Sequences | 20:02 | Pairwise Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 70 | EMBOSS Water | 9:10 | Pairwise Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 71 | Clustal Omega: Most Reliable Multiple Sequence Alignment Tool | 19:18 | Multiple Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 72 | Clustal Omega Alignment Format | 5:07 | Alignment Format | Bioinformatics File Formats |
| 73 | Jalview | 13:42 | Multiple Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 74 | T-Coffee: Iterative Multiple Sequence Alignment Tool | 8:37 | Multiple Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 75 | MUSCLE: Accurate Multiple Sequence Alignment Tool | 21:07 | Multiple Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 76 | MEGA - Multiple Sequence Alignment | 4:23 | Multiple Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 77 | MEGA (Alignment Format) | 5:32 | Alignment Format | Bioinformatics File Formats |
| 78 | MAFFT - Fastest Multiple Sequence Alignment Tool | 8:22 | Multiple Sequence Alignment & Analysis | Sequence Alignment & Analysis |
| 79 | PHYLIP - Multiple Sequence Alignment Format | 4:34 | Alignment Format | Bioinformatics File Formats |
| 80 | Stockholm Alignment Format | 3:10 | Alignment Format | Bioinformatics File Formats |
| 81 | Aln2Plot | 2:30 | Sequence Analysis | Sequence Alignment & Analysis |
| 82 | MEGA | 21:20 | Phylogenetic Analysis | Phylogenetic Analysis |
| 83 | iTOL: Creating Publishable Phylogenetic Figures | 13:42 | Phylogenetic Tree Visualization & Analysis | Phylogenetic Analysis |
| 84 | FigTree | 21:26 | Phylogenetic Tree Visualization & Analysis | Phylogenetic Analysis |
| 85 | Quick2D | 4:33 | Secondary Structure Prediction | Secondary Structure Prediction |
| 86 | Ali2D | 4:09 | Secondary Structure Prediction | Secondary Structure Prediction |
| 87 | Jpred: Prediction Secondary Structure of the Proteins | 4:54 | Secondary Structure Prediction | Secondary Structure Prediction |
| 88 | HHrepID | 5:15 | Secondary Structure Prediction | Secondary Structure Prediction |
| 89 | DeepCoil | 3:22 | Secondary Structure Prediction | Secondary Structure Prediction |
| 90 | REPPER - Predict Gapless Repeats in Proteins | 2:25 | Secondary Structure Prediction | Secondary Structure Prediction |
| 91 | HMMER - Hidden Markov Model Based Protein Profiles Database | 13:16 | Protein Analysis | Protein Databases & Analysis |
| 92 | SignalP: Prediction of Signal Peptides | 7:57 | Protein Analysis | Protein Databases & Analysis |
| 93 | TargetP: Prediction of Protein Localization | 9:21 | Protein Analysis | Protein Databases & Analysis |
| 94 | Pfam - Understand the Relation of a Protein to its Family and Clan | 15:55 | Protein Family Database | Protein Databases & Analysis |
| 95 | PROSITE - A Database of Protein Domian, Families and Functional Sites | 13:46 | Protein Family Database | Protein Databases & Analysis |
| 96 | ScanProsite - Scanning Protein for Important Protein Sites Against PROSITE Databas | 7:36 | Motif & Domain Analysis | Protein Databases & Analysis |
| 97 | Marcoil - Predict Coiled Coil Domains in Proteins | 4:05 | Motif & Domain Analysis | Protein Databases & Analysis |
| 98 | SMART | 6:44 | Motif & Domain Analysis | Protein Databases & Analysis |
| 99 | PDB - Ligands | 5:23 | PDB | Protein Databases & Analysis |
| 100 | MODELLER: Most Commonly Used Homology Modelling | 36:13:00 | 3D Structure Prediction | 3D Structure Prediction |

