

INDEX

Entries in bold text refer to a section of the book.

- 2-break operation *see* DCJ
- 2-colorability problem 271–272
- 3-colorability problem 276
- abstraction 320
- acceptor sites 68, 81
- acyclic graphs 70
- adenovirus 119, 119, 124
- adjacencies 181, 184
- adjacency 177
 - list 294–295
 - matrix 294–295
- adjacency-based ancestral reconstruction 213–218
- algorithms
 - anchors 309
 - choosing 333–334
 - hashing 259–261
 - polynomial-time 180
 - rounding 25
 - stopping rule 285
- algorithms, specific
 - DCJSORT 184
 - Get-Predecessor-Successor (R) 217
 - GRAAL (GRAPh ALigner) 309–311
 - GreedyReversalSort 175–176
 - GRIMM-Synteny algorithm 209
 - PathBLAST 309
- alignment problem 66–67, 77
- alignments **77–80**
 - edit distance 173
 - local 79
 - matches and mismatches 67
 - multiple 80
 - phylogenetic trees 194
 - whole-genome 209
- alleles 4, 14
 - bi-allelic marker 24
- complex 18–19, 18
- disease 101
- major and minor 24
- Alu sequence 40
- Amenta, N. *et al.* 261
- amino acids 67
 - amino terminus 127
 - match weights matrix 80
 - residues 291
 - selection pressure 118
 - signals in 129
 - substitution matrices 91
- analysis of variance (ANOVA) 13
- ancestral karyotype reconstruction 211–212
- ancestral reconstruction 214–216
 - adjacency-based 213–218
 - base-level 206–207
 - rearrangement-based 212–217
- anchors (algorithms) 309
- animal influenza viruses 148–164, 155
- antiviral drugs 150
- approximation algorithms 176
- arbitrary dependencies **138–139**
- archaea 119, 190–191, 195
- arcs (graphs) 44–48, 69–70
- association(s)
 - association test 16–17
 - chromosome populations 14
 - common disease 20
 - epistasis, effect of 19
 - vs. linkage 15–16
 - Linkage Disequilibrium 10
- Avian Flu 148, 150
- Bacillus subtilis* 118, 121, 124
- backtracking (graphs) 72
- bacteria replication 116

Index

351

- bacterial genomes 113, 116–118
- bait protein 293, 298
- baker's yeast 303, 309, 311
- base (nucleotide) 94, 94
- base-level reconstruction 206–207
- base-pair 96
- Bayes' Law 100, 100–102, 101, 102, 105
- Bayesian estimation of species trees (BEST) 254
- Bayesian inference 102–103
 - arbitrary dependencies **138–139**
 - MrBayes 253, 254
 - prior probability 103, 103, 103, 104
 - uninformative priors 103
- Bayesian information criterion (BIC) 337
- Bayesian model 342
- Bayesian posterior probabilities (BPP) 253
- Bergeron, Ann 187, 180
- BEST (Bayesian estimation of species trees) 254
- bi-allelic marker 24
- bias 293, 299
- BIC (Bayesian information criterion) 337
- big cats (*Panthera*) 248–263
- binding affinity 140, 151
- binding partners 126
- binding sites (*see also* TF binding sites)
 - clusters 142
 - dependencies 143
 - identification 143, 141
 - positions 138
 - prediction 140–141, 140
 - search for 140–143
- binding specificity 130
- Bininda-Emonds, O. R. P. 254
- binomial probability distribution 102
- bins (classes) 14
- biochemical interaction networks 305
- BioGRID database 303
- Bioinformatics Algorithms* 167
- biological function, discovering **303–306**
- biomolecules 126–127, 127, 151
- bipartite graph 184
- bipartitions **254–258**, 255–256, 258–263
- bitstrings 256–263
- Blanchette M. et al. 207
- BLAST algorithm 309
- blood pressure 13–14
- Bombyx mori* (silkworm) 169
- Bonferroni correction 16
- Boot Split Distance method (BSD) 195
- bootstrapping 195, 253
- Borellia burgdorferi* 116–118
- Boreoeutherian common ancestor 203, 207, 217
- Boyd, S. 342
- BPP (Bayesian posterior probability) 253
- branch-and-bound algorithms 284
- breakpoints 168, 177–178, 209, 212, 219
- Brenner, Sydney 64
- brewer's yeast (*Saccharomyces cerevisiae*) 126, 318
- Brujin, Nicolaas de 52, 55, 63
- BSD (Boot Split Distance) 195
- cancer 168, 220–221, 220
- CARs (continuous ancestral regions) 217
- cases and controls 4–5, 16
- cats (felids) 229, 248–263, 250, 253
- causal loci 8, 15
- causal mutation 4–6, 8
- cDNAs 319
- CDRV (Common Disease Rare Variant) 20
- ceiling function 177
- cell division tree 192
- cells 3–4
- cellular interactions 126–129
- centralities (networks) 296
- Chargaff parity rules 124, 124
- Charleston, Michael 234, 245
- chimeric protein sets 191
- chimpanzees 95, 205, 207
- ChIP (Chromatin Immunoprecipitation) 130, 130, 143, 157
- Chi-square* (χ^2) statistic 135–136, 138
- Chi-square* (χ^2) test 11
- chloroplasts 191
- chromatid 157, 207
- chromatin structure 143
- chromosome painting 212
- chromosomes 6–9, 94–95, 168–170, 207–208
 - circular 118, 168, 181
 - disease 100–101, **219–221**
 - human genome 211
 - intervals 94
 - linear 180–181
 - mammalian common ancestor 211
 - paternity inference 103
 - super-chromosome 180
- cis*-regulatory module (CRM) 142
- Citoscape software 295
- classes (bins) 14
- Classical MultiDimensional Scaling (CMDS)
 - 196–199
- Clay Mathematics Institute 48
- cluster analysis 196
- clustering 296, 297, 297, 304
- CMDS *see* Classical MultiDimensional Scaling
- coalescent trees 7, 8
- coding potential 68
- codons 67, 118
- coevolution 227, 228–229, 230–235, **233–235**, 244
- collision (bitstrings) 261
- common ancestor 6–7, 203, 207, 211, 217, 250
- Common Disease Rare Variant (CDRV) 20
- comparative genomics 202–206, 205–207

