

Advances in Biological Science Research

A Practical Approach

Edited by
Surya Nandan Meena and Milind Mohan Naik



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Contents

Contributors	xxi
Preface	xxv
Acknowledgments	xxix

1. Bioinformatics methods: application toward analyses and interpretation of experimental data

Shyamalina Haldar

1.1	Aim of the chapter	1
1.2	DNA sequencing	1
1.3	Identification of organisms from nucleotide sequence	2
1.3.1	What is BLAST?	2
1.3.2	Methods for nucleotide BLAST	2
1.3.3	Interpretation of BLAST results	4
1.3.4	Construction and interpretation of phylogenetic tree	5
1.3.5	Sequence deposition	6
1.4	Microbial ecology statistics	7
1.4.1	Species composition/species richness	7
1.4.2	Species abundance	7
1.4.3	Species diversity	10
1.5	Biostatistics	13
1.5.1	Sampling statistics	14
1.5.2	Testing of hypothesis	15
1.5.3	Probability distribution	15
1.6	Advanced bioinformatics tools in biological sciences	17
1.6.1	Sequence analysis	17
1.6.2	Phylogenetic analysis	17
1.6.3	Sequence databases	18
1.7	Conclusion	18
	References	18

2. Genome sequence analysis for bioprospecting of marine bacterial polysaccharide-degrading enzymes

Md Imran and Sanjeev C. Ghadi

2.1	Introduction	21
2.2	Marine polysaccharides and polysaccharide-degrading bacteria: an overview	22

2.3	Identification of polysaccharide-degrading genes through genome annotation	23
2.4	Identification of polysaccharide-degrading genes in newly sequenced bacterial genome: a guide for beginners	27
2.5	Genome sequence analysis unravels organization of polysaccharide-degrading genes as polysaccharide utilization loci	28
2.6	Genome annotation: a potential tool for the elucidation of glycometabolism pathways	28
2.7	CAZy database: a promising tool for the classification of polysaccharide-degrading genes/enzymes identified in newly sequenced genomes	29
2.8	Validation of computationally identified polysaccharide-degrading genes in the genomes of marine bacteria	30
	Acknowledgments	30
	References	30
3.	Proteomics analysis of <i>Mycobacterium</i> cells: challenges and progress	
	<i>Suvidha Samant and Abhishek Mishra</i>	
3.1	Introduction	35
3.2	Proteome analysis of axenic mycobacteria	37
3.3	Proteome analysis of mycobacteria-infected cells	39
3.4	Proteome analysis of mycobacteria-containing host vacuoles	39
3.5	Conclusion	40
	References	41
4.	Plant proteomics: a guide to improve the proteome coverage	
	<i>Chhaya Patole and Laurence V. Bindschedler</i>	
4.1	Introduction	45
4.2	Hurdles associated with plant proteins sample preparation for mass spectrometry-based proteomics	46
4.3	Primary considerations to design suitable workflows for plant proteomics	46
4.3.1	Effective protein sample preparation: extraction and recovery from difficult plant samples	50
4.3.2	Contaminant removal from or during protein digestion	53
4.3.3	Overcoming the high-dynamic range of protein concentrations for the discovery of low-abundant proteins	54
4.3.4	Digestion of plant proteins	58
4.3.5	Overcoming technical and biological variations	59

