

Index

A

Abundance-based coverage estimator (ACE), 8, 24
Abundance data, 3–12, 14, 15
Acetogens, 60
Actinomycetes, 183
Akaike Information Criterion (AIC), 6
Alginate beads, 173, 174
Ampicillin, 185, 187, 188
Amplification, 83–97
Anaerobic methanotrophs (ANME), 61–78
Anaerobic oxidation of methane (AOM),
61–64, 66–70, 72–76, 78
Antibiotic resistance, 167, 168
Archaea, 20, 30
ATP synthesis, 61
Axial Seamount, 28, 30

B

Bacteria, 20, 21, 25, 27, 28, 30, 31
Bacterial growth efficiency (BGE), 109–111
Beggiatoa, 71
Beta-binomial, 13
Bioassay-guided fractionation, 140
Biofilms, 126, 181–190
Biogeographical distribution, 31
Bioinformatic, 24–28
BLAST, 27, 28
BLASTN, 27, 28

C

Capture–recapture, 10
Cell–cell signaling, 146
CGA. *See* Community genome array
Chao1, 24
Chemostat, 104, 105, 110, 111
Chimeric structures, 91
Chloroflexi, 94–96

Cholera, 122, 124, 126–127
Climate, 61
Co-culture, 139–140, 152
Cold seeps, 64, 67, 68, 75
Colwellia sp., 184
CommOligo, 51
Community genome array (CGA), 36, 41, 48–52
Consortium, 61, 65
Cooperation, 61, 62
Coverage, 8, 9, 12, 14
Crenarchaeota, 60, 66
Cross-feeding, 139
Cultivable variants, 137–139, 141, 143, 149
Cultivation, 196–198, 201, 202
Culture independent molecular tools, 20

D

Deep biosphere, 60, 66
Deltaproteobacteria, 60, 61
Desulfobulbus, 64
Desulfosarcina/Desulfococcus, 64
Diffusion chamber(s), 133–140, 152, 153
DNA
amplification, 50, 52
isolation, 89–92
Domesticated strains, 137, 150
Domestication, 132, 137–140, 149
Dominant populations, 31
Dormancy, 123, 144, 146, 147, 149, 150,
152, 154–156, 181, 184, 188–190
DOTUR, 28, 29

E

eDNA
definition, 165
humic substances, 170
representation, 167, 170

Electron shuttles, 77
 Elemental composition, 200
 emPCR, 23
 Energy yields, 61, 66
 Eukarya, 20
 Euryarchaeota, 60
 “Everything is everywhere” hypothesis, 31
 Exosymbionts, 196
 Expression
 E. coli, 167, 168, 171
 METREX, 173
 P. putida, 172
 S. lividans, 168, 171, 172
 Extinction culturing, 112
 Extraterrestrial, 200–201
 Extreme environments, 197, 200
 Extremophilic, 74

F

FGA. *See* Functional gene array
 Finite mixture, 13
 Flow cytometry, 85–87, 93
 Flow through reactor, 72
 Fluorescence activated cell sorting (FACS),
 86–87
 Fluorescence in situ hybridization (FISH),
 63, 64, 71, 85–87
 Fluorescent antibody staining, 124, 126
 Fluoroquinolone, 186
 Free energy change, 62
 Frequency count, 3–9, 11, 15
 Functional gene array (FGA), 36, 39–42,
 46–52
 Fuzznuc, 27

G

Gas hydrate, 62, 70, 71
 Gene expression profile, 124
 Genome, 83–97
 Genomics, 70
 Genus, 24, 27, 28
 Geochemical gradients, 69
 GeoChip, 39–41, 46–48
 Global assignment of sequence taxonomy
 (GAST), 27, 28
 Global transcription pattern, 124
 Goodness-of-fit, 5, 9
 Great plate count anomaly, 102, 115–117,
 132, 140, 141, 143–156
 Growth advantage in stationary phase
 (GASP), 153, 154
 Growth limitations, 134

Growth-promoting signals, 141,
 143–145, 149
 Growth strategies, 132, 148–150,
 152
 Growth yields, 63, 64
 GS20, 23, 24
 GSFLX, 23, 26, 27

H

Heat shock protein (*hsp70*), 166
Helicobacter pylori, 124
 Helper species, 143, 146
 High-pressure, 72
hipA gene, 185
 Homopolymer, 23
 Hybridization, 86
 Hydrogen transfer, 61, 62
 Hydrostatic pressure, 60, 70, 73
 Hydrothermal vents, 68

I

Ichip, 132–137, 142, 153
 Incidence-based coverage estimator
 (ICE), 14
 Incidence data, 10–14
 Independence, 15
 Indirubin, 168
 In vitro enrichments, 65–78
 Ion microprobe mass spectrometry, 63
 Isocyanide synthase, 168

J

Juan de Fuca Ridge, 28

K

K-selected, 111

L

Latent infections, 132, 156
 Libraries
 combinatorial, 163
 cosmid eDNA, 174
 eDNA, 167
 Library size, 172–173
 454 Life Science A primer, 23
 Life’s signatures, 199
 Lipid biomarkers, 62, 65, 66
 Low-abundance organisms, 31
 Low-abundance taxa, 22

