

Contents

Chapter 1: Introduction	1
1.1 Prelude	1
1.2 What is Bioinformatics.....	2
1.3 Book's Organization	3
Chapter 2: An Introduction to the Python Language	5
2.1 Features of the Python Language	5
2.2 Variables and Pre-Defined Functions.....	8
2.2.1 Variable Types	8
2.2.2 Assigning Values to Variables	9
2.2.3 Numerical and Logical Variables.....	10
2.2.4 Containers	13
2.2.5 Variable Comparison	17
2.2.6 Type Conversion	18
2.3 Developing Python Code	19
2.3.1 Indentation.....	19
2.3.2 User-Defined Functions.....	21
2.3.3 Conditional Statements	22
2.3.4 Conditional Loops.....	25
2.3.5 Iterative Loop Statements.....	26
2.3.6 List Comprehensions.....	28
2.3.7 Help	29
2.4 Developing Python Programs	29
2.4.1 Data Input and Output	30
2.4.2 Reading and Writing From Files	31
2.4.3 Handling Exceptions	34
2.4.4 Modules.....	36
2.4.5 Putting It All Together	37
2.5 Object-Oriented Programming	39
2.5.1 Defining Classes and Creating Objects	39
2.5.2 Special Methods	42

Contents

2.5.3 Inheritance	43
2.5.4 Modularity	45
2.6 Pre-Defined Classes and Methods	45
2.6.1 Generic Methods for Containers	45
2.6.2 Methods for Lists	48
2.6.3 Methods for Strings	50
2.6.4 Methods for Sets	52
2.6.5 Methods for Dictionaries	53
2.6.6 Assigning and Copying Variables	54
Bibliographical Notes and Further Reading	55
Exercises and Programming Projects	56
Exercises	56
Programming Projects	57
 Chapter 3: Cellular and Molecular Biology Fundamentals	 59
3.1 The Cell: The Basic Unit of Life	59
3.2 Genetic Information: Nucleic Acids	61
3.2.1 Transcription: RNA Synthesis	62
3.2.2 Translation: Protein Synthesis	63
3.3 Genes: Discrete Units of Genetic Information	67
3.3.1 Gene Structure	67
3.3.2 Regulation of Gene Expression	70
3.4 Human Genome	71
3.5 Biological Resources and Databases	73
Bibliographic References and Further Reading	77
Exercises	77
 Chapter 4: Basic Processing of Biological Sequences	 79
4.1 Biological Sequences: Representations and Basic Algorithms	79
4.2 Transcription and Reverse Complement	83
4.3 Translation	84
4.4 Seeking Putative Genes: Open Reading Frames	87
4.5 Putting It All Together	90
4.6 A Class for Biological Sequences	91
4.7 Processing Sequences With BioPython	94
4.8 Sequence Annotation Objects in BioPython	98
Exercises and Programming Projects	104
Exercises	104
Programming Projects	105

Chapter 5: Finding Patterns in Sequences	107
5.1 Introduction: Importance of Pattern Finding in Bioinformatics	107
5.2 Naive Algorithm for Fixed Pattern Finding	108
5.3 Heuristic Algorithm: Boyer-Moore.....	110
5.4 Deterministic Finite Automata.....	113
5.5 Finding Flexible Patterns: Regular Expressions	117
5.5.1 Definitions and Regular Expressions in Python	117
5.5.2 Examples in Biological Sequence Analysis.....	122
5.5.3 Finding Protein Motifs	125
5.5.4 An Application to Restriction Enzymes.....	127
Bibliographic Notes and Further Reading	129
Exercises and Programming Projects	129
Exercises	129
Programming Projects.....	130
Chapter 6: Pairwise Sequence Alignment	133
6.1 Introduction: Comparing Sequences and Sequence Alignment	133
6.2 Visual Alignments: Dot Plots	134
6.3 Sequence Alignment as an Optimization Problem.....	138
6.3.1 Problem Definition and Complexity	138
6.3.2 Objective Function: Substitution Matrices and Gap Penalties	139
6.3.3 Implementing the Calculation of the Objective Function	142
6.4 Dynamic Programming Algorithms for Global Alignment	146
6.4.1 The Needleman-Wunsch Algorithm	146
6.4.2 Implementing the Needleman-Wunsch Algorithm	149
6.5 Dynamic Programming Algorithms for Local Alignment.....	152
6.5.1 The Smith-Waterman Algorithm	152
6.5.2 Implementing the Smith-Waterman Algorithm	154
6.6 Special Cases of Sequence Alignment	157
6.7 Pairwise Sequence Alignment in BioPython.....	159
Bibliographical Notes and Further Reading	160
Exercises and Programming Projects	161
Exercises	161
Programming Projects.....	162
Chapter 7: Searching Similar Sequences in Databases	163
7.1 Introduction.....	163
7.2 BLAST Algorithm and Programs	165
7.2.1 Overview of the BLAST Algorithm.....	165
7.2.2 BLAST Programs	166