4.4	Advances and applications in plant proteomics	61
4.4.1	Proteogenomics to help annotation of open reading frames (ORFs) in newly sequenced genomes	61
4.4.2	Understanding plant development and responses to environmental clues	62
4.5	Conclusion and future perspective	62
	References	63
5.	Structural analysis of proteins using X-ray diffraction technique	
	<i>Umesh B. Gawas, Vinod K. Mandrekar and Mahesh S. Majik</i>	
5.1	Introduction	69
5.2	Historical background	70
5.3	X-ray crystallography	71
5.4	Protein X-ray crystallography	72
5.5	Advances in protein crystallography	74
5.6	Case study: extended spectrum β-lactamases	76
5.7	Conclusion	80
	Acknowledgments	80
	References	80
6.	Technological advancements in industrial enzyme research	
	<i>Vazhakatt Lilly Anne Devasia, R. Kanchana, Poonam Vashist and Usha D. Muraleedharan</i>	
6.1	Introduction	85
6.2	Enzyme discovery	86
6.3	Enzyme customization	89
6.4	Improvement of existing enzymes through mutagenic approaches	90
6.4.1	By site-directed mutagenesis	90
6.4.2	By random mutagenesis	91
6.5	High-throughput screening of genetic variants for novel enzyme production	93
6.6	Immobilization of enzymes	93
6.7	Enzyme inhibitor studies	94
6.8	Enzyme promiscuity and multifunctional enzyme studies	95
6.9	Sequence-dependent approach of the novel gene encoding the target enzyme/protein	96
6.10	Function-based identification of the novel gene	96
6.11	Identification of the novel gene by sequencing techniques	97
6.12	Improvement of enzymatic catalysis by microbial cell surface display	98
6.13	Conclusion	99
	References	99

7. Biotechnological implications of hydrolytic enzymes from marine microbes

Poonam Vashist, R. Kanchana, Vazhakatt Lilly Anne Devasia, Priyanka V. Shirodkar and Usha D. Muraleedharan

7.1	Introduction	103
7.2	Applications of marine hydrolases	104
7.2.1	Biorefineries	105
7.2.2	Pharmaceuticals and cosmeceuticals	105
7.2.3	Food industry	106
7.2.4	Feed industry	108
7.2.5	Biopolymer industry	108
7.2.6	Detergent industry	109
7.2.7	Textile industry	109
7.2.8	Leather industry	110
7.2.9	Paper and pulp industry	110
7.2.10	Organic synthesis	111
7.2.11	Waste treatment	111
7.2.12	Nanoparticle synthesis	112
7.3	Prospecting the use of hydrolytic enzymes from marine microbes	112
	References	113
	Further reading	118

8. Recent advances in bioanalytical techniques using enzymatic assay

Kanchanmala Deshpande and Geetesh K. Mishra

8.1	Introduction	119
8.1.1	Why biosensors?	120
8.1.2	Emergence of biosensors	120
8.2	Classification of biosensors	121
8.2.1	Enzyme biosensor	122
8.2.2	Overcoming limitations in enzyme-based biosensors	124
8.2.3	Application of enzyme biosensor	126
8.3	Enzyme biosensors for environmental monitoring	127
8.4	Enzyme biosensors for food quality monitoring	128
8.5	Future prospects and conclusions	129
	References	131
	Further reading	134

9. Microbial lectins: roles and applications

Hetika Kotecha and Preethi B. Poduval

9.1	Introduction	135
9.2	Roles and mechanism of lectin action	136
9.3	Applications of microbial lectins	141
9.3.1	Lectins in diagnostics	141
9.3.2	Lectins in bioremediation	141