M

M_0 , 11, 12
 Maximum likelihood, 5, 7, 9, 12–14
 MazF, 188, 190
 Metagenomic, 22, 24, 36, 41–42, 48
 Metagenomics, 84
 definition, 165
Methanococcoides, 64
 Methanogens, 60–62, 75, 76
 Methanomicrobiales, 64
Methanosarcinales, 62, 64
 Methanotrophs, 59–78
 Methods of enumeration, 125–126
 Methyl coenzyme M reductase (MCR), 64
 M_h , 11–14
 Microarray
 applications, 43–48
 CGA (*see* Community genome array)
 data analysis, 52
 DNA/RNA amplification, 43, 44, 47, 50, 52
 FGA (*see* Functional gene array)
 metagenomic array, 41–42
 microbial activity, 47
 microbial detection, 43–45
 PhyloChip (*see* PhyloChip)
 POA (*see* Phylogenetic oligonucleotide array)
 protein arrays, 43
 quantitation, 52
 sensitivity, 49–50
 software, 51
 specificity, 50–51
 target enrichment, 37
 types, 37–43
 use with isotopes, 42, 43
 WGA (*see* Whole-genome open reading frame array)
 Microbe-animal symbioses, 67
 Microbial bistability, 147
 Microbial cell individuality, 143
 Microbial diversity, 164–166, 172
 Microcolonies, 85, 90, 94
 Microdroplets, 85
 Microfluidics, 87–89, 93
 Micromanipulation, 85–86
 Micronutrients, 103, 104
 Microsensor profiling, 68, 69, 75
M. luteus, 184
 Monoclonal antibody staining, 122
 M_r , 11, 12
 M_{th} , 12–14
 Mud volcano, 62, 64, 70, 71
 Multiple displacement amplification (MDA), 89–92

Multiple list, 10
 Multiple recapture, 10, 11
 Multiplexing, 26
 MUSCLE, 27

N

Negative binomial, 9
 Noise in gene networks, 146
 Noncultivable, 198, 199
 Nonculturable cells, 125–126
 Non-parametric, 2, 7–9, 12–14, 24, 30
 Nonparametric maximum likelihood estimate (NPMLE), 7, 8, 14
 Nonribosomal peptide synthases (NRPS), 163, 166, 168, 169, 175
 Nonspore-forming bacteria, 122
 North Atlantic Deep Water (NADW), 28, 29
 Nutrient-limited, 103–110
 Nutrient transport, 106, 108

O

Oligotrophic microbes, 177
 Operational taxonomic units (OTUs), 2, 3, 21, 25, 26, 28–31

P

Pangenomic, 90
 Parametric incidence models, 12–13
 Parametric stochastic abundance model, 5, 7
 Pathogenicity, 123, 125
 Penalty parameter, 8
 Permeases, 106–108
 Persister cells, 153, 154, 181, 184–185, 187, 189, 190
 Persisters, 181–190
 Phi29 DNA polymerase, 89
 pH optimum, 73, 74
 PhyloChip, 39, 47
 Phylogenetic oligonucleotide array (POA), 36, 37–39
 Phylogenetic reconstruction, 95
 Phylotypes, 21, 22, 24, 28
 Phylum, 24, 84, 87, 88, 93, 94, 96, 97
 PicoTiterPlate™, 23, 26
 POA. *See* Phylogenetic oligonucleotide array
 Poisson distribution, 5
 Polyketide synthases (PKS), 163, 166–169, 175
 Polymerase chain reaction (PCR), 21–26
 Predicting occurrence of cholera, 126
 Proteomics, 70

Pseudomonads, 183
 Pyrosequencing, 26, 28, 92, 93
 454 Pyrosequencing, 22, 24

Q

Quorum sensing, 144, 148, 150

R

Radioisotope, 42, 43
 Rare biosphere, 28–31
 Rasch model, 13
 Redox sensitivity, 75
 Reductants, 76
 RelE, 188, 190
 Revival, 146, 147, 155, 156
 Ribosomal database project (RDP) classifier,
 27, 28
 Ribosomal RNA (rRNA), 20, 21, 24–28,
 37–39, 43, 44, 47, 111
 Right truncation point, 6
 RNA amplification, 43, 44, 47
 R-selected, 111

S

Sanger sequencing, 92, 93
 Scout model, 144, 147, 148, 151–156
 Secondary metabolites
 definition, 162
 Seed populations, 31
 Semi continuous culture technique, 73
 Siderophores, 181, 184
 Signal induction of growth, 148
 Signatures of life, 199, 200
 Single cell genomics, 84, 85, 92, 97
 Slow grower(s), 142, 143
 Slow-growing bacteria, 106, 111, 112
 Slow growth, 61, 72, 77
 Software, 3, 8, 9, 13, 14, 16
 Solexa, 22, 23
 SOLiD™, 22
 Species, 2–16
 Species richness, 2–5, 7, 9, 13–16
 Specific growth rate, 104, 106
 16S rRNA. *See* Ribosomal RNA
 Stable isotope probing (SIP), 37

Standard error (SE), 5, 7, 8, 14, 16
 Stochastic change in gene expression, 144
 Stochastic exit from dormancy, 147–148
 Streptomycin, 163
 Sulfate-methane transition zones (SMTZ),
 66, 67
 Sulfate-reducing bacteria (SRB), 61–64,
 68, 75–77
 Survival, 122, 123, 144–146, 154–156
 Symbiosis, 196
 Synergistic growth, 139
 Syntrophic, 61, 62, 77, 196, 202

T

“Tag” sequences, 24
 Temperature optimum, 74
 Terragines, 167–168
 Thiotrophic bacteria, 67
 TM7, 84, 87–91, 94–97
 Tuberculosis, 182, 188
 Tuning parameter, 6, 7
 Turbomycins A and B, 168

U

Uncultivability, 190
 Uncultivable species, 137–141, 152
 Unculturable bacteria, 190

V

Vectors, 166, 167, 171, 172
 Viability, 123
 Viable but nonculturable (VBNC), 132,
 146, 153, 155–156
Vibrio cholerae, 122–125
 Violacein, 168
 Virulence, 123, 125
 V6 region, 24–26, 28, 29

W

WGA. *See* Whole-genome open reading
 frame array
 Whole cell screening, 173
 Whole-genome open reading frame array
 (WGA), 36, 42, 48, 50