

Days	Name	Durations	Category	Main Category
1	Why Python in Bioinformatics	9:16	Introduction	Python
1	Introduction to Python and it's Intallation	8:25	Introduction	Python
2	Comments	5:42	Introduction	Python
2	Basic Input and output	15:37	Introduction	Python
3	Mathematical Operations	7:20	Introduction	Python
3	Strings	21:51	Iterable Objects	Python
4	Dictionaries	10:57	Iterable Objects	Python
4	Lists	28:47:00	Iterable Objects	Python
5	Lists(pt 2) and Tuples	10:37:00	Iterable Objects	Python
5	Sets	7:35	Iterable Objects	Python
6	If-Else	9:19	Control Flow	Python
6	For Loop and calc of Mol. weight	10:56	Control Flow	Python
7	While Loop	9:37	Control Flow	Python
7	Reading Files	13:45	File Handling	Python
8	CSV	8:41	File Handling	Python
8	Writing Files	7:17	File Handling	Python
9	Consolidate(merge) multiple DNA and Protein Sequences into one FASTA file	9:24	File Handling	Python
9	OS	31:47:00	File Handling	Python
10	Function	26:41:00	Functions & Modules	Python
10	With	8:50	Functions & Modules	Python
11	Error Handling	15:31	Error Handling	Python
12	Introduction to BioPython & Installation	10:18	Introduction	BioPython
12	Bio.Seq Create a Seq Object	7:38	Sequence Analysis	BioPython
13	Bio.Seq Seq Object Behaves Like a String	9:54	Sequence Analysis	BioPython
13	Bio.Seq Central Dogma in Play Through Python	8:41	Sequence Analysis	BioPython
14	Bio.Seq Unkown & Mutable Sequences	6:53	Sequence Analysis	BioPython

24	AlignIO - Information Mapping of Alignments	2:33	Alignment Parsing and Analysis	BioPython
25	AlignIO - Format Alignments	3:55	Alignment Parsing and Analysis	BioPython
25	AlignIO - Slicing Alignments	6:05	Alignment Parsing and Analysis	BioPython
26	Bio.Blast - Querying NCBI BLAST Through Python	11:41	BLAST Database Searching	BioPython
27	Bio.Blast - Parsing BLAST Results	14:51	Parsing BLAST results	BioPython
28	Bio.Entrez - Accessing ENTREZ Using Python	9:32	Biological Data Retrieval	BioPython
29	Bio Entrez Use Esummary To Get Summary Of Your Accessions	8:59	Biological Data Retrieval	BioPython
30	Bio.Entrez - Use EFetch to Download Complete Records	13:56	Biological Data Retrieval	BioPython
31	Bio.Entrez - Use EGQuery to Do Global Queries for Search Counts	7:24	Biological Data Retrieval	BioPython
32	Bio.Entrez - Use Elink To Search For Database Links Of Records	3:41	Biological Data Retrieval	BioPython
33	Bio.Entrez - Use ESearch to Search the Entrez Databases	8:20	Biological Data Retrieval	BioPython
34	Bio.Entrez - Use Espell To Get Correct Spellings For Your Search Terms	5:21	Biological Data Retrieval	BioPython
35	Bio.Entrez - Download GenBank and Entrez Records	14:17	Biological Data Retrieval	BioPython
36	Bio.Entrez - Taxonomy Database Searching	7:05	Biological Data Retrieval	BioPython
37	Bio.Entrez - Download PubMed Articles	8:28	Biological Data Retrieval	BioPython
38	Bio.Entrez - Use EFetch to Download Complete Records	13:56	Biological Data Retrieval	BioPython
39	Bio.PDB - Reading a PDB (3D Structure) File	11:59	Parsing a PDB Structure file	BioPython
39	Bio.Phylo - Calculating Distance Matrix Between Sequences For Phylogenetic Analysis	4:18	Phylogenetic Analysis	BioPython