9.3.3	Lectins in bioflocculation	142
9.3.4	Lectins in fluorescent staining	143
9.3.5	Lectin and probiotics	143
9.4	Conclusion	143
	References	144
	Further reading	147
10.	Biodegradation of seafood waste by seaweed-associated bacteria and application of seafood waste for ethanol production	
	<i>Sanika Samant, Milind Mohan Naik, Diviya Chandrakant Vaingankar, Saijiya Yusuf Mujawar, Prachi Parab and Surya Nandan Meena</i>	
10.1	Introduction	149
10.2	Materials and methods	151
10.2.1	Collection of marine seaweed samples	151
10.2.2	Enrichment of <i>Ulva</i> -associated bacteria	151
10.2.3	Isolation of calcium carbonate solubilizing marine <i>Ulva</i> -associated bacteria	151
10.2.4	Investigating seafood waste (fish, crab, prawn waste) utilizing potential of selected calcium carbonate-solubilizing bacteria	151
10.2.5	Agarase production by marine <i>Ulva</i> sp.-associated bacteria	152
10.2.6	Production of protease by <i>Ulva</i> sp.-associated bacteria	152
10.2.7	Phosphate solubilization by acid-producing <i>Ulva</i> sp.-associated bacteria	152
10.2.8	Cellulase production by <i>Ulva</i> sp.-associated bacteria	152
10.2.9	Production of chitinase by <i>Ulva</i> sp.-associated bacteria	153
10.2.10	Degradation of fish/crab/prawn waste using microbial consortia developed using <i>Ulva</i> sp.-associated bacteria	153
10.2.11	Identification of seaweed-associated bacteria	154
10.3	Results and discussion	154
10.4	Application of seafood waste for bioethanol production	157
	Acknowledgments	158
	References	158
11.	Phosphate solubilization by microorganisms: overview, mechanisms, applications and advances	
	<i>Neha Prabhu, Sunita Borkar and Sandeep Garg</i>	
11.1	Introduction	161
11.2	Phosphate-solubilizing microorganisms: an overview	161

11.2.1	Screening microorganisms for phosphate solubilization	163
11.3	Phosphate solubilizing microorganisms: mechanisms	164
11.3.1	Inorganic phosphate-solubilization mechanisms	165
11.3.2	Organic phosphate solubilization mechanisms	167
11.4	Phosphate-solubilizing microorganisms: applications and advances	167
11.4.1	Biofertilizer	167
11.4.2	Phytoremediation	169
11.5	Conclusion	171
	References	171
12.	Metagenomics a modern approach to reveal the secrets of unculturable microbes	
	<i>Kashif Shamim, Sajiya Yusuf Mujawar and Milind Mutnale</i>	
12.1	Introduction	177
12.2	History of metagenomic approach	178
12.3	Approach, strategies, and tools used in the metagenomic analysis	179
12.3.1	Isolation of metagenomic DNA	180
12.3.2	Cloning vector and host	182
12.3.3	Screening of metagenomic clones	182
12.3.4	Sequencing and bioinformatics analysis of the metagenomic clones	183
12.4	Application of the metagenomic approach	183
12.5	Conclusion remarks	186
	Acknowledgments	189
	References	189
13.	Halophilic archaea as beacon for exobiology: recent advances and future challenges	
	<i>Abhilash Sundarasami, Akshaya Sridhar and Kabilan Mani</i>	
13.1	Introduction	197
13.2	Missions with exobiological significance	198
13.2.1	1960–2000	198
13.2.2	2000–10	200
13.2.3	2010–18	201
13.3	Extremophiles—a general overview	202
13.4	Halophiles in the universe	204
13.5	Modes of energy generation in halophilic archaea	205
13.6	Radiation resistance in halophilic archaea	206
13.7	Halophilic archaea from ancient halite crystals	207
13.8	Adaptation of halophilic archaea to extreme temperatures and pH	208