352 Index

- comparisons, network 295–300
- Complete Genomics 58
- computation time 234 (*see also* run times of algorithms)
- computational complexity
 - large, noisy data sets 316
 - objective function 322
 - penalizing 337
- computational problems 268–277, 320 (*see also* glycan motif finding problem; heuristic solutions; NP-hard problems)
- 2-colorability 271–272
- 3-colorability 276
- cophylogeny 229–233
- Fixed-tree Maximum Parsimony 278
- genome rearrangements **171–175**
- global alignment 77
- machine learning 333
- Median Problem 213
- motif finding 148
- network alignment **306–312**
- NP-completeness 76
- optimization 267
- regression 339
- tractable vs. intractable 48–49
- “computational thinking” 250
- conditional probability 97, 99–100, 138
- confounding factors 16, 17–18
- Congdon, P. 342
- connected graphs 44, 70
- consensus
 - base 137
 - methods 157–158
 - model 132
 - nucleotides 131, 135–136
 - sequence 131–132, 140–141
 - consensus representation 131–132
 - consensus tree algorithm 256
 - consensus trees 248, 250–251, **254–263** (*see also* evolutionary histories)
 - consensus trees, majority 251–252, 254, 256, 258–259, 261–263, 262–263
 - conserved regions 40
 - conserved segment 209
 - constructive proof 61
 - contingency table 160
 - continuous ancestral regions (CARs) 217
 - continuous data (real-valued data) 338–339
 - controls and cases 4–5, 16
 - Cooties 228, 229–232
 - cophylogeny 245
 - cophylogeny data 241
 - cophylogeny reconstruction problem 227, 229–233, 232, 234, 239
 - Jane software 235, 239
 - jungles technique 234
 - cospeciation events 230–232, 242–243
 - cost (numerical)
 - cophylogeny reconstruction **233–235**, 239, 239–241
 - phylogeny estimation 278–283
 - traveling salesman problem 235–237
 - trees 278–283, 284–285
 - CRM *see cis*-regulatory module
 - cross-species genomic changes 121–122, 124, 190–193, 207–210 (*see also* horizontal gene transfer)
 - cumulative GC skew 114–115
 - cumulative skew diagrams **112–124**
 - cut based network 304
 - cycles (graphs) *see* acyclic graphs; Eulerian cycle; Hamiltonian Cycle Problem; supercycle
 - cyclic genomes 49
 - cytoplasm 4
 - cytosine nucleotide (C) 23, 118, 119
 - D-statistic 10
 - Dantzig, George 32
 - Darwin, Charles 189, 228, 245, 249
 - data
 - de-noising 303
 - noisy 293, 316
 - normalized 319
 - real-valued (continuous) data 338–339
 - data collection 293, 303
 - data sources, combining 339–341
 - databases
 - BioGRID 303
 - DIP (Database of Interacting Proteins) 292
 - GenBank 113, 130, 253
 - HPRD 303
 - JASPAR 130
 - largest molecular 253
 - sequence data 268
 - TRANSFAC 130
 - Davis, B.W. *et al.* 251, 253, 254
 - DCJ (double-cut-and-join) model 180, 180, 184, 218
 - DCJSORT algorithm 184
 - de Bruijn graphs 52–54, 61 (*see also* directed graphs)
 - de Bruijn, Nicolaas 52, 55, 63
 - deamination 118–119, 119
 - degree distributions 296, 300–302
 - degree of a node 296, 303, 304
 - degree of a vertex 43–45
 - deoxyribonucleic acid (DNA) *see* DNA entries
 - dependencies, arbitrary **138–139**
 - depth-first traversal 257
 - d_{HP} distance 180, 183
 - diameter of a network 297
 - dinucleotides 119, 134
 - DIP (Database of Interacting Proteins) 292
 - directed graphs 45–47, 59–60 (*see also* de Bruijn graph)