40	Bio.Phylo - Converting Phylogenetic Tree Data Formats	3:28	Phylogenetic Analysis	BioPython
41	Bio.Phylo - Printing Out Phylogenetic Tree In Ascii	2:17	Phylogenetic Analysis	BioPython
42	Bio.Phylo - Reading Phylogenetic Trees	6:28	Phylogenetic Analysis	BioPython
42	Bio.Phylo - Visualization And Manipulation Of Phylogenetic Trees	9:36	Phylogenetic Analysis	BioPython
43	Bio.Phylo - Writing Out Phylogenetic Data	4:04	Phylogenetic Analysis	BioPython
43	Bio.motifs - Creating a WebLogo of Motifs		Protein Sequence Analysis	BioPython
44	Bio.motifs - MEME Analysis		Protein Sequence Analysis	BioPython
44	Introduction to R in Bioinformatics & R Installation	9:47	Introduction	R
45	The R User Interface	6:23	Introduction	R
45	Comments	4:16	Introduction	R
46	Variable Declaration and Objects	5:24	Variables & Functions	R
47	Built-in Functions & ARGS	4:31	Variables & Functions	R
48	Sample & Replacement	9:09	Variables & Functions	R
49	Write Your Own Functions And Arguments	5:39	Variables & Functions	R
50	Scripts	7:36	Variables & Functions	R
51	Packages	4:00	Packages	R
52	Install Packages	5:25	Packages	R
53	Library & Initialize Packages	2:27	Packages	R
54	Getting Help with Help Packages	3:42	Packages	R
55	Atomic Vectors	2:42	Vectors & Data Types	R
56	Doubles	3:30	Vectors & Data Types	R
57	Integers	3:23	Vectors & Data Types	R
58	Characters	4:43	Vectors & Data Types	R
59	Logicals	2:27	Vectors & Data Types	R
60	Attributes and Names	4:46	Vectors & Data Types	R
61	Dim & Dimensions	5:46	Vectors & Data Types	R
62	Matrix & Matrices	4:42	Vectors & Data Types	R
63	Arrays	3:42	Vectors & Data Types	R

64	Class	3:12	Vectors & Data Types	R
65	Factors	6:40	Vectors & Data Types	R
66	Coercion	4:27	Vectors & Data Types	R
67	Lists	6:41	Vectors & Data Types	R
68	Data Frames	6:30	Biological Data Analysis	R
69	Loading Biological Data	7:55	Biological Data Analysis	R
70	Saving Biological Data	5:26	Biological Data Analysis	R
71	R Notation & Selecting Values from Biological Dataset	4:09	Biological Data Analysis	R
72	Positive Integers for subsetting Biological Dataset(DataFrame)	5:25	Biological Data Analysis	R
73	Negative Integers for subsetting Biological Dataset(DataFrame)	5:28	Biological Data Analysis	R
74	Zero Notation for subsetting Biological Datasets (DataFrames)	1:09	Biological Data Analysis	R
75	Blank Spaces For Biological Data Subsetting	3:20	Biological Data Analysis	R
76	Dollar Signs for Biological Dataset Subsetting	2:58	Biological Data Analysis	R
77	Modifying Values in Existing DataFrames/Datasets	7:06	Biological Data Analysis	R
78	NA Values in Biological Dataset	5:24	Biological Data Analysis	R
79	Figuring out NA Values in Biological Dataset	2:06	Biological Data Analysis	R
80	Logical Subsetting in Biological Datasets	9:45	Biological Data Analysis	R
81	If Else Statement	4:15	Control Flow	R
82	Comments	4:16	Introduction	R
83	For Loops & Biological Data Binding	16:30	Control Flow	R
84	While Loops & Reading Multiple Biological Datasetswhile Loops & Reading Multiple Biological Datasets	16:16	Control Flow	R
85	Introduction to ggplot2 for Biological Datasets	10:46	Data Visualization: ggplot2	R