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| 101 | SwissModel: Homology Modeling Through Web-server | 12:52 | 3D Structure Prediction | 3D Structure Prediction |
| 102 | HHPred | 14:09 | 3D Structure Prediction | 3D Structure Prediction |
| 103 | M4T | 9:26 | 3D Structure Prediction | 3D Structure Prediction |
| 104 | IntFold | 8:41 | 3D Structure Prediction | 3D Structure Prediction |
| 105 | ROBETTA: ab initio Protein Structure Prediciton | 14:39 | 3D Structure Prediction | 3D Structure Prediction |
| 106 | Homology Modeling Using MOE | 12:34 | 3D Structure Prediction | 3D Structure Prediction |
| 107 | UCSF CHIMERA | 25:23:00 | 3D Structure Visualization | 3D Structure Visualization |
| 108 | PyMol | 40:48:00 | 3D Structure Visualization | 3D Structure Visualization |
| 109 | WhatCheck | 8:40 | 3D Structure Evaluation | 3D Structure Evaluation |
| 110 | ProCheck | 12:40 | 3D Structure Evaluation | 3D Structure Evaluation |
| 111 | ERRAT | 6:44 | 3D Structure Evaluation | 3D Structure Evaluation |
| 112 | Verify3D | 8:31 | 3D Structure Evaluation | 3D Structure Evaluation |
| 113 | RAMPAGE | 3:29 | 3D Structure Evaluation | 3D Structure Evaluation |
| 114 | SAVES | 5:31 | 3D Structure Evaluation | 3D Structure Evaluation |
| 115 | PROSA | 10:05 | 3D Structure Evaluation | 3D Structure Evaluation |
| 116 | MOE: Protein Ligand Docking | 9:23 | Molecular Docking | Molecular Docking |
| 117 | MOE: Protein Protein Docking | 11:38 | Molecular Docking | Molecular Docking |
| 118 | SwissDock Protein Ligand Docking | 19:16 | Molecular Docking | Molecular Docking |
| 119 | Autodock Vina Protein Ligand Docking | Not Yet Available | Molecular Docking | Molecular Docking |
| 120 | MOE: Structure Based Drug Desinging | 16:19 | Molecular Docking | Molecular Docking |
| 121 | MOE: Docking Library of Compounds | 19:48 | Molecular Docking | Molecular Docking |
| 122 | ClusPro Protein Protein Docking | 21:44 | Molecular Docking | Molecular Docking |
| 123 | Patchdock Protein Protein Docking | 17:39 | Molecular Docking | Molecular Docking |
| 124 | PEPFOLD 3 Peptide Structure Prediction | 13:14 | Molecular Docking | Molecular Docking |
| 125 | Zdock Protein Protein/Ligand docking | 19:35 | Molecular Docking | Molecular Docking |
| 126 | MDockPEP Protein Peptide Docking | 10:06 | Molecular Docking | Molecular Docking |
| 127 | Discovery Studio+ | 12:03 | Molecular Docking | Molecular Docking |
| 128 | PDBsum Docking Complex Evaluation | 18:49 | Docking Complex Evaluation | Docking Complex Evaluation |
| 129 | Pdbepisa Docking Complex Evaluation | 23:27 | Docking Complex Evaluation | Docking Complex Evaluation |
| 130 | SwissADME | 15:31 | Docking Complex Evaluation | Docking Complex Evaluation |
| 131 | GeneMark: Gene Prediction from Eukaryotic Genomes | 16:51 | Gene Prediction | Gene Prediction |
| 132 | Prodigal: Gene Prediction from Microbial Genomes | 25:46:00 | Gene Prediction | Gene Prediction |
| 133 | GenScan - Prediction of Genes from Green Monkey and Finding a Novel Gene | 10:40 | Gene Prediction | Gene Prediction |
| 134 | AUGUSTUS - Prediction of Novel Genes in Star Fish or Any Genome | 17:27 | Gene Prediction | Gene Prediction |

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| 135 | UniRef And Retrieve Protein Clusters | 11:35 | UniProt | Bioinformatics Databases |
| 136 | UniParc And Find the Non-Redundant Entries | 4:38 | UniProt | Bioinformatics Databases |