13.9	Growth of halophilic archaea in the presence of perchlorates	209
13.10	Saline environments in space	209
13.10.1	Mars	209
13.10.2	Europa	210
13.10.3	Enceladus	210
13.11	Methods for detecting halophilic archaea in saline econiches	210
13.12	Conclusion	211
	References	212
4.	Bacterial probiotics over antibiotics: a boon to aquaculture	
	<i>Samantha Fernandes and Savita Kerkar</i>	
14.1	Introduction	215
14.2	The probiotic approach	216
14.3	Antimicrobial mechanism of probiotics	217
14.3.1	Production of antagonistic compounds	217
14.3.2	Competitive exclusion	217
14.3.3	Immunomodulation	218
14.3.4	Production of other beneficiary compounds	219
14.4	Screening and development of probiotics	219
14.4.1	In vitro screening for antimicrobial activity	219
14.4.2	Mucus adhesion, colonization, and growth profile	221
14.4.3	Pathogenicity test	221
14.4.4	Organism identification	222
14.4.5	Route of delivery, dosage, and frequency	222
14.4.6	In vivo validation	223
14.4.7	Shelf life	223
14.4.8	Economic evaluation	224
14.5	Recent probiotics used in aquaculture	224
14.6	Conclusion and future perspectives	224
	Acknowledgments	228
	References	228
5.	Recent advances in quorum quenching of plant pathogenic bacteria	
	<i>Gauri A. Achari and R. Ramesh</i>	
15.1	Introduction	233
15.2	Overview of the different quorum sensing molecules of plant pathogenic bacteria	234
15.3	Mechanisms of quorum quenching	236
15.3.1	Inhibition of synthesis of quorum sensing signal	236
15.3.2	Inhibition of sensing of quorum sensing signal	236

15.3.3	Degradation of quorum sensing molecules	237
15.4	Quorum quenching against plant pathogens	239
15.5	Transgenic plants expressing quorum quenching molecules	240
15.6	Summary and future research needs	241
	Acknowledgments	242
	References	242
16.	Trends in production and fuel properties of biodiesel from heterotrophic microbes	
	<i>Gouri Raut, Srijay Kamat and Ameeta RaviKumar</i>	
16.1	Introduction	247
16.2	Growth of different sources of biodiesel on various substrates	248
16.2.1	Screening of lipid-producing microorganisms	248
16.3	Harvesting of cellular biomass from fermentation broth	252
16.4	Cell lysis	253
16.5	Lipid extraction	255
16.6	Transesterification/FAME preparation—conventional two-step, one-step, use of lipases	257
16.6.1	Transesterification process	257
16.7	Determination of fuel properties of heterotrophic microbes	261
16.7.1	Cetane number	261
16.7.2	Viscosity	262
16.7.3	Density	262
16.7.4	Higher heating value	263
16.8	Conclusions and future perspectives	264
	Acknowledgments	264
	References	265
17.	Advances and microbial techniques for phosphorus recovery in sustainable wastewater management	
	<i>Meghanath Shambhu Prabhu and Srikanth Mutnuri</i>	
17.1	Introduction	275
17.2	Technologies for phosphorus recovery	277
17.2.1	The process of struvite crystallization	277
17.2.2	Recovery of struvite from wastes	278
17.2.3	Source of magnesium for struvite formation	278
17.3	Struvite crystallization technologies	279
17.3.1	Lab-scale studies	279
17.3.2	Biological struvite precipitation	279
17.3.3	Struvite formation within wastewater treatment plants: pilot-scale studies	282
17.4	Use of struvite as fertilizer and its potential market	283
17.4.1	Use of struvite to increase soil fertility	283

17.4.2	World and India's fertilizer requirements	284
17.5	Economic feasibility of struvite recovery process	285
17.6	Conclusion	285
	References	286
18.	Genotoxicity assays: the micronucleus test and the single-cell gel electrophoresis assay	
	<i>Avelyno D'Costa, M.K. Praveen Kumar and S.K. Shyama</i>	
18.1	Introduction	291
18.1.1	Micronucleus test	292
18.1.2	Comet assay (single-cell gel electrophoresis)	295
18.2	Conclusion	298
	References	299
19.	Advances in methods and practices of ectomycorrhizal research	
	<i>Lakshangy S. Charya and Sandeep Garg</i>	
19.1	Introduction	303
19.2	Benefits of ECM association	304
19.3	Cultivation and physiology of ECM fungi	305
19.3.1	Cultivation media for ECM fungi	305
19.3.2	Isolation methods of ECM fungi	306
19.4	Identification methods of ECM fungi	308
19.4.1	Conventional methods	308
19.4.2	Case study	309
19.4.3	Challenges in the identification of ECM	310
19.4.4	Advances in identification of ECM	310
19.5	Assessment and quantification of ECM	310
19.5.1	Conventional methods of assessment and quantification of ECM	311
19.5.2	Molecular tools of assessment and quantification of ECM	312
19.6	Stress response and pigments/phenolics in ECM fungi	313
19.7	Application in forestry: ECM fungi as bioinoculants	315
19.7.1	Types of ectomycorrhizal inoculants	316
19.7.2	Ectomycorrhizal inoculants in field applications	318
19.8	Conclusion	318
19.9	Future prospects	320
	Acknowledgments	320
	References	320
	Further reading	325