Index

353

- diseases
 - alleles 101
 - cancer 168, 220–221, 220
 - carriers 100
 - chromosomal aberrations **219–221**
 - complex 16
 - development 167
 - estimating risk 100–102
 - genes 100
 - parasites 245
 - proteins 304
 - recessive 100
 - SNPs 94
 - tests 98–99, 303
- distance matrix 193, 196
- distance metrics 171
 - BSD method 195
 - d_{DCJ} distance 183
 - d_{HP} distance 180, 183
 - edit distance 171–173, 173
 - genome rearrangement **171–175**
 - minimum-evolution method 252
 - reversal distance 212–213
- distribution degree 300–302
- distribution law 84
- diversification 250
- DNA (deoxyribonucleic acid) 167–168
 - cDNAs 319
 - double-stranded DNAs 119, 119, 124, 167–168
 - fragments 56–57
 - horizontal transfer 121–122, 124
 - motif 157
 - replication 111, 191
 - signals 129
 - single-stranded 118
 - structure 124
- DNA and RNA, regulatory interactions 316–319
- DNA sequencing 23, **36–40**, 63
 - Complete Genomics 58
 - the early days 49–50, 56
 - largest molecular database 253
 - modeling regulatory motifs 130
 - motif finding problem 157
 - next generation technologies 58
 - and the overlap puzzle 36–40
 - phylogeny estimation 277–285
 - sequencing machines 40, 55
 - WebLogo 133
- Dobzhansky, Theodosius 6, 173–175, 207, 221
- dogs 213–214
- Dollo parsimony model 253
- donor sites 68, 81
- dot-plot 170–171, 180
- double-stranded DNAs (dsDNAs) 119, 119, 124, 167–168
- Double-Cut-and-Join* *see DCJ*
- drift, genetic 8, 95
- Drmanac, Radoje 55–56, 58, 64
- Drosophila pseudoobscura* (fruit fly) 142, 173, 174, 207
- drugs 150, 304, 305, 305–306
- dsDNAs *see double-stranded DNAs*
- Duffy locus 17–18
- duplication events 242–243
- dynamic programming 66–92, 91, 239, 282
- “earthquakes” (genomic) 208
- ECPs *see Eulerian Cycle Problems*
- edge lists (adjacency lists) 294–295
- edges (trees) 229, 239
- edges (vertices) 271–272, 291
- edit distance 171–173
- efficiency of a method (*see computational complexity; time complexity*)
- endosymbiotic events 191–192
- epidemics 148
- epistasis 18–19
- epithelial cells 150, 155
- equivalence of conditions 45, 59
- Erdos–Renyi random graph model 300
- Escherichia coli* 116, 118, 118, 190–191
- ethnicity 17–18
- eukaryotes 68, 128, 142, 191–192, 207
- Euler, Leonhard 40, 55, 63
- Eulerian assembly 58
- Eulerian cycle 45–48, 53–54, 60–61
- Eulerian Cycle Problem (ECP) 43–44, 49, 50–52
- Eulerian graphs 54
- Eulerian path 45
- Euler’s Theorem for directed graphs 44–48, **58–61**
 - (*see also* Königsberg Bridge Problem)
 - Theorem I 45–47, 58, 59–60
 - Theorem II 47, 59–61
- evolution 111, 268
 - and alignment 77
 - mammalian 203–204
 - and mutagenesis 119
 - rates of 303
 - simulation of 237
- evolutionary conservation 142
- evolutionary histories 250–251, 267 (*see also* consensus trees)
- evolutionary trees 173, 248, **250–254**, 268, 277–286 (*see also* phylogenetic trees; phylogenies)
- exhaustive searches 273, 274–276, 282–284
- exons 68, 68, 81–83, 81, 81–82
- false-negative error rate 16
- false-positive error rate 16
- family traits 15, 101, 168

354 Index

- fast solutions 233, 234, 236, 259–261, 303 (*see also heuristic solutions*)
- feasible region 31
- felids (cats) 229, 248–263, 250, 253
- figs (*Ficus*) 228, 228, 228–229, 241–243
- finches (Estrildidae) 228–229, 241, 244
- Fisher's exact test 152, 160
- fissions 180, 218
- Fitch's method 214–216, 216–217
- fitness 111–112, 142, 236, 239–241
- Fixed-tree Maximum Parsimony problem 278
- flow-based network 304
- fluorescence 57, 96, 103, 319
- forensic DNA tests 94, 96
- Forest of Life (FOL) analysis 193–199
- FRAG_NEW 252
- fragment assembly 37–40, 49–50
 - directed graphs 45
 - Eulerian Cycle Problem 50–52
 - Hamiltonian Cycle Problem 49–51
 - read multiplicities 54
- Frank, A. C. 118
- Frontiers at the Interface of Computing and Biology (NRC Committee) 250
- fruit fly (*Drosophila pseudoobscura*) 142, 173, 174, 207
- F*-test 14
- fungi 311
- fusions 180, 181, 208, 218, 220
- galactose (Gal) 126–127, 155
- gap penalties 80
- gaps in a network pathway 309
- gaps in sequences 66–67, 206–207
- Gaussian bell curve 338–339
- GBPs *see* glycan binding proteins
- GC-skew (guanine–cytosine) 112, 113–114, 114–115, 118, 119, 119
- GDV (graphlet degree vector) 304–305, 309–310
- GenBank 113, 130, 253
- gene expression 58, 139, 318–319, 342
- gene mapping 209
- gene order data 212
- gene pairs, corresponding 179
- gene permutations 175–178
- gene recognition 67, 68, 68, **81–83**, 91
- generalized random graphs model 300
- genes 4
 - genetic algorithms 234–237, 242, 244
 - genetic code *see* genotype
 - genetic fingerprint 95
 - genome assembly 49
 - genome rearrangement problem **171–175**, 173, 186 (*see also* rearrangements)
 - Applications of Genome Rearrangements* 187
 - genome reconstruction 205–207
- genome sequencing 37, 56, 190–193, 202–204, 209 (*see also* DNA sequencing)
- genome sequencing projects 202, 220, 268
- genome sorting problem 175–176
- genomes 118, 119, 167–168, 173, 191
- genomics (*see also* Tree of Life (TOL))
 - changes 112, 112–113
 - comparative 202–206
 - “earthquakes” 208
 - genomic anchors 179
 - RNAi functional 305
- genotype (genetic code) 3, 4–5, 5, 14, 94
- genotyping cost, tag SNPs 24
- Genscan software 135
- geometric graphs 301–302, 302, 303
- Get-Predecessor-Successor (R) algorithm 217
- Gibbs sampling algorithm 334
- Gilbert, Walter 38, 63, 113
- global alignment problem 77
- global network alignments 307–308
- global optimum solution 285
- global polarity switch 113–115
- global properties (networks) 295–296
- global-alignment (sequences) 77, 91
- glycan arrays 148, 151, 156–157, 160, 161, 163
- glycan binding proteins (GBPs) 155, 156, 158
- glycan motifs 148, **157–161**
- glycan structures 152–153, 160
- glycans 153, 156–157
- glycans and hemagglutinin interaction 148, 150–151, 151, 156–157, 156–157
- glycans ligands 156–157
- glycobiology 151, 163
- glycoconjugates 153
- glycoproteins 150, 153
- glycosidic bond 152–153
- glycosylations 153
- GRAAL (GRAph ALigner) 309–311
- graph isomorphism 295–296
- graph theory 43, 63
- GraphCrunch software 295, 300
- graphlet count estimation 303
- graphlet degree vector (GDV) 304–305
- graphlets 298–299
- graphs 43–48, **69–70**, 271–272, 291 (*see also*
 - Eulerian graphs; networks
 - arbitrary dependencies 138
 - binding site prediction 140–141
 - connected 44, 70
 - de Bruijn graphs 52–54, 61
 - directed 45–47, 59–60
 - exon–intron 81–82
 - geometric 301–302, 303
 - hypergraphs 86
 - oriented 69
 - RIGs (residue interaction graphs) 291