| 137 | Genome Reference Consortium (GRC) | 7:48 | NCBI | Bioinformatics Databases |
| 138 | BioProject | 6:39 | NCBI | Bioinformatics Databases |
| 139 | BioSystems | 4:16 | NCBI | Bioinformatics Databases |
| 140 | BioSample | 2:56 | NCBI | Bioinformatics Databases |
| 141 | Sequence Read Archive (SRA) | 7:14 | NCBI | Bioinformatics Databases |
| 142 | Introduction to Gene Expression Omnibus Database | 9:15 | NCBI | Bioinformatics Databases |
| 143 | Gene Expression Omnibus - Platforms | 5:42 | NCBI | Bioinformatics Databases |
| 144 | Gene Expression Omnibus - Samples | 4:15 | NCBI | Bioinformatics Databases |
| 145 | Gene Expression Omnibus - Series | 4:00 | NCBI | Bioinformatics Databases |
| 146 | Gene Expression Omnibus - Datasets | 4:44 | NCBI | Bioinformatics Databases |
| 147 | STRING: Comprehensive Protein-Protein Interaction Database | 13:16 | PPI Database | PPI Database |
| 148 | Gene Structure Display Server 2.0 | 8:35 | Genomics Tools | Genomics Tools |
| 149 | Molecular Dynamics Simulation - Pre-processing of Protein Structure and Removal of Unnc | 12:33 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 150 | pdb2gmx - Construction of Topology File for Simulation | 9:00 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 151 | Defining a Solvant Box for Simulation | 4:14 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 152 | Solvation - Adding Water Molecules in Solvant Box | 5:30 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 153 | Generating Input Run File Replacement of Water Molecues With Ions | 6:55 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 154 | genion - Replacement of Water Molecules With Ions | 4:18 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 155 | Energy Minimization - Relaxing and Fixing the Structure for Simulation | 11:25 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 156 | GRACE - Visualization and Analysis of Minimized Structure | 4:11 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 157 | Equilibration of Protein Structure NVT ENSEMBLE Phase 1 | 8:37 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 158 | Equilibration of Protein Structure NPT ENSEMBLE Phase 2 | 8:09 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 159 | mdrun - Executing Simulation Analysis | 3:46 | Molecular Dynamics Simulations: GROMACS | Molecular Dynamics Simulation |
| 160 | Virulence Factor Database | | Vaccine Development | Drug Designing & Discovery |
| 161 | Database of Essential Genes | | Vaccine Development | Drug Designing & Discovery |
| 162 | Drug Databank | | Vaccine Development | Drug Designing & Discovery |
| 163 | Sortaller | | Vaccine Development | Drug Designing & Discovery |
| 164 | Algpred | | Vaccine Development | Drug Designing & Discovery |
| 165 | Allertop | | Vaccine Development | Drug Designing & Discovery |
| 166 | Vaxijen | | Vaccine Development | Drug Designing & Discovery |
| 167 | Antigenpro | | Vaccine Development | Drug Designing & Discovery |
| 168 | CD-HIT | | Vaccine Development | Drug Designing & Discovery |

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| 169 | Netct1.2 | | Vaccine Development | Drug Designing & Discovery |
| 170 | MHC I | | Vaccine Development | Drug Designing & Discovery |
| 171 | MHC II | | Vaccine Development | Drug Designing & Discovery |
| 172 | Netmhc II | | Vaccine Development | Drug Designing & Discovery |
