

| Days | Name   | Durations | Category                           | Main Category |
|------|--|-----------|------------------------------------|---------------|
| 1    | Introduction to Linux for Bioinformatics             | 22:31     | Getting Familiar With Linux        | Linux         |
| 2    | PWD - Print Working Directory                        | 1:26      | Getting Familiar With Linux        | Linux         |
| 3    | CD - Changing Directories                            | 5:03      | Getting Familiar With Linux        | Linux         |
| 4    | MKDIR - Making Directories                           | 8:12      | Getting Familiar With Linux        | Linux         |
| 5    | MV - Moving Files, Directories and Data              | 5:10      | Getting Familiar With Linux        | Linux         |
| 6    | RM - Deleting Files and Directories                  | 1:23      | Getting Familiar With Linux        | Linux         |
| 7    | Which & Whereis - Find Programs You Installed        | 3:43      | Getting Familiar With Linux        | Linux         |
| 8    | Find - Finding User Created Files                    | 3:38      | Getting Familiar With Linux        | Linux         |
| 9    | LS - Listing Files and Directories on Linux          | 6:45      | Getting Familiar With Linux        | Linux         |
| 10   | Piping and Redirection of Data                       | 3:34      | Piping and Control Data Flow       | Linux         |
| 11   | Cat - Visualization and Inspection of Text Data      | 3:55      | Pre-processing Biological Datasets | Linux         |
| 12   | Head - Reading Specified Number of Lines from Top    | 3:49      | Pre-processing Biological Datasets | Linux         |
| 13   | Tail- Reading Specified Number of Lines from Bottom  | 2:22      | Pre-processing Biological Datasets | Linux         |
| 14   | Touch - Modifying File Statistics and Creating Files | 7:03      | Pre-processing Biological Datasets | Linux         |
| 15   | Stat - Statistics of File & Directories              | 2:46      | Pre-processing Biological Datasets | Linux         |
| 16   | Wget - Retrieval of Genome Assemblies                | 6:48      | Pre-processing Biological Datasets | Linux         |
| 17   | Curl - Retrieval of Bioinformatics Files             | 2:25      | Pre-processing Biological Datasets | Linux         |
| 18   | Vim - Create and Edit Text Files                     | 5:58      | Pre-processing Biological Datasets | Linux         |

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| 19 | Diff - Find Sequence Differences in Files  | 2:34  | Pre-processing Biological Datasets             | Linux |
| 20 | GZIP - Compress and Archive Files Efficiently  | 6:05  | Processing and Analysis of Biological Datasets | Linux |
| 21 | GUNZIP - Extract Compressed Content  | 2:14  | Processing and Analysis of Biological Datasets | Linux |
| 22 | Tar - Create Archives of Genome Data   | 4:18  | Processing and Analysis of Biological Datasets | Linux |
| 23 | Grep - Finding Uncharacterized Proteins in Human Genome  | 8:55  | Processing and Analysis of Biological Datasets | Linux |
| 24 | Cut - Subsetting Required Textual Data from Text Files   | 5:48  | Processing and Analysis of Biological Datasets | Linux |
| 25 | Sort - Sorting Data  | 4:22  | Processing and Analysis of Biological Datasets | Linux |
| 26 | Uniq - Finding Unique Data Items   | 10:32 | Processing and Analysis of Biological Datasets | Linux |
| 27 | WC - Statistics of the Data Within File  | 2:45  | Processing and Analysis of Biological Datasets | Linux |
| 28 | CP - Copying Files and Files Contents  | 3:43  | Processing and Analysis of Biological Datasets | Linux |
| 29 | Column - Proper Visualiation of Delimited Datasets   | 4:38  | Processing and Analysis of Biological Datasets | Linux |
| 30 | Getting Started With Molecular Dyanmics Simulation - Pre-processing of Protein Structure and Removal of Unncessary Structural Features | 12:33 | Molecular Dynamics Simulations: GROMACS        | Linux |
| 31 | pdb2gmx - Construction of Topology File for Simulation   | 9:00  | Molecular Dynamics Simulations: GROMACS        | Linux |
| 32 | Defining a Solvant Box for Simulation  | 4:14  | Molecular Dynamics Simulations: GROMACS        | Linux |
| 33 | Solvation - Adding Water Molecules in Solvant Box  | 5:30  | Molecular Dynamics Simulations: GROMACS        | Linux |

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| 34 | Generating Input Run File<br>Replacement of Water Molecules With Ions  | 6:55  | Molecular Dynamics Simulations: GROMACS | Linux |
| 35 | genion - Replacement of Water Molecules With Ions                      | 4:18  | Molecular Dynamics Simulations: GROMACS | Linux |
| 36 | Energy Minimization - Relaxing and Fixing the Structure for Simulation | 11:25 | Molecular Dynamics Simulations: GROMACS | Linux |
| 37 | GRACE - Visualization and Analysis of Minimized Structure              | 4:11  | Molecular Dynamics Simulations: GROMACS | Linux |
| 38 | Equilibration of Protein Structure NVT ENSEMBLE Phase 1                | 8:37  | Molecular Dynamics Simulations: GROMACS | Linux |
| 39 | Equilibration of Protein Structure NPT ENSEMBLE Phase 2                | 8:09  | Molecular Dynamics Simulations: GROMACS | Linux |
| 40 | mdrun - Executing Simulation Analysis                                  | 3:46  | Molecular Dynamics Simulations: GROMACS | Linux |