Index

355

- segment 82
- supercycle 60–61
- greedy algorithms (greedy heuristics) 26, 28–30, 72, 236, 284, 308
- GreedyReversalSort algorithm 175–176
- GRIMM-Synteny algorithm 209
- Groodies 229–232
- guanine nucleotide (G) 23, 112–113, 119, 121
- guilt-by-association (GBA) 334
- H protein *see* hemagglutinin
- H1N1 virus 150–151
- Haeckel, Ernst (19C) 189
- Haemophilis influenzae* 63, 113, 115, 121
- Hamilton, William 41, 55
- Hamiltonian Cycle Problem (HCP) 43–45, 45, 48–50, 49, 50, 63
- Hannenhalli, Sridhar 140, 180, 212
- haplotype block 24, 25, 26, 27, 31–32
- Hardy–Weinberg equilibrium 15
- harmonic series 30
- hashing 259–261
- Hb (TF protein) *see* Hamiltonian Cycle Problem
- Helicobacter pylori* 121–124, 122, 122, 309
- helix–coil transitions 91
- hemagglutinin (HA) 148, 149, 155, 163–164
- hemagglutinin–glycans binding specificity 155
- hemagglutinin–glycans interaction 148, 150–151, 151, 156–157
- Hemmer, H. 254
- hemoglobin 94
- hemophilia B 128, 128
- heterozygous SNP 94
- heuristic solutions 234, 276, 295, 303, 333–334 (*see also* fast solutions; greedy algorithm; NP-hard problems)
- maximum parsimony 284–286
- multiple genome rearrangements (MGR) 213
- PAUP* software 253, 256
- phylogeny estimation 267
- stopping rule 285
- HGP (Human Genome Project) 202, 220
- HGT (horizontal gene transfer) 121–122, 124, 190–193, 195–198, 232
- hidden event 100
- Hidden Markov Models 91
- hidden variables 98, 102, 103
- higher-order PWM 134–135
- high-LD regions *see* haplotype blocks
- hill-climbing heuristics 334
- Histone modifications 143
- HIV 229, 232, 245
- homologous gene sequences 171
- homologous proteins 79, 309
- homologous recombination 95
- homologs (homologous traits) 191
- homology 305
- homozygous SNP 94
- horizontal gene transfer (HGT) *see* HGT
- host species 227
- host specificity 155
- host switches 148, 151, 155, 232, 239, 242–243
- host trees (host phylogenies) 229, 238–239
- HPRD database 303
- HPV-IA 120
- hubs (nodes) 297
- human (*Homo sapiens*) 63, 169, 202–204, 207, 211, 214
- chromosomes 207, 211
- disease causes 219–221
- epithelial cells 155
- influenza viruses 155, 161
- population patterns 24
- Human Genome Project (HGP) 202, 220
- human viruses
 - adenovirus 119, 119, 124
 - cytomegalovirus 119
 - influenza virus 155, 161
- hypergeometric distribution 160
- Hyseq 58
- Icosian Game 41–42, 43–44, 48
- in vivo* identification of binding sites 130
- indegree of a vertex 47–48
- indigo birds 228–229, 241, 244
- induced subgraph 298–299
- inference *see* network inference; paternity inference; regulatory network inference
- inference (statistical) 342 (*see also* Bayesian inference)
- infinite sites assumption 8, 10
- influenza virus
 - animals to humans 148–164, 155
 - classification 150
 - host specificity 155
 - human 155, 161
 - strains 155
 - switches 148, 151, 151–157, 155
 - transmission efficiency 155
 - types 149
 - vaccines 150
 - virion 149
- Information Content 133
- inheritance
 - chromosomes 6
 - DNA 4
 - natural selection 111, 237, 244
 - recessive 17
 - SNPs 94
- insertion and deletion events 168, 207, 211
- integer programming 30–32, 31
- integral constraint 32