| 173 | Galaxy Refine | | Vaccine Development | Drug Designing & Discovery |
| 174 | Modrefiner | | Vaccine Development | Drug Designing & Discovery |
| 175 | IEDB Conservancy | | Vaccine Development | Drug Designing & Discovery |
| 176 | IEDB Immunogenicity | | Vaccine Development | Drug Designing & Discovery |
| 177 | Toxinpred | | Vaccine Development | Drug Designing & Discovery |
| 178 | Elliprosuite | | Vaccine Development | Drug Designing & Discovery |
| 179 | Doscotope2.0 | | Vaccine Development | Drug Designing & Discovery |
| 180 | BCpreds | | Vaccine Development | Drug Designing & Discovery |
| 181 | Bepipred | | Vaccine Development | Drug Designing & Discovery |
| 182 | ABCpred | | Vaccine Development | Drug Designing & Discovery |
| 183 | Cofactor | | Vaccine Development | Drug Designing & Discovery |
| 184 | Castp | | Vaccine Development | Drug Designing & Discovery |
| 185 | C-Immsim | | Vaccine Development | Drug Designing & Discovery |
| 186 | Jcat | | Vaccine Development | Drug Designing & Discovery |
| 187 | IFNepitope | | Vaccine Development | Drug Designing & Discovery |
| 188 | Maestro | | Vaccine Development | Drug Designing & Discovery |
| 189 | SnapGene | | Vaccine Development | Drug Designing & Discovery |
| 190 | DNASTAR | | Vaccine Development | Drug Designing & Discovery |
| 191 | CLC Sequence Viewer | | Vaccine Development | Drug Designing & Discovery |
| 192 | Why Python in Bioinformatics | 9:16 | Introduction | Python |
| 193 | Introduction to Python and it's Intallation | 8:25 | Introduction | Python |
| 194 | Comments | 5:42 | Introduction | Python |
| 195 | Basic Input and output | 15:37 | Introduction | Python |
| 196 | Mathematical Operations | 7:20 | Introduction | Python |
| 197 | Strings | 21:51 | Iterable Objects | Python |
| 198 | Dictionaries | 10:57 | Iterable Objects | Python |
| 199 | Lists | 28:47:00 | Iterable Objects | Python |
| 200 | Lists(pt 2) and Tuples | 10:37:00 | Iterable Objects | Python |
| 201 | Sets | 7:35 | Iterable Objects | Python |
| 202 | If-Else | 9:19 | Control Flow | Python |

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|-----|---|----------|--------------------------------|-----------|
| 203 | For Loop and calc of Mol. weight | 10:56 | Control Flow | Python |
| 204 | While Loop | 9:37 | Control Flow | Python |
| 205 | Reading Files | 13:45 | File Handling | Python |
| 206 | CSV | 8:41 | File Handling | Python |
| 207 | Writing Files | 7:17 | File Handling | Python |
| 208 | Consolidate(merge) multiple DNA and Protein Sequences into one FASTA file | 9:24 | File Handling | Python |
| 209 | OS | 31:47:00 | File Handling | Python |
| 210 | Function | 26:41:00 | Functions & Modules | Python |
| 211 | With | 8:50 | Functions & Modules | Python |
| 212 | Error Handling | 15:31 | Error Handling | Python |
| 213 | Introduction to BioPython & Installation | 10:18 | Introduction | BioPython |
| 214 | Bio.Seq Create a Seq Object | 7:38 | Sequence Analysis | BioPython |
| 215 | Bio.Seq Seq Object Behaves Like a String | 9:54 | Sequence Analysis | BioPython |
| 216 | Bio.Seq Central Dogma in Play Through Python | 8:41 | Sequence Analysis | BioPython |
| 217 | Bio.Seq Unkown & Mutable Sequences | 6:53 | Sequence Analysis | BioPython |
| 218 | Bio.Alphabet Understanding the Alphabets of Biology | 7:37 | Sequence Analysis | BioPython |
| 219 | Bio.Alphabet IUPAC and Types of Sequence Representations | 10:34 | Sequence Analysis | BioPython |
