

Index

- D*-split, 112
- \mathcal{X} -tree, 25, 91, 139
- μ -distance, 179
- p*-split, 219
- 3-SAT, 169

- abstract network, 71
- acyclic agreement forest, 281
- acyclic DLT scenario, 298
- acyclic graph, 5
- Adams consensus tree, 65
- additive distances, 51, 254
- adjacent, 3
- affine gap penalty, 16
- agreement forest, 276
- Aho algorithm, 301
- Aho graph, 301
- alignment, rooted phylogenetic networks, 181
- ancestor, 8
- ancestral recombination graph, 79, 236
- apex of a reticulation, 162
- arc, 7
- ARG, 79, 236
- Arlequin, software, 335

- backbone clusters, 194
- backbone tree, 194
- balanced average distance, 57
- balanced edge length, 57
- balanced minimum evolution, 56
- balanced minimum evolution tree, 59
- Bayes' Theorem, 45
- Beagle, software, 335
- bicombining network, 140
- bicombining node, 76, 140
- biconnected component, 6
- bifurating node, 8
- bifurcation, rooted phylogenetic network, 140
- Bio-PhyloNetwork, software, 335
- bipartite graph, 6, 94
- blocks, 15
- BLOSUM matrix, 15, 20
- BME, 56
- bootstrapping, 44

- bottom-up algorithm, 11
- branch, 7, 24
- branch-and-bound, 36
- branch-swapping methods, 38
- breadth-first traversal, DAG, 11
- breadth-first traversal, tree, 10
- Buneman graph, 98
- Buneman index, 109
- Buneman tree, 110
- burn in, 47

- canonical split network, 98
- Cass algorithm, 212
- caterpillar chain, 278
- chain reduction, 278, 283
- character, 22, 217
- character state, 22
- child, 8
- circular cladogram, network, 322
- circular cladogram, tree, 315
- circular distance matrix, 254
- circular network algorithm, 72, 105, 190, 254, 259, 310, 330, 332
- circular ordering, 103
- circular phylogram, network, 326
- circular phylogram, tree, 324
- circular splits, 102
- clade, 11
- cladogram, 312
- clique, 131
- cluster, 11, 128, 129
- cluster containment problem, 168
- cluster distance, trees, 62
- cluster network, 76, 134, 193, 334
- cluster reduction, 282
- cluster weight, 128
- cluster-popping algorithm, 135, 193, 274, 288
- collapsible, 304
- CombineTrees, software, 335
- combining view, 81, 327
- compatible, binary characters, 217
- compatible, clusters, 130
- compatible, splits, 71, 90
- composite taxon, 195

359 **Index**

- condensed multiple alignment, 216
- connected component of a graph, 6
- connected graph, 6
- Consecutive Ones problem, 103
- consensus cluster network, 274
- consensus split network, 266, 332
- consensus super cluster network, 275
- consensus tree, 265
- contact edge, 327
- contained tree, split network, 121
- contraction, edge, 6, 27
- contraction, split, 121
- convex hull, 187, 219
- convex hull algorithm, 72, 101, 187, 253, 332
- cut edge, 6
- cut node, 6
- cycle, 5

- DAG, 8, 70
- DAG traversals, 10
- data-display network, 71
- decomposable distance matrix, 119
- decomposable set of clusters, 151
- decomposition property, 151
- decomposition, divide-and-conquer, 156, 194
- degree of a node, 5
- deletion, 14
- Dendroscope, software, 77, 81, 82, 193, 202, 215, 299, 328, 331, 334
- dense rooted triples, 304
- descendant, 8
- digraph, 4
- directed acyclic graph, 8
- directed cycle, 5
- directed edge, 4
- directed graph, 4
- directed path, 5
- displayed cluster, 129
- displayed tree, 144
- displayed trees distance, softwired networks, 177
- distance function, 50
- distance matrix, 50, 250
- distance-based methods, 50
- distances represented by splits, 251
- distortion of a split, 274
- divide-and-conquer, decomposition-based, 195
- DLT, 289
- DLT scenario, 294
- duplication-loss, 291