356 Index

- integration, numerical 114
- interaction maps 302
- interaction specificity 127, 156
- interactome detection 302–303
- intergenic regions *see* adjacencies
- International Union of Pure and Applied Chemistry (IUPC) 132
- intractable problems 48–49, 213 (*see also* NP-completeness)
- introns 67–68, 68, 81–83, 253
- inversions *see* reversals
- isomers 153
- IUPC *see* International Union of Pure and Applied Chemistry (IUPC)
- jaguar (*P. onca*) 248–263
- JAK-STAT signal transduction pathway 127
- Jane software 235, **237–245**
- Janecka, J. E. *et al.* 254
- JASPAR database 130
- Johnson, W. E. *et al.* 252, 253
- joint probability 97–98, 326
- Jones, Neil 167
- jungles technique 234
- K12 genome 190–191
- karyotypes 207, 211–212
- Königsberg Bridge Problem 40, 43–45, 63
- lagging DNA strand 116, 118, 120, 121
- Laplace prior 133
- large data sets 316
- large populations 244
- LD *see* Linkage Disequilibrium (LD)
- leading DNA strand 116, 118, 120, 121
- leaf nodes 152
- least-cost solutions, dynamic programming 239
- leopard (*P. pardus*) 248–263
- Levy, S. 140
- lice 228, 230, 241
- ligands, glycans 156–157
- likelihood models 102, 103, 340
- likelihood of a model, model likelihood 106, 323–324, 333–334
- linear chromosomes 116, 168, 180–181, 207
- linear constraints 30–32, 31, 31
- linear programming 30–32
- linear regression 339
- linkage 8, 15–16, 95, 152
- Linkage Disequilibrium (LD) 10–12, 12, 15, 15, 18, 20, 24
- Linkage Equilibrium 10, 15
- links (graphs) 291
- lion (*P. leo*) 248–263
- l*-mer 49–50, 54, 56, 58
- Lobry, J.R. 118
- local alignments (sequences) 79, 91
- local network alignments 307
- local network properties 298–300
- loci (genetic) 4
 - alleles 14
 - causal 8, 15
 - complex alleles 18–19
 - Duffy locus 17–18
 - orthologous gene 209
 - polymorphic 14
- logarithmic approximation ratio 32
- Logo representation 133
- long-range LD 15, 18
- loops (graphs) 69
- loss events 242–243
- low-LD regions *see* recombination hotspots
- l*-treelet, glycan motif 158–161
- l*-tuple DNA motif 157
- Ma, J. *et al.* 209–210, 213, 218
- machine learning 316, 333, 342
- MAF *see* minor allele frequencies (MAF)
- major alleles 24, 25
- majority consensus trees 251–252, 254, 256, 258–259, 261–263, 262–263
- malaria 94, 245
- mammalian genomes 202–204
- Margoliash, Emanuel 190
- markers 4, 15, 17–19, 175, 176, 209
- Markov chain Monte Carlo method 334, 342
- Markov model 135, 138
- mass spectrometry 163
- Massively Parallel Signature Sequencing (MPSS) 64
- match scoring 140
- MATCH software 140
- match weights 80
- matches 67
- matching *see* alignment; sequences, similarity of matrices (*see also* Position Weight Matrix)
 - adjacency matrix 294–295
 - amino acid match weights 80
 - matrix vs. star models 293
 - polymorphisms 8
 - probability **132–135**
 - tree distance matrix 193
- matrix technique 91
- Maxam, A. W. 113
- maximum common subsequence problem 80
- maximum common subword problem 80
- maximum independent set (graphs) 274–276
- maximum likelihood methods 195, 253, 323–328
- maximum parsimony 277–286, 284–286
- MDD (Maximum Dependence Decomposition) **135–138**
- mean 338

Index

357

- Median Problem 213
- meiosis 8
- Mendel, Gregor J. 4
- mental health 94
- Merkle, Daniel 234
- Methanoscincina* (archaea) 191
- methods (computational)
 - Boot Split Distance 195
 - clustering 304
 - evolutionary histories 268
 - exhaustive searches 273, 274–276
 - Fitch's method 214–216
 - guilt-by-association (GBA) 334
 - jungles technique 234
 - Markov chain Monte Carlo 334, 342
 - maximum likelihood 195, 253
 - minimum-evolution 252, 252
 - MPSS 64
- Metropolis–Hastings algorithm 334
- MGR (multiple genome rearrangements 213
- mice 202–203, 205, 207, 213, 214
- microarrays 64, 96, 318–319 (*see also* nanoball arrays)
 - analysis 157
 - gene expression 342
 - how they work 56–58
 - paternity inference 103, 106
 - probe sequence 96
- microbial genomes 118, 119, 190, 193
- microchips 5, 8, 15, 55–58, 56–58 (*see also* microarrays)
- Middendorf, Martin 234
- Millennium Problems 48
- minimization 30–32
- minimum cost reconstructions 233–235
- minimum test collection problem 25–26
- minimum-evolution method 252
- minor allele frequency (MAF) 16, 24
- minor alleles 24, 25
- Mirzabekov, Andrey 55–56, 64
- mismatches
 - in an alignment 67
 - base pair strands 118
 - in a network pathway 309
 - pairs of amino acids 80
- missing data 33
- mitochondria 119, 124, 191, 253, 254
- Mixtacki, Julia 167
- model likelihood 106, 323–324, 333–334
- modeling software *see* software packages
- models (*see also* algorithms)
 - classes of 317
 - computational thinking 250
 - likelihood models 102, 103, 340
 - machine learning 316, 333, 342
 - network 300–303
- sensitivity 143
- sequence-based 143
- modulo function 260
- molecular dynamics 164
- monosaccharide residues 153
- monosaccharides 152–153, 157, 160
- most recent common ancestor (MRCA) 6–7 (*see also* common ancestor)
- motifs, regulatory 126–143, 133, 148
- MPSS *see* Massively Parallel Signature Sequencing
- MrBayes software 253, 254
- MRCA (most recent common ancestor) 6–7, 15
- mRNA 116, 128
- mtDNA 252
- multiple alignments 80, 193, 194, 206–207
- multiple chromosomes 180–185, 180
- multiple genome rearrangements (MGR) 213
- Murphy, W. J. 253, 253
- mutation pressure 118, 119
- mutations 4–6, 8
 - drift 8, 95
 - Factor IX 128
 - genome rearrangements 168
 - hemagglutinin 155
 - point mutations 168
 - single nucleotide 24
 - SNPs 18–19, 95
 - spontaneous deamination 118
 - transcription-induced 120
- mutualism 228
- Nadeau, J. 209
- nanoball arrays 58
- National Research Council (NRC) 250
- natural selection 111, 237, 244
- Naughton, B. T. *et al.* 141
- nDNA (nuclear genes) 253
- nearest neighbor interchange (NNI) 284–285
- Nearly Universal Trees (NUTs) 194, 195–199, 195–198
- negative (purifying) selection 142, 202
- negative skew 115
- Neighbor Joining algorithm 252
- neighbors (nodes) 297
- neighbors (treospace) 252, 284–285, 285
- Neofelis* (clouded leopard) 248–263
- “net of life” 190
- network alignment 306–312
- network alignment algorithms 308–309
 - analysis software 295, 300
 - comparisons 295–300
 - diameter 296
 - flow 304
 - growth 302
 - inference 321, 334
 - models 300–303