| 220 | Bio.Alphabet Concatenation of Multiple Seq Records Using Generic Alphabets | 9:47 | Sequence Analysis | BioPython |
| 221 | SeqRecord Creating Seq Records | 12:27 | Sequence Analysis | BioPython |
| 222 | SeqRecords & FASTA | 4:35 | Sequence Analysis | BioPython |
| 223 | SeqRecords & GenBank | 3:28 | Sequence Analysis | BioPython |
| 224 | SeqRecord Formatting Records | 3:47 | Sequence Analysis | BioPython |
| 225 | SeqRecord Comparison & Reading Multiple FASTA Files from Directory | 5:47 | Sequence Analysis | BioPython |
| 226 | SeqIO Reading a Sequence File | 10:32 | Sequence Data Parsing | BioPython |
| 227 | SeqIO Parsing a Sequence File | 7:16 | Sequence Data Parsing | BioPython |
| 228 | SeqIO Parsing a Compressed Sequence File & Creating a Dictionary of Sequences | 6:10 | Sequence Data Parsing | BioPython |
| 229 | SeqIO - Write Sequences and SeqRecords Into Files | 11:42 | Sequence Data Parsing | BioPython |
| 230 | SeqIO Extracting Annotations and Pattern-wise Sequence Data Extraction | 10:35 | Sequence Data Extraction | BioPython |
| 231 | AlignIO - Reading and Parsing a Multiple Sequence Alignment File | 8:19 | Alignment Parsing and Analysis | BioPython |
| 232 | AlignIO - Writing Alignments and Multiple Sequence Alignment Records | 5:28 | Alignment Parsing and Analysis | BioPython |
| 233 | AlignIO - Conversion of Alignment Formats | 4:01 | Alignment Parsing and Analysis | BioPython |
| 234 | AlignIO - Manipulating Alignments | 2:57 | Alignment Parsing and Analysis | BioPython |
| 235 | AlignIO - ClustalW Python Wrapper - Align Multiple Sequences | 7:47 | Alignment Parsing and Analysis | BioPython |
| 236 | AlignIO - Pairwise2 - Align Two Sequences | 7:31 | Alignment Parsing and Analysis | BioPython |

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| 271 | Install Packages | 5:25 |
| 272 | Library & Initialize Packages | 2:27 |
| 273 | Getting Help with Help Packages | 3:42 |
| 274 | Atomic Vectors | 2:42 |
| 275 | Doubles | 3:30 |
| 276 | Integers | 3:23 |
| 277 | Characters | 4:43 |
| 278 | Logicals | 2:27 |
| 279 | Attributes and Names | 4:46 |
| 280 | Dim & Dimensions | 5:46 |
| 281 | Matrix & Matrices | 4:42 |
| 282 | Arrays | 3:42 |
| 283 | Class | 3:12 |
| 284 | Factors | 6:40 |
| 285 | Coercion | 4:27 |
| 286 | Lists | 6:41 |
| 287 | Data Frames | 6:30 |
| 288 | Loading Biological Data | 7:55 |
| 289 | Saving Biological Data | 5:26 |
| 290 | R Notation & Selecting Values from Biological Dataset | 4:09 |
| 291 | Positive Integers for subsetting Biological Dataset(DataFrame) | 5:25 |
| 292 | Negative Integers for subsetting Biological Dataset(DataFrame) | 5:28 |
| 293 | Zero Notation for subsetting Biological Datasets (DataFrames) | 1:09 |
| 294 | Blank Spaces For Biological Data Subsetting | 3:20 |
| 295 | Dollar Signs for Biological Dataset Subsetting | 2:58 |
| 296 | Modifying Values in Existing DataFrames/Datasets | 7:06 |
| 297 | NA Values in Biological Dataset | 5:24 |
| 298 | Figuring out NA Values in Biological Dataset | 2:06 |
| 299 | Logical Subsetting in Biological Datasets | 9:45 |
| 300 | If Else Statement | 4:15 |
| 301 | Comments | 4:16 |
| 302 | For Loops & Biological Data Binding | 16:30 |
| 303 | & Reading Multiple Biological Datasetswhile Loops & Reading Multiple Biolog | 16:16 |
| 304 | Introduction to ggplot2 for Biological Datasets | 10:46 |

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| Packages | R |