86	ggplot2: Key components	8:25	Data Visualization: ggplot2	R
87	ggplot2: Human Mitochondrial Proteome & Aesthetics (Size, Shape, Color)	26:02:00	Data Visualization: ggplot2	R
88	ggplot2: Facetting of Human Genome	22:25	Data Visualization: ggplot2	R
89	ggplot2: Smooth Out the Biological Data	8:43	Data Visualization: ggplot2	R
90	ggplot2: Boxplots for Human Mitochondrial Proteome	7:55	Data Visualization: ggplot2	R
91	ggplot2 :Histograms for Human Mitochondrial Pattern Finding	6:02	Data Visualization: ggplot2	R
92	ggplot2: Frequency Plots for Human Mitochondrial Information Frequency Mining	6:12	Data Visualization: ggplot2	R
93	ggplot2: Bar Charts Human Mitochondrial Knowledge Mining	10:43	Data Visualization: ggplot2	R
94	ggplot2 - Scaling and Limiting Data Visualization	3:53	Data Visualization: ggplot2	R
95	ggplot2 - Changing Labels and Finalizing Visualization	8:41	Data Visualization: ggplot2	R
96	ggtree - Phylogenetic Tree Visualization	5:41	Data Visualization: ggplot2	R
97	ggplot2 - Saving the Visualizations in High Resolution	4:44	Data Visualization: ggplot2	R
98	Introduction to Linux for Bioinformatics	22:31	Getting Familiar With Linux	Linux
99	PWD - Print Working Directory	1:26	Getting Familiar With Linux	Linux
100	CD - Changing Directories	5:03	Getting Familiar With Linux	Linux
101	MKDIR - Making Directories	8:12	Getting Familiar With Linux	Linux
102	MV - Moving Files, Directories and Data	5:10	Getting Familiar With Linux	Linux
103	RM - Deleting Files and Directories	1:23	Getting Familiar With Linux	Linux
104	Which & Whereis - Find Programs You Installed	3:43	Getting Familiar With Linux	Linux
105	Find - Finding User Created Files	3:38	Getting Familiar With Linux	Linux
106	LS - Lisiting Files and Directories on Linux	6:45	Getting Familiar With Linux	Linux

107	Piping and Redirection of Data	3:34	Piping and Control Data Flow	Linux
108	Cat - Visualization and Inspection of Text Data	3:55	Pre-processing Biological Datasets	Linux
109	Head - Reading Specified Number of Lines from Top	3:49	Pre-processing Biological Datasets	Linux
110	Tail- Reading Specified Number of Lines from Bottom	2:22	Pre-processing Biological Datasets	Linux
111	Touch - Modifying File Statistics and Creating Files	7:03	Pre-processing Biological Datasets	Linux
112	Stat - Statistics of File & Directories	2:46	Pre-processing Biological Datasets	Linux
113	Wget - Retrieval of Genome Assemblies	6:48	Pre-processing Biological Datasets	Linux
114	Curl - Retrieval of Bioinformatics Files	2:25	Pre-processing Biological Datasets	Linux
115	Vim - Create and Edit Text Files	5:58	Pre-processing Biological Datasets	Linux
116	Diff - Find Sequence Differences in Files	2:34	Pre-processing Biological Datasets	Linux
117	GZIP - Compress and Archive Files Efficiently	6:05	Processing and Analysis of Biological Datasets	Linux
118	GUNZIP - Extract Compressed Content	2:14	Processing and Analysis of Biological Datasets	Linux
119	Tar - Create Archives of Genome Data	4:18	Processing and Analysis of Biological Datasets	Linux
120	Grep - Finding Uncharacterized Proteins in Human Genome	8:55	Processing and Analysis of Biological Datasets	Linux
121	Cut - Subsetting Required Textual Data from Text Files	5:48	Processing and Analysis of Biological Datasets	Linux
122	Sort - Sorting Data	4:22	Processing and Analysis of Biological Datasets	Linux
123	Uniq - Finding Unique Data Items	10:32	Processing and Analysis of Biological Datasets	Linux
124	WC - Statistics of the Data Within File	2:45	Processing and Analysis of Biological Datasets	Linux
125	CP - Copying Files and Files Contents	3:43	Processing and Analysis of Biological Datasets	Linux