358 Index

- network alignment algorithms (*cont.*)
 - motifs 298–300
 - projections 305
 - properties 296
 - structure 298–299
 - topology 296, **303–306**, 311–312
- networks 291 (*see also* graphs)
- neuraminidase (N) gene 150, 150
- “newspaper problem” 36–40
- NNI (nearest neighbor interchange) 284–285
- Nobel Prize 38
- node degree (graphs) 296, 303, 304
- nodes (graphs) 138, 229, 239, 291
- noisy data 293, 303, 316, 323
- non-coding regions (introns) 67–68, 168, 253
- non-consensus nucleotides 135–136
- non-oriented paths (graphs) 69
- non-trivial bipartitions 255
- normalization 98, 100, 135, 319
- normally distributed data 338
- NP-completeness 48, 76, 296
- NP-hard problems 268–277, **275–277**, 283
 - cophylogeny reconstruction 234
 - genome sorting 176
 - integer programming 32
 - tag SNP selection 26
 - traveling salesman 236
- nucleic acids 112, 127, 152, 161, 319
- nucleosomes 143, 143
- nucleotide(s) 4, 167–168
 - bases 94, 130
 - combination letter codes 132
 - consensus 131, 135–136
 - counting 112–113, 124
 - non-consensus 135–136
 - relative frequencies 112
 - string of (*l*-mer) 49–50
 - substitutions of 168
- null hypothesis 232–233
- NUTs (Nearly Universal Trees) 194, 195–199
- objective function 30, 322
- observed event 100
- observed variables 98, 102, 103
- odds ratio (OR) 19, 105, 107
- Okazaki fragments 116, 118
- oligosaccharides 151, 153, 161
- O(n²) time 271, 272
- operations, counting 270–271
- optimization problems 267, 277–286, 342
- orderings 236–237, 237–241
- organelles 4, 119
- organismal trees 190
- oriented graphs 69
- origin (ori) of replication 115–116, 118, 122
- Origin of the Species* 189, 228, 249
- orthologous genes (orthologs) 157, 193–194, 209
- outdegree of a vertex 47–48, 53
- overfitting 337
- overlap puzzle 36–40
- Oxford Gene Technology 58
- p*-value 11
- paired-end reads 220–221
- pandemics 148–149, 155
- Panthera* genus 248–263
- papillomavirus 120
- PAR *see* Population Attributable Risk
- parasite tree 229, 239
- parasites 227, 229, 245
- parasitism 228, 229
- parents 4, 6–8, 236–237, 237
- parsimony 172, 213, 214, 218, 253, 277–286
- partial subgraph 298–299
- partition function 85
- partitioning 18
- paternity inference 96–107, **103–107**, 104–105, 106–107
- paternity tests 93–94, 96
- path score (graphs) 70
- PathBLAST algorithm 309
- pathogenic strain genomes 190
- pathogenicity islands 122, 191
- paths (graphs) 45, 69, 69, 70, 71
- pattern matching *see* optimal alignment
- Pauling, Linus B 190
- PAUP* software 253, 256
- penalties (negative weights) 67
- permutations (gene) 175–178
- Pevzner, Pavel 167, 180, 209, 212
- pharmacology 305–306
- phenotypes 3–5, 8, 12, 12–14, 190
- phylogenetic analysis 212, 268
- phylogenetic footprints 142
- phylogenetic trees 193–199, 251–254, 267 (*see also* evolutionary trees; phylogenies)
 - bipartitions 255–256
 - coevolution 227
 - early 189
 - edit distance 173
 - Fitch’s method 214–216
 - Groodies and Cooties 229–234
 - mammalian comparative genomics 203–204
 - maximum likelihood methods 195
 - pantherines 249, 251–254
 - phenotypes 190
 - phylogenetic relationships 306
 - topology comparison 195
- phylogenetics 248
- phylogenies 248–250 (*see also* evolutionary trees; phylogenetic trees)
- estimating 267, **277–286**