| Packages | R |
| Packages | R |
| Vectors & Data Types | R |
| Vectors & Data Types | R |
| Vectors & Data Types | R |
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| Biological Data Analysis | R |
| Control Flow | R |
| Introduction | R |
| Control Flow | R |
| Control Flow | R |
| Data Visualization: ggplot2 | R |

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| 305 | ggplot2: Key components | 8:25 | Data Visualization: ggplot2 | R |
| 306 | ggplot2: Human Mitochondrial Proteome & Aesthetics (Size, Shape, Color) | 26:02:00 | Data Visualization: ggplot2 | R |
| 307 | ggplot2: Facetting of Human Genome | 22:25 | Data Visualization: ggplot2 | R |
| 308 | ggplot2: Smooth Out the Biological Data | 8:43 | Data Visualization: ggplot2 | R |
| 309 | ggplot2: Boxplots for Human Mitochondrial Proteome | 7:55 | Data Visualization: ggplot2 | R |
| 310 | ggplot2 :Histograms for Human Mitochondrial Pattern Finding | 6:02 | Data Visualization: ggplot2 | R |
| 311 | ggplot2: Frequency Plots for Human Mitochondrial Information Frequency Minir | 6:12 | Data Visualization: ggplot2 | R |
| 312 | ggplot2: Bar Charts Human Mitochondrial Knowledge Mining | 10:43 | Data Visualization: ggplot2 | R |
| 313 | ggplot2 - Scaling and Limiting Data Visualization | 3:53 | Data Visualization: ggplot2 | R |
| 314 | ggplot2 - Changing Labels and Finalizing Visualization | 8:41 | Data Visualization: ggplot2 | R |
| 315 | ggtree - Phylogenetic Tree Visualization | 5:41 | Data Visualization: ggplot2 | R |
| 316 | ggplot2 - Saving the Visualizations in High Resolution | 4:44 | Data Visualization: ggplot2 | R |
| 317 | Introduction to Linux for Bioinformatics | 22:31 | Getting Familiar With Linux | Linux |
| 318 | PWD - Print Working Directory | 1:26 | Getting Familiar With Linux | Linux |
| 319 | CD - Changing Directories | 5:03 | Getting Familiar With Linux | Linux |
| 320 | MKDIR - Making Directories | 8:12 | Getting Familiar With Linux | Linux |
| 321 | MV - Moving Files, Directories and Data | 5:10 | Getting Familiar With Linux | Linux |
| 322 | RM - Deleting Files and Directories | 1:23 | Getting Familiar With Linux | Linux |
| 323 | Which & Whereis - Find Programs You Installed | 3:43 | Getting Familiar With Linux | Linux |
| 324 | Find - Finding User Created Files | 3:38 | Getting Familiar With Linux | Linux |
| 325 | LS - Lisiting Files and Directories on Linux | 6:45 | Getting Familiar With Linux | Linux |
| 326 | Piping and Redirection of Data | 3:34 | Piping and Control Data Flow | Linux |
| 327 | Cat - Visualization and Inspection of Text Data | 3:55 | Pre-processing Biological Datasets | Linux |
| 328 | Head - Reading Specified Number of Lines from Top | 3:49 | Pre-processing Biological Datasets | Linux |
| 329 | Tail- Reading Specified Number of Lines from Bottom | 2:22 | Pre-processing Biological Datasets | Linux |
| 330 | Touch - Modifying File Statistics and Creating Files | 7:03 | Pre-processing Biological Datasets | Linux |
| 331 | Stat - Statistics of File & Directories | 2:46 | Pre-processing Biological Datasets | Linux |
| 332 | Wget - Retrieval of Genome Assemblies | 6:48 | Pre-processing Biological Datasets | Linux |
| 333 | Curl - Retrieval of Bioinformatics Files | 2:25 | Pre-processing Biological Datasets | Linux |
| 334 | Vim - Create and Edit Text Files | 5:58 | Pre-processing Biological Datasets | Linux |
| 335 | Diff - Find Sequence Differences in Files | 2:34 | Pre-processing Biological Datasets | Linux |
