

Contents

1	Nucleotide Analysis	1
1.1	Sequence Retrieval	2
1.2	Primer Designing	6
1.3	Designing Degenerate Primers	11
1.4	Reading of Sequence Trace Files Using Finch TV	14
1.5	Troubleshooting DNA Sequencing Problems	18
1.6	Editing Sequence Data	24
1.7	Sequence Assembly—CAP3 Program	28
1.8	Checking for Vector Contamination	32
1.9	Restriction Mapping Using NEBcutter	35
1.10	Gene Prediction Using ORF Finder (Open Reading Frame Finder)	40
1.11	Gene Prediction Using FGENESB	47
1.12	Dot-Plot	49
1.13	Global Sequence Alignment	56
1.14	Local Sequence Alignment	61
1.15	Basic Local Alignment Search Tool (BLAST)—Nucleotide BLAST	64
1.16	Interpreting BLAST Result	70
1.17	Multiple Sequence Alignment: T-Coffee for Small Alignments	76
1.18	Multiple Sequence Alignment—MUSCLE for Medium Alignments	84
1.19	Multiple Sequence Alignment—MAFFT for Large Alignments	87
1.20	Multiple Sequence Alignment and Phylogenetic Analysis Using MEGA	92

2	DNA Marker Analysis	117
2.1	Genetic Analysis Using NTSYSpc (Numerical Taxonomy System)	117
2.2	Principal Coordinate Analysis (PCORDA) Using NTSYSpc	124
2.3	Population Genetic Analysis Using PowerMarker	129
2.4	Dissimilarity Analysis—DARwin5 (Dissimilarity Analysis and Representation for Windows)	134
3	RNA Analysis	141
3.1	Predicting RNA Secondary Structure	141
3.2	Finding Repeats	145
4	Protein Sequence Analysis	149
4.1	Protein Sequence Retrieval from UniProtKB	149
4.2	Visualization of Features in a Multiple Sequence Alignment	154
4.3	Predicting Signal Peptides in Proteins Using SignalP 4.1 Server	156
4.4	Predicting Transmembrane Segments and Signal Peptides in Proteins Using Phobius	162
4.5	Predicting Subcellular Location Using TargetP	166
4.6	Protein BLAST (blastp)	171
4.7	Position-Specific Iterated (PSI)-BLAST	176
4.8	Creating Pattern from Alignment	180
4.9	Pattern-Hit Initiated (PHI)-BLAST	182
4.10	Domain Enhanced Lookup Time Accelerated-BLAST (DELTA-BLAST)	185
5	Protein Structure Analysis	191
5.1	Protein Primary Structure Analysis—ProtParam	191
5.2	Protein Secondary Structure Prediction	196
5.2.1	Secondary Structure Prediction Using SOPMA	197
5.2.2	Secondary Structure Prediction Using PSIPRED	201
5.3	Protein Tertiary Structure Prediction by Homology Modelling	204
5.3.1	Homology Modelling Using SwissModel	208
5.3.2	Protein Tertiary Structure Prediction by Threading (Fold Recognition)	215
5.4	Protein Tertiary Structure Analysis	223
5.4.1	RAMPAGE	223
5.4.2	Protein Structure Analysis Using SAVeS	226
5.5	Protein Structure Visualization	230
5.5.1	RasMol	230
5.5.2	PyMol	238
5.6	Protein Structure Alignment/Superimpose Using SuperPose	246
5.7	Protein Cleft Analysis	252

6 Protein–Ligand Interactions	257
6.1 Protein–Ligand Docking Using AutoDock4.1 and MGLTools . . .	257
6.2 Protein–Protein Docking Using ClusPro2.0	268
Appendix: Online Resources on Bioinformatics	275
References	279



<http://www.springer.com/978-981-10-1856-5>

Bioinformatics - A Student's Companion

Syed Ibrahim, K.; Gurusubramanian, G.; Zothansanga;
Yadav, R.P.; Senthil Kumar, N.; Pandian, S.K.; Borah, P.;
Mohan, S.

2017, XV, 283 p. 333 illus., Hardcover

ISBN: 978-981-10-1856-5