Index

359

- GRAAL 311
- host 238–239
- MrBayes 253, 254
- phylogenomics 192, 193–195
- pigs 150, 155
- pocket gophers 228, 230, 241
- point mutations 168, 171, 171–173
- points, related (graphs) 301
- Poisson-distribution 15
- polarity switch, global 113–115
- pollination 228, 241
- poly A sites 129
- polymerase enzymes 128, 317
- polymers **83–86**
- polymorphic locus 14
- polymorphic markers 4
- polymorphisms 8, 12 (*see also SNPs*)
- polynomial-time algorithm 180, 268–269, 271, 276
- polyten chromosome reversals 173
- Population Attributable Risk (PAR) 19
- population size 241, 244
- population substructure 17–18
- Position Weight Matrix (PWM) **132–135**
 - binding site positions 143
 - binding site prediction 141
 - binding sites search 140–143
 - higher-order PWM 134–135
- positive skew 115
- posterior probability 103, 105
- power 16–17, 16
- power-law 296, 301–302
- PPI networks 291–292, 294–295, 298, 302–306, 304, 305
- predecessor synteny block 216–217
- premiums (positive weights) 67
- prey proteins 293, 298
- primates, non-human 229, 245
- prior probability 103, 103, 103, 104, 132, 335–337
- probability
 - BPP 253
 - conditional 97, 99–100, 138
 - density function 338
 - distributions, binomial 102
 - joint 97–98
 - machine learning 316
 - matrix 132
 - models 323–324
 - Position Weight Matrix (PWM) 141
 - unconditional 97, 99
- problems *see* computational problems
- profile methods 157–158
- prokaryotes 68, 190, 191–192
- promoter region 317
- protein function prediction 303
- protein structure networks 291
- protein-binding DNA microarrays 129, 157
- protein-coding regions 67–68 (*see also exons*)
- protein–DNA interaction 130
- protein–/non-protein coding regions 67–68
- protein–protein interactions *see* PPI networks
- proteins **4, 152**
 - chimeric 191
 - connectivity 303
 - disease-related 304
 - identifying features 127
 - regulatory 127
 - structure 161
 - trans-membrane 127
- protists 311
- pseudo count *see* prior probability
- pull-down experiments 302
- purifying selection 142, 202
- PWM *see* Position Weight Matrix (PWM)
- quadratic time 269
- random walk (graphs) 60
- randomized rounding 32
- rare variants (RVs) 19–20
- rats 213, 214
- read generation 37–38, 49, 55
- reads 37, 54–55, 220–221
- real-valued data 338–339
- rearrangements 186
 - ancestral reconstruction 212–213
 - fission and fusion 180, 208
 - inversions (reversals) 208
 - large-scale 207–210, 211
 - operation types 181, 208
- recessive disease 100
- recessive inheritance 17
- reciprocal translocation 208
- recombination events 8, 10, 15, 24, 95
- reconstruction *see* ancestral genome reconstruction; cophylogeny reconstruction problem
- reconstructions 230–235
- recursive algorithm 158
- regression 339
- regulation 128, 317–319, 322
- regulatory DNA and RNA interactions 316–319
- regulatory motifs 126–143, 133
- regulatory networked inference **337–338**
- regulatory networks 139, 299, 315–342, 316
- regulatory regions 142, 157
- relative entropy 133
- relative nucleotide frequencies 112
- relative risk (RR) 12
- replication 112, 119
 - DNA 111
 - fidelity 111
- mechanism 115–116

360 Index

- replication (*cont.*)
 - origin (ori) 118
 - terminus (ter) 115–116
 - and transcription 118, **120–124**
- residue interaction graphs (RIGs) 291
- residues 153, 157, 291
- resolution of synteny blocks 209
- respiratory system 150, 155
- Restriction Fragment Length Polymorphisms (RFLP)
 - 252
- reversal distance 212–213
- reversals (inversions) 170
 - cumulative skew, HGT 122
 - DCJ model 181, 218
 - phylogeny reconstruction 173
 - polytene chromosome 173
 - signed reversals **178–180**
 - sorting by reversals 212
 - unsigned reversals **175–178**
- reverse transcription 319
- RFLP (Restriction Fragment Length Polymorphisms) 252
- rhesus genome 214
- r statistic 11
- RIGs (residue interaction graphs) 291
- RNA (ribonucleic acid) 4, 86, 111, 112
 - DNA interactions 316–319
 - folding 239
 - regulatory interactions 316–319
 - secondary structures 91
 - viruses 119, 149
- RNAi functional genomics 305
- Robertsonian translocation 208
- rooted trees 251, 256
- rounding algorithm 25
- rRNA 190, 191
- run times of algorithms 234
 - 3-colorability 276–277
 - estimating 270–271, 282–283
 - heuristics 285–286
 - polynomial-time 268–269, 271
 - stopping rule 285
- RVs *see* rare variants (RVs)
- Saccharomyces cerevisiae* (brewer's yeast) 126, 318
- sampling issues 16–17
 - bias 293
 - correcting for unobserved data *see* prior probability
 - with DNA microchips 8
 - sample size 16, 138
 - under-sampling 14
- Sanger, Frederick 38, 56, 63, 113
- Sankoff, D. 212
- scale-free network 296, 300
- Science* (1988), DNA arrays 57
- scoring 67
- alignment scores 77
- match scoring 140
- optimum solutions 285
- paths 70
- sequences 141
- search algorithms 309
- seed-and-extend approach 309–310
- segment graph 82
- segmental duplication 211
- segmentation (sequence) 67
- segregating sites 4
- selection algorithms 258–259, 259–261
- SELEX 129
- sensitive models 143
- sequence analysis
- sequence insertions 121–122
- sequence windows 113, 114
- sequence-based models 143, 143
- sequenced genomes 112
- sequences 66, 66–67, 122, 131–132, 309
- sequencing machines (DNA) 40, 55
- serotonin 94
- set-covering problem 26–30, 26, 28–30
- Sex Life of Flowers* 228
- shortest path algorithms 234
- sialic acids 155, 157
- sickle-cell anemia 17–18, 94
- signaling molecules 151
- signatures (molecular) 126
- signed permutations 180
- signed reversals **178–180**, 180
- silk worm (*Bombyx mori*) 169
- simian virus 113
- simplex algorithm (Dantzig) 32
- simulation of evolution 237
- single-copy genes 253
- single-nucleotide polymorphisms *see* SNPs
- single-stranded DNA 118
- sink vertex 70
- skew 118, 121 (*see also* GC-skew)
- skew plot 113
- skewed distributions 296
- skin color 17
- small-world networks model 300
- snow leopard (*P. uncia*) 248–263
- SNPs (single-nucleotide polymorphisms) 4, 93, 94–96
 - (*see also* haplotype blocks; tag SNPs)
 - and disease 6, 8, 15
 - paternity inference 103, 104–105, 106–107
- software
 - Citoscape 295
 - FRAG_NEW 252
 - Genscan 135
 - GraphCrunch 295, 300
 - heuristic 234
 - Jane 235, **237–245**