| 336 | GZIP - Compress and Archive FilesEfficiently | 6:05 | Processing and Analysis of Biological Datasets | Linux |
| 337 | GUNZIP - Extract Compressed Content | 2:14 | Processing and Analysis of Biological Datasets | Linux |
| 338 | Tar - Create Archives of Genome Data | 4:18 | Processing and Analysis of Biological Datasets | Linux |

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| 339 | Grep - Finding Uncharacterized Proteins in Human Genome | 8:55 | Processing and Analysis of Biological Datasets | Linux |
| 340 | Cut - Subsetting Required Textual Data from Text Files | 5:48 | Processing and Analysis of Biological Datasets | Linux |
| 341 | Sort - Sorting Data | 4:22 | Processing and Analysis of Biological Datasets | Linux |
| 342 | Uniq - Finding Unique Data Items | 10:32 | Processing and Analysis of Biological Datasets | Linux |
| 343 | WC - Statistics of the Data Within File | 2:45 | Processing and Analysis of Biological Datasets | Linux |
| 344 | CP - Copying Files and Files Contents | 3:43 | Processing and Analysis of Biological Datasets | Linux |
| 345 | Column - Proper Visualization of Delimited Datasets | 4:38 | Processing and Analysis of Biological Datasets | Linux |
| 346 | Introduction to BioConductor | | BioConductor | R |
| 347 | Installing Packages from BioConductor | | BioConductor | R |
| 348 | Retrieving Biological Sequence in R | | Sequence Retrieval | R |
| 349 | Reading and Writing the FASTA File | | Bioinformatics File Parsing and Writing | R |
| 350 | Getting the Detail of a Sequence Composition | | Sequence Analysis | R |
| 351 | Pairwise Sequence Alignment | | Sequence Alignment | R |
| 352 | Multiple Sequence Alignment | | Sequence Alignment | R |
| 353 | Phylogenetic Analysis and Tree Plotting | | Phylogenetics Analysis | R |
| 354 | Handling BLAST Results | | Database Searching | R |
| 355 | Pattern Finding in a Sequence | | Sequence Analysis | R |
| 356 | Performing ID Conversions | | BioConductor | R |
| 357 | Handling Annotation Databases in R | | BioConductor | R |
| 358 | Performing ID Conversions | | BioConductor | R |
| 359 | The KEGG Annotation of Genes | | Gene Enrichment Analysis | R |
| 360 | The GO Annotation of Genes | | Gene Enrichment Analysis | R |
| 361 | The GO Enrichment of Genes | | Gene Enrichment Analysis | R |
| 362 | The KEGG Enrichment of Genes | | Gene Enrichment Analysis | R |
| 363 | BioConductor in the Cloud | | BioConductor | R |
| 364 | Introduction to dplyr | | Data Transformation with dplyr | R |
| 365 | Filter Rows with filter() | | Data Transformation with dplyr | R |
| 366 | Select Columns with select() | | Data Transformation with dplyr | R |
| 367 | Add New Variables with mutate() | | Data Transformation with dplyr | R |
| 368 | Grouped Summaries with summarize() | | Data Transformation with dplyr | R |
| 369 | Grouped Mutates (and Filters) | | Data Transformation with dplyr | R |
| 370 | Introduction to tidyr | | Tidy Data with tidyr | R |
| 371 | Data Tidying | | Tidy Data with tidyr | R |
| 372 | Data Spreading & Gathering | | Tidy Data with tidyr | R |

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|-----|---|-------|-----------------------------------|---|
| 373 | Data Separating & Pull | | Tidy Data with tidyr | R |
| 374 | Missing Values | | Tidy Data with tidyr | R |
| 375 | Case Study with tidyr | | Tidy Data with tidyr | R |