7.2.3 Significance of the Alignments	167
7.3 Implementing Our Own BLAST	168
7.4 Using BLAST Through BioPython.....	171
Bibliographical Notes and Further Reading	176
Exercises and Programming Projects	176
Exercises	176
Programming Projects.....	177
Chapter 8: Multiple Sequence Alignment	179
8.1 Introduction: Problem Definition and Complexity.....	179
8.2 Classes of Optimization Algorithms for Multiple Sequence Alignment	180
8.2.1 Dynamic Programming	180
8.2.2 Heuristic Algorithms	182
8.3 Implementing Progressive Alignments in Python	186
8.3.1 Representing Alignments: Class <i>MyAlign</i>	186
8.3.2 Pairwise Alignment: Class <i>AlignSeq</i>	188
8.3.3 Implementing Multiple Sequence Alignment: Class <i>MultipleAlign</i> ..	190
8.4 Handling Alignments in <i>BioPython</i>	193
Bibliographical Notes and Further Reading	195
Exercises and Programming Projects	195
Exercises	195
Programming Projects.....	197
Chapter 9: Phylogenetic Analysis	199
9.1 Introduction: Problem Definition and Relevance	199
9.2 Classes of Algorithms for Phylogenetic Analysis	201
9.2.1 Distance-Based Methods	202
9.2.2 Maximum Parsimony	206
9.2.3 Statistical Methods	207
9.3 Implementing Distance-Based Algorithms in Python	207
9.3.1 Implementing Binary Trees.....	208
9.3.2 Implementing the UPGMA Algorithm.....	211
9.4 BioPython Functions for Phylogenetic Analysis	216
Bibliographical Notes and Further Reading	218
Exercises and Programming Projects	218
Exercises	218
Programming Projects.....	220
Chapter 10: Motif Discovery Algorithms	221
10.1 Introduction: Problem Definition and Relevance	221

10.2 Brute-Force Algorithms: Exhaustive Search	226
10.3 Branch-and-Bound Algorithms	227
10.4 Heuristic Algorithms	232
Bibliographic Notes and Further Reading	235
Exercises and Programming Projects	235
Exercises	235
Programming Projects.....	236
Chapter 11: Probabilistic Motifs and Stochastic Algorithms	237
11.1 Representing and Searching Probabilistic Motifs.....	237
11.2 Stochastic Algorithms: Expectation-Maximization.....	244
11.3 Gibbs Sampling for Motif Discovery.....	247
11.4 Probabilistic Motifs in BioPython	250
Bibliographic Notes and Further Reading	252
Exercises and Programming Projects	253
Exercises	253
Programming Projects.....	253
Chapter 12: Hidden Markov Models	255
12.1 Introduction: What Are Hidden Markov Models?	255
12.2 Algorithms and Python Implementation	260
12.2.1 Joint Probability of an Observed Sequence and State Path	261
12.2.2 Probability of an Observed Sequence Over All State Paths	262
12.2.3 Probability of the Remainder of an Observed Sequence	264
12.2.4 Finding the Optimal State Path	265
12.2.5 Learning the Parameters of an HMM Model	267
12.3 HMMs for Database Search	271
Bibliographic Notes and Further Reading	272
Exercises and Programming Projects	273
Chapter 13: Graphs: Concepts and Algorithms	275
13.1 Graphs: Definitions and Representations.....	275
13.2 A Python Class for Graphs.....	277
13.3 Adjacent Nodes and Degrees	279
13.4 Paths, Searches, and Distances	281
13.5 Cycles	286
Bibliographic Notes and Further Reading	287
Exercises and Programming Projects	287
Exercises	287
Programming Projects.....	288

Chapter 14: Graphs and Biological Networks.....	289
14.1 Introduction.....	289
14.2 Representing Networks With Graphs.....	290
14.2.1 A Python Class for Metabolic Networks.....	290
14.2.2 An Example Metabolic Network for a Real Organism.....	296
14.3 Network Topological Analysis	297
14.3.1 Degree Distribution	298
14.3.2 Shortest Path Analysis	300
14.3.3 Clustering Coefficients.....	301
14.3.4 Hubs and Centrality Measures.....	304
14.4 Assessing the Metabolic Potential.....	307
Bibliographic Notes and Further Reading.....	309
Exercises and Programming Projects	310
Exercises	310
Programming Projects.....	310
Chapter 15: Assembling Reads Into Genomes: Graph-Based Algorithms	313
15.1 Introduction to Genome Assembly and Related Challenges	313
15.2 Overlap Graphs and Hamiltonian Cycles	314
15.2.1 Problem Definition and Exhaustive Search	314
15.2.2 Overlap Graphs.....	317
15.2.3 Hamiltonian Circuits	320
15.3 DeBruijn Graphs and Eulerian Paths	325
15.3.1 DeBruijn Graphs for Genome Assembly	325
15.3.2 Eulerian Paths	327
15.4 Genome Assembly in Practice	332
Bibliographic Notes and Further Reading.....	334
Exercises and Programming Projects	334
Exercises	334
Programming Projects.....	335
Chapter 16: Matching Reads to Reference Sequences.....	337
16.1 Introduction: Problem Definition and Applications	337
16.2 Pre-Processing the Patterns: Tries	337
16.2.1 Definitions and Algorithms	337
16.2.2 Implementing Tries in Python	340
16.3 Pre-Processing the Sequence: Suffix Trees	344
16.3.1 Definitions and Algorithms	344
16.3.2 Implementing Suffix Trees in Python	349
16.4 Burrows-Wheeler Transforms	352

16.4.1 Definitions and Algorithms	352
16.4.2 Implementation in Python	357
16.4.3 Aligning References to Genomes in Practice	362
Bibliographic Notes and Further Reading	362
Exercises and Programming Projects	363
Exercises	363
Programming Projects.....	363
Chapter 17: Further Reading and Resources.....	365
17.1 Complementary Books	365
17.2 Journals and Conferences	366
17.3 Formal Education.....	368
17.4 Online Resources	369
Final Words	373
Bibliography.....	375
Index	383