Index

361

- MATCH 140
- MrBayes 253, 254
- PAUP* 256
- Tarzan 234
- TreeMap 234
- WebLogo 133
- software run times *see* run times of algorithms
- sorting 175–176, 176, 184, 212, 258–259
- source vertex 70
- Southern, Sir Edwin 55–56, 58, 64
- Spanish flu 148
- speciation events 229, 230–231, 230–231, 237–241, 239
- species trees 190
- specificity of interaction 127, 156
- splice sites 68, 81, 129
- splicing 68, 128
- spoke models 293
- standard deviation 338
- star trees 254, 261–263
- statistical hypothesis testing 232
- statistical inference 342
- statistical tests
 - of association 12
 - case-control test 16
 - Chi-square (χ^2)* test 11
 - correlation between two events 9–12
 - Fisher's exact test 152, 160
 - F*-test 14
- Stats Mode (Jane software) 244
- Stephens, P. J. *et al.* 221
- stopping rule (algorithms) 285
- strict consensus trees 251, 254, 256
- string of (*l*-mer) 131
- Student's *t* distribution 13, 14
- Sturtevant, A. H. 173–175, 207
- subgraphs 158, 296
- subpath (graphs) 71
- substitutions (nucleotides) 168
- substrate specificity 127
- successors 216–217
- Sul, S.-J. *et al.* 261
- super-chromosome 180
- supercomputers 233
- supercycle (graphs) 60–61
- superstring nucleotides) 49–52
- Swine Flu 148–149, 150–151, 150
- synteny blocks 179, 209–210, 213, 216–217
- systems biology 316
- systems pharmacology 305–306
- t*-statistic 14
- tag SNPs 23–33, 24, 25–29, 31, 33, 33
- tandem duplication 211
- tanglegram 230
- Tarzan software 234
- Taylor, B. 209
- telomeres 168, 176, 180–181, 207
- terminal residues 157
- terminus (ter) 115–116, 118
- Tesler, Glenn 209
- test accuracy 98, 99
- test for associations 14
- tests, statistical *see* statistical tests
- test's power 12
- tetraglucose 152
- TFs (transcription factors) 126, 127–130, 142–143, 317–318
- TF binding sites (TFBS) 127, 317 (*see also* binding sites)
 - additional hallmarks 141–143
 - destruction 19
 - identification 141, 143
 - models 129–134
 - multiple rare variants 19
- TF proteins 142, 143
- TF-DNA 128–129, 133, 133, 141, 143
- tiger (*P. tigris*) 248–263
- time complexity (*see also* run times of algorithms)
 - O(n²)* time 271, 272
 - polynomial-time 268–269, 271, 276
 - quadratic time 269
- topology 195, 296, 303–306, 311–312
- tractable vs. intractable problems 48–49
- transcription 111, 112, 115–116, 116, 118, 119, 319
- transcription factors *see* TF entries
- transcriptional regulation 128, 317–319
- transcription-induced mutations 120
- TRANSFAC database 130
- translocations 122, 180, 181, 218
- trans-membrane protein 127
- transmission efficiency, influenza virus correlation 155
- transpositions 181, 211
- Traveling Salesman Problem 76, 235–237
- tree distance matrix 193
- Tree of Life (TOL) 189–192, 268
- treelets 158–161
- TreeMap software 234
- treespace 284–285
- trivial bipartitions 255, 257
- true (network) alignments 308
- unconditional probability 97
- uninformative priors (Bayesian inference) 103
- unique bipartitons 258–259
- universal gene core 194
- universal hashing functions 261–263
- University of Leipzig, Germany 234
- University of Sydney, Australia 234

362 Index

- unobserved data *see* prior probability
unrooted trees 251, 263, 278
unsigned reversals **175–178**

vaccines 150, 229
variables, observed and hidden 98, 102
variants 4–5
Venn diagram 97
vertices (graphs) 69–70, 271–272
 degree of a vertex 43–45
 indegree of a vertex 47–48, 53
 outdegree of a vertex 47–48, 53
 sink vertex 70
 source vertex 70
vessel theory of influence pandemics
 155
viral genomes 113, 119
viral glycan-binding protein 155
viral RNAs 150

Virchow, Rudolf 192
virus replication 116

walks (graphs) 69
wasps 228, 241–243
WebLogo sequencing software 133
weighting, event cost 232
weights 67, 70, 79–80
Woese, C. R. and coworkers 190
word-based algorithms 157
World Health Organization 149
Wright Fisher model 7

X- and Y-linked DNA sequences 253

Yancopoulos, S. and colleagues 180
yeast 293, 295, 318

Zuckerkandl, Emile 190