| 376 | Nontidy Data | | Tidy Data with tidyr | R |
| 377 | Introduction to ArrayExpress - Getting Started With MicroArray Analysis | 9:55 | MicroArray Analysis: BioConductor | R |
| 378 | Introduction to BioConductor - Installing MicroArray Packages | 5:05 | MicroArray Analysis: BioConductor | R |
| 379 | Getting Started with R Studio Project for MicroArray Analysis | 4:50 | MicroArray Analysis: BioConductor | R |
| 380 | Downloading MicroArray Raw Data from ArrayExpress | 4:19 | MicroArray Analysis: BioConductor | R |
| 381 | Creating Raw Intensities MicroArray Data Structure and Log2 Transformation | 14:40 | MicroArray Analysis: BioConductor | R |
| 382 | Principle Component Analysis of Raw Expression Dataset | 15:44 | MicroArray Analysis: BioConductor | R |
| 383 | Plot Visualization of Raw Intensity Data to Interpret the Median Intensities of the Samples | | MicroArray Analysis: BioConductor | R |
| 384 | ArrayQualityMetrics - Automated Quality Control for Microarray Datasets | | MicroArray Analysis: BioConductor | R |
| 385 | Annotating the Probe IDs with Gene Symbols and Names | | MicroArray Analysis: BioConductor | R |
| 386 | Excluding Probe IDs with Multiple Mappings from the ExpressionSet | | MicroArray Analysis: BioConductor | R |
| 387 | Filtering out the Genes that are Above Threshold | | MicroArray Analysis: BioConductor | R |
| 388 | Heatmap Visualization of the Normalized Gene Expression Values | 11:51 | MicroArray Analysis: BioConductor | R |
| 389 | Intensity-based Filtration of Low-Intensity Transcripts | | MicroArray Analysis: BioConductor | R |
| 390 | Normalization of Raw Intensities Values | | MicroArray Analysis: BioConductor | R |
| 391 | Relative Log Expression Analysis and Visualization | | MicroArray Analysis: BioConductor | R |
| 392 | Removal of the Probe IDs that Match to Multiple Genes | | MicroArray Analysis: BioConductor | R |
| 393 | Robust Multi-Array Summarization and Background Correction of the Raw MicroArray Data | | MicroArray Analysis: BioConductor | R |
| 394 | LIMMA - Data Preparation for Linear Modelling | | MicroArray Analysis: BioConductor | R |
| 395 | Factors Preparation | | MicroArray Analysis: BioConductor | R |
| 396 | Analysis of Gene Expression Levels of a Single Gene Among Different Conditions | | MicroArray Analysis: BioConductor | R |
| 397 | LIMMA - Applying Linear Model on a Single Gene Expression Data | | MicroArray Analysis: BioConductor | R |
| 398 | Data Visualization of the Gene Expression of a Single Gene | | MicroArray Analysis: BioConductor | R |
| 399 | Applying t-test to Find if Genes are Differentially Expression | | MicroArray Analysis: BioConductor | R |
| 400 | LIMMA - Applying Linear Model for Differential Gene Expression Analysis | | MicroArray Analysis: BioConductor | R |
| 401 | Extraction of Differentially Expressed Genes from the Fitted Linear Model | | MicroArray Analysis: BioConductor | R |
| 402 | Setting a Threshold for Differentially Expressed Genes | | MicroArray Analysis: BioConductor | R |
| 403 | Volcano Plot - Visualization of the Genes that are Differentially Expressed | 8:36 | MicroArray Analysis: BioConductor | R |
| 404 | Matching the DEGs with Background Genes to Find Overlap | | MicroArray Analysis: BioConductor | R |
| 405 | topGO - Gene Enrichment & Ontology Analysis | | MicroArray Analysis: BioConductor | R |
| 406 | topGO - KEGG & REACTOME Pathway Analysis | | MicroArray Analysis: BioConductor | R |