20.	Photocatalytic and microbial degradation of Amaranth dye	
	<i>Pranay P. Morajkar, Amarja P. Naik, Sandesh T. Bugde and Bhanudas R. Naik</i>	
20.1	Introduction	327
20.2	Advanced photocatalytic amaranth degradation using titanium dioxide	329
20.2.1	Characterization of TiO ₂ supported mesoporous Al ₂ O ₃ catalyst	331
20.2.2	Amaranth adsorption versus photocatalytic- degradation kinetics	333
20.2.3	Identification of photodegradation products using LC-ESI-HRMS technique	336
20.2.4	Toxicity of photodegradation products	337
20.3	Bioremediation of amaranth dye	338
20.4	Coupling of photocatalysis with bioremediation methods	339
	References	342
21.	Role of nanoparticles in advanced biomedical research	
	<i>R.K. Kunkalekar and Umesh B. Gawas</i>	
21.1	Introduction	347
21.2	Cancer therapy	348
21.3	Metal nanoparticles as drug delivery and anticancer agents	349
21.3.1	Gold nanoparticles	350
21.3.2	Silver nanoparticles	351
21.4	Metal oxide nanoparticles as drug delivery and anticancer agent	352
21.4.1	Iron oxide nanoparticles	353
21.4.2	Miscellaneous	354
21.5	Carbon-based nanoparticles as drug delivery and anticancer agents	354
21.5.1	Graphene oxide/reduced graphene oxide for drug delivery	355
21.6	Conclusions	356
	Acknowledgments	356
	References	357
22.	Iron-oxygen intermediates and their applications in biomimetic studies	
	<i>Sunder N. Dhuri and Sarvesh S. Harmalkar</i>	
22.1	Introduction	363
22.2	Mononuclear nonheme iron(III)-superoxo complexes	367
22.3	Mononuclear nonheme iron(III)-peroxo complex	368
22.4	Mononuclear nonheme iron(III)-hydroperoxo complex	369

22.5	Mononuclear high-valent iron(IV)-oxo complex	370
22.6	Mononuclear nonheme iron(V)-oxo complex	371
22.7	Application of iron-oxygen intermediates in biomimetics	373
22.8	Summary	373
	Acknowledgments	374
	References	374
23.	Frontiers in developmental neurogenesis	
	<i>Shanti N. Dessai</i>	
23.1	Introduction to neurogenesis	381
23.1.1	Developmental neurogenesis	381
23.2	Signaling pathway cross talk of developmental neurogenesis	382
23.2.1	Notch	383
23.2.2	Wingless/Integrated	384
23.2.3	Hedgehog/Sonic hedgehogs	385
23.2.4	Fibroblast growth factor	385
23.2.5	Neuronal progenitor cell environment	386
23.3	Tools to study developmental neurogenesis	386
23.3.1	In vitro models	387
23.3.2	Time-lapse analysis	389
23.3.3	Transcriptome, metabolomics, and single-cell "omics"	390
23.3.4	Real-time analysis of progenitors in both embryonic and postnatal studies by tissue explants/slice assays	390
23.4	Conclusion	391
	References	391
24.	Analytical methods for natural products isolation: principles and applications	
	<i>Mahesh S. Majik, Umesh B. Gawas and Vinod K. Mandrekar</i>	
24.1	Introduction	395
24.2	Extraction techniques	396
24.3	Isolation and purification techniques	398
24.4	High-performance liquid chromatography	400
24.4.1	Analysis of chromatograms obtained from HPLC/GC	401
24.5	Spectroscopic methods for characterization	401
24.5.1	Ultraviolet-visible spectroscopy	402
24.5.2	Infrared spectroscopy	402
24.5.3	Mass spectrometry	402
24.5.4	Nuclear magnetic resonance spectroscopy	402
24.6	Chemical profiling of marine sponges: case studies	403
24.6.1	Marine sponge, <i>Haliclona cribriculis</i>	405
24.6.2	Marine sponge, <i>Fasciospongia cavernosa</i>	405
24.6.3	Marine sponge, <i>Axinella donnani</i>	407