126	Column - Proper Visualiation of Delimited Datasets	4:38	Processing and Analysis of Biological Datasets	Linux
127	Introduction to BioConductor		BioConductor	R
128	Installing Packages from BioConductor		BioConductor	R
129	Retrieving Biological Sequence in R		Sequence Retrieval	R
130	Reading and Writing the FASTA File		Bioinformatics File Parsing and Writing	R
131	Getting the Detail of a Sequence Composition		Sequence Analysis	R
132	Pairwise Sequence Alignment		Sequence Alignment	R
133	Multiple Sequence Alignment		Sequence Alignment	R
134	Phylogenetic Analysis and Tree Plotting		Phylogenetics Analysis	R
135	Handling BLAST Results		Database Searching	R
136	Pattern Finding in a Sequence		Sequence Analysis	R
137	Performing ID Conversions		BioConductor	R
138	Handling Annotation Databases in R		BioConductor	R
139	Performing ID Conversions		BioConductor	R
140	The KEGG Annotation of Genes		Gene Enrichment Analysis	R
141	The GO Annotation of Genes		Gene Enrichment Analysis	R
142	The GO Enrichment of Genes		Gene Enrichment Analysis	R
143	The KEGG Enrichment of Genes		Gene Enrichment Analysis	R
144	BioConductor in the Cloud		BioConductor	R
145	Introduction to dplyr		Data Transformation with dplyr	R
146	Filter Rows with filter()		Data Transformation with dplyr	R
147	Select Columns with select()		Data Transformation with dplyr	R
148	Add New Variables with mutate()		Data Transformation with dplyr	R
149	Grouped Summaries with summerize()		Data Transformation with dplyr	R
150	Grouped Mutates (and Filters)		Data Transformation with dplyr	R

151	Introduction to tidyr		Tidy Data with tidyr	R
152	Data Tidying		Tidy Data with tidyr	R
153	Data Spreading & Gathering		Tidy Data with tidyr	R
154	Data Separating & Pull		Tidy Data with tidyr	R
155	Missing Values		Tidy Data with tidyr	R
156	Case Study with tidyr		Tidy Data with tidyr	R
157	Nontidy Data		Tidy Data with tidyr	R
158	Introduction to ArrayExpress - Getting Started With MicroArray Analysis	9:55	MicroArray Analysis: BioConductor	R
159	Introduction to BioConductor - Installing MicroArray Packages	5:05	MicroArray Analysis: BioConductor	R
160	Getting Started with R Studio Project for MicroArray Analysis	4:50	MicroArray Analysis: BioConductor	R
161	Downloading MicroArray Raw Data from ArrayExpress	4:19	MicroArray Analysis: BioConductor	R
162	Creating Raw Intensities MicroArray Data Structure and Log2 Transformation	14:40	MicroArray Analysis: BioConductor	R
163	Principle Component Analysis of Raw Expression Dataset	15:44	MicroArray Analysis: BioConductor	R
163	Box Plot Visualization of Raw Intensity Data to Interpret the Median Intensities of the Samples		MicroArray Analysis: BioConductor	R
164	ArrayQualityMetrics - Automated Quality Control for Microarray Datasets		MicroArray Analysis: BioConductor	R
165	Annotating the Probe IDs with Gene Symbols and Names		MicroArray Analysis: BioConductor	R
166	Excluding Probe IDs with Multiple Mappings from the ExpressionSet		MicroArray Analysis: BioConductor	R
167	Filtering out the Genes that are Above Threshold		MicroArray Analysis: BioConductor	R
168	Heatmap Visualization of the Normalized Gene Expression Values	11:51	MicroArray Analysis: BioConductor	R
169	Intensity-based Filtration of Low-Intensity Transcripts		MicroArray Analysis: BioConductor	R

