

INDEX

A

Affymetrix 1–9, 183, 184, 185, 187, 189,
190, 197, 198, 202
Amplex red 170, 173, 176, 178
Assessment 128, 138, 147, 155–165, 197, 208

B

Biclustering 18, 55–72, 91–101, 159
Bioinformatics 13, 15, 18
Biological network inference 155–165

C

Cancer samples 1–9, 111, 112
Cardiac development 207, 218
Classification 41–54, 146
Cloud computing 26, 27, 29, 30, 31, 32, 33, 35
Clustering 18, 21, 27, 35, 41–53, 56,
57, 59, 64, 70, 79, 96, 97, 98, 99, 108, 111, 112,
113, 114, 115, 159, 187, 190, 195, 199, 203,
213, 219
Correlation 19, 29, 56, 57, 58, 59, 62, 63, 64,
65, 66, 68, 70, 71, 100, 124, 125, 126, 129, 131,
133, 134, 140, 159, 160, 187, 212, 216

D

Data analysis 11–22, 25–38, 41, 57,
64, 95, 96, 97, 141, 147, 148, 195, 199,
212–213
Databases 17, 18, 19, 56, 77,
78, 84, 109, 110, 113, 114, 118, 127, 146, 200,
202, 218
Data mining 78, 83, 87, 95, 101, 144
Dissection 169, 171, 172, 174, 175, 177

E

Euthanasia 170, 171, 172
Expression microarray 108, 212
Expression patterns 92, 161, 191

F

Functional pathways 21, 162
Functional prediction 41–54

G

Gene expression 2, 11,
12, 16, 17, 29, 30, 31, 41, 43, 52, 53, 55–72, 91,
92, 93, 94, 95, 96, 99, 100, 101, 137, 138, 140,
141, 143, 144, 146, 147, 148, 149, 150, 151,
152, 156, 159, 160, 163, 182, 183, 189, 195,
200, 203, 204, 212, 213, 218, 219
Gene ontology 17, 20,
21, 29, 95, 97, 106, 110, 113, 118, 119, 125,
163, 200, 216, 217
Gene regulatory networks (GRNs) 96, 137–153,
155, 156, 157, 158, 159, 160, 161, 162, 163,
164, 216, 217, 218
Gene target 11, 13, 19, 216
Glioblastoma 195–205
Gold standard 156, 160,
161, 162, 163, 164, 165
Graph theory 140, 155, 156

H

Hierarchical clustering 44, 46, 111, 114, 190,
213, 219

L

Lactate 126, 170, 171, 172, 173,
176, 177, 178

M

Measure 19, 59, 62, 63,
66, 70, 71, 99, 100, 101, 105, 106, 107, 108,
114, 120, 128, 131, 137, 161, 162, 163, 172,
176, 177, 193, 209, 210
Meta-analyses 208, 218–219
Metabolomics 124, 169–178
MetaMirClust 75–88
Microarray data analysis 12–13, 25–38,
105–115, 141, 212–213
Microarray profiling 208, 212
Microarrays 1–9, 12–13,
15, 20, 21, 25–38, 41–54, 55, 56, 57–59, 64, 66,
70, 71, 91, 92, 93, 96, 105–115, 117–120, 126,
137–153, 155–165, 182, 183, 184, 185, 191,
195–205, 207–219

microRNA 1–9, 11–22, 32, 34, 75–88,
 181–193, 207–213, 214, 219
 cluster 75–88
 inhibition 183, 184,
 188, 191
 microarray 1–9
 replacement 183, 191
 Multivariate data analysis 43, 212, 213

N

Next-generation sequencing (NGS) 12, 13–15,
 16, 17, 18, 20, 21, 25, 28, 31, 32, 78, 84
 Normalization 1–9, 13, 17,
 31, 43, 60, 61, 126, 190, 200, 202, 208,
 212–213, 219

O

Ontologies 20, 21, 29, 106, 107, 118, 119, 165

P

Pathways 1, 20,
 21, 56, 75, 77, 91, 105, 123, 127, 128, 129,
 138, 139, 140, 146, 149, 150, 151, 162, 182,
 191, 199, 200, 204, 205, 207, 216, 217, 218

Prediction 13, 17, 18, 19, 20, 22, 29, 41–54,
 128, 129, 133, 138, 140, 144, 160, 193, 203, 216
 Proteome 110, 125, 126, 198

S

Semantic similarity 106, 107, 108, 114,
 115, 118, 119–120
 Sequence features 125, 126, 131, 132, 133, 134
 Skeletal muscle 169–178, 211
 Synteny 77, 78
 Systems biology 117, 137, 138, 152, 155, 164

T

Transcriptome 34, 162, 185, 186,
 187, 189, 190, 191, 199, 200
 Transfection 76, 184, 186, 188, 192
 Translation 124, 125, 130, 132,
 133, 134, 146, 182, 216

U

Undetected proteins 124, 126, 132

Z

Zero-inflated Poisson regression 127