24.7	Conclusion	407
	Acknowledgments	408
	References	408
25.	Advanced bioceramics	
	<i>Kiran Suresh Naik</i>	
25.1	Introduction	411
25.2	Classification of biomaterials	412
25.3	Applications and properties of bioceramics	413
25.3.1	Hydroxyapatite	413
25.3.2	β -Tricalcium phosphate (β -TCP)	414
25.3.3	Alumina (Al_2O_3)	414
25.3.4	Zirconia	414
25.3.5	Bioglass and glass ceramics	415
25.4	Conclusion and future perspectives	415
	Acknowledgments	415
	References	416
26.	Production of polyhydroxyalkanoates by extremophilic microorganisms through valorization of waste materials	
	<i>Bhakti B. Salgaonkar and Judith M. Bragança</i>	
26.1	Introduction	419
26.2	Synthesis of polyhydroxyalkanoates	421
26.3	Classification of PHAs	423
26.3.1	Biosynthetic origin	423
26.3.2	Monomer size	424
26.3.3	Monomers units	424
26.3.4	Nature of the monomers	424
26.4	Screening, extraction, and characterization of polyhydroxyalkanoates	424
26.4.1	Screening for PHA	424
26.4.2	PHA extraction	426
26.4.3	PHA characterization	426
26.5	Advances in the applications of PHAs	428
26.5.1	Food industry	428
26.5.2	Medical industry	428
26.5.3	Agricultural industry	429
26.6	Extremophilic microorganisms	430
26.7	Extremophilic microorganisms producing PHAs	430
26.8	PHAs from renewable resources and agroindustrial wastes	432
26.9	Conclusions	437
	Acknowledgments	437
	References	438

27.	Techniques for the mass production of Arbuscular Mycorrhizal fungal species	
	<i>James Dsouza</i>	
27.1	Introduction	445
27.2	Pot/substrate-based mass production system	446
27.3	The AM host plants	447
27.4	Root trap cultures	448
27.5	Plant trap cultures	448
27.6	Soil as inoculum	449
27.7	Microenvironment	449
27.8	Conclusion	450
	References	450
28.	Metagenomics: a gateway to drug discovery	
	<i>Flory Pereira</i>	
28.1	Introduction	453
28.2	Approaches to accelerate antibiotic discovery	454
28.2.1	Mining unusual habitats as a source of novel secondary metabolites	454
28.2.2	Revolutionary cultivation techniques	454
28.2.3	Next-generation sequencing techniques in mining for bioactive compounds	456
28.3	Metagenomic or environmental or community genomic sequencing	458
28.3.1	Sequence-based metagenomics	458
28.3.2	Function-based metagenomics	458
28.4	How metagenomics facilitates drug discovery	460
28.5	Conclusion	463
	References	464
29.	Application of 3D cell culture techniques in cosmeceutical research	
	<i>Surya Nandan Meena and Chellandi Mohandass</i>	
29.1	Introduction	469
29.2	Two-dimensional cell system in cosmeceutical research	469
29.3	Role of three-dimensional cell culture system in cosmeceutical research	470
29.4	Key features of 3D cell culture	470
29.5	Diverse application of 3D cell culture	471
29.6	Preparation of 3D reconstructed human skin model	472
29.6.1	The traditional approach for 3D skin model preparation	472
29.6.2	Bioprinting technology for preparation of 3D skin models	474

29.7	Application of 3D skin models in cosmeceutical research	474
29.7.1	Skin whitening or melanin content	474
29.7.2	Skin antiaging study using 3D in vitro skin model	475
29.7.3	Antioxidant activity	475
29.7.4	Antiinflammatory activity	476
29.7.5	Wound healing assay	476
29.7.6	Skin corrosion test	476
29.7.7	Skin cell irritation test	477
29.7.8	Skin penetration assay	477
29.7.9	Phototoxicity study	477
29.7.10	Genotoxicity assay	478
29.7.11	Skin absorption assay	478
29.8	Conclusion	478
	Acknowledgments	479
	References	479
30.	Advances in isolation and preservation strategies of ecologically important marine protists, the thraustochytrids	
	<i>Varada S. Damare</i>	
30.1	Introduction	485
30.2	Occurrence and ecological significance	486
30.3	Isolation	487
30.3.1	Isolation of thraustochytrids	488
30.3.2	Isolation of labyrinthulids	494
30.4	Preservation of cultures	495
30.5	Summary and future prospects	495
	Acknowledgments	495
	References	496
31.	Advances in sampling strategies and analysis of phytoplankton	
	<i>Priya M. D'Costa and Ravidas K. Naik</i>	
31.1	Introduction	501
31.2	Sampling strategies	502
31.2.1	Choice of research vessel	502
31.2.2	Sampling in coastal waters	503
31.2.3	Aspects to be considered	504
31.3	Analysis of phytoplankton	504
31.3.1	Phytoplankton taxonomy	504
31.3.2	Analysis of phytoplankton community structure	505
31.3.3	Analysis of benthic diatoms	507
31.3.4	Analysis of dinoflagellate cysts	508
31.3.5	Study of fouling diatoms/biofilms	508
31.3.6	Analysis of epibiotic phytoplankton	509

31.3.7	Study of picophytoplankton	509
31.3.8	Phytoplankton pigment analysis	510
31.3.9	Analysis of viability and photosynthetic parameters of phytoplankton populations	511
31.3.10	Toxin analysis	513
31.4	Primary productivity	514
31.4.1	Estimation of primary productivity using remote sensing	515
31.4.2	Monitoring of HABs using remote sensing	515
31.5	Future perspectives	515
	Acknowledgments	516
	References	516
	 Index	 523

Bioinformatics methods: application toward analyses and interpretation of experimental data

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1.1 Aim of the chapter

This chapter aims to describe the tools and the techniques that are being applied globally for analysis and assessment of biological data. The chapter has been divided into three sections (nucleic acid: 1.2 and 1.3; microbial ecology: 1.4; bio statistics: 1.5).

(1) Section I deals with the bioinformatics methods applied for molecular analyses of nucleic acids. (2) Section II deals with the statistical formulae used to interpret microbial ecological data. (3) Section III describes statistical methods used to compare the biological observations to draw significant conclusions. Care has been taken to present the methods in a stepwise manner with examples for better understanding.

1.2 DNA sequencing

DNA sequencing is the process of determining the order of nucleotides within a DNA molecule. There are two methods of DNA sequencing: Maxam–Gilbert sequencing and Sanger sequencing. The former is a chemical method that chemically modifies the DNA nucleotides and subsequently cleaves the DNA backbone at the sites neighboring to the modified nucleotides [1]. However, due to technical complexity and use of hazardous chemicals, this method is not currently used for standard molecular biology.

Sanger sequencing is the method of DNA sequencing in which dideoxynucleotide phosphates (ddNTPs) are incorporated by DNA polymerase during in vitro DNA replication. Modified ddNTPs terminate DNA strand elongation since they lack a 3'-OH group required for the formation of a