- edge, 3
- edge assignment map, 151, 159
- edge coloring, 93
- edge length, 323
- edge weight, 323
- edge-weighted tree, 27
- edit distance, 14
- EEEP, software, 335
- embedded network, 140
- evolutionary network, 71
- explicit network, 71

- FastME, 59
- Felsenstein's algorithm, 43
- finite metric space, 122
- fit, split decomposition, 119
- Fitch algorithm, 34
- Fitch-Hartigan, 34
- flat prior, 45
- four-point condition, 51

- gall, 156
- galled network, 162, 201, 334
- galled tree, 156, 240
- GalledTree, software, 336
- Gamma distribution, 31
- gap extension penalty, 17
- gap open penalty, 17
- gap penalty, 16
- gaps, 14
- gene duplication, 289
- gene loss, 289
- gene phylogeny, 289
- general time reversible model, 31
- geodesically pruned quasi-median network, 232
- global alignment, 17
- guide tree, 21, 316

- Hamming distance, 33, 50
- haplotype, 75, 216
- haplotype network, 75
- hardwired, 76, 193
- hardwired cluster distance, 173
- hardwired clusters, 146
- hardwired interpretation, 147
- hardwired network, 148
- Hasegawa-Kishino-Yano model, 31
- Hasse diagram, 133, 243
- homologous, 13, 20
- horizontal gene transfer, 289
- HybridInterleave, software, 336
- hybridization network, 77, 275, 335

- identifiable models, 32
- identity, 172
- immediate dominator, 142
- in-edge, 4
- incident, 3
- incomparable, 292
- incomparable edges, 9
- incomparable nodes, 9
- incompatibility graph, 91, 130
- incompatible, binary characters, 217
- incompatible, clusters, 130
- incompatible, splits, 90
- indegree, 4
- indistinguishable networks, 172
- induced clusters, 129
- induced graph, 5
- induced phylogenetic network, 143
- induced phylogenetic tree, 61
- induced splits, 88
- infinite sites, 235

360 **Index**

- inner circular cladogram, tree, 316
- inorder traversal, tree, 10
- insertion, 14
- internal node, 7
- isolation index, 111
- isomorphic rooted networks, 177
- isomorphism distance function, 178

- Jukes-Cantor model, 29
- Jukes-Cantor transformation, 51
- jungle, 337

- Kuratowski map, 125

- large parsimony problem, 35
- LCA, lowest common ancestor, 140
- leaf node, 7, 139
- length, edge, 26
- level of a node, 313
- level, rooted phylogenetic network, 160
- level- k network, 160, 303, 334
- LEVEL2, software, 336
- linear gap penalty, 16
- local algorithm, 47
- local alignment, 18, 19
- local-tree graph, 237
- lower edge, 9
- lower node, 8
- lowest common ancestor, 140, 292
- lowest common ancestor, taxa, 64
- lowest stable ancestor, 142
- LSA consensus tree, 65, 143
- LSA tree, 142, 318
- LSA* tree, 318

- majority consensus tree, 64, 265, 335
- Markov chain Monte Carlo, 46
- MARLON, software, 336
- matching, 182
- Max Clique, 131
- maximum acyclic agreement forest, 281
- maximum agreement forest, 278
- Maximum Compatibility problem, 131
- maximum likelihood estimation, 40
- maximum parsimony method, 33, 272
- maximum parsimony problem, 33
- maximum weighted matching, 182
- MC³, 48
- MCMC, 46
- median closure, 220
- median network, 220, 332, 333
- median sequence, 220
- median-joining, 227, 332, 333
- metric, 50
- Metropolis-coupled Markov chain Monte Carlo, 48
- Metropolis-Hastings algorithm, 46
- minimum galled network, 164
- minimum galled tree, 157
- minimum spanning network, 229, 332, 335
- minimum spanning tree, 229

- MLE, 40
- model of sequence evolution, 32
- model tree, 29
- molecular clock hypothesis, 52
- monophyletic group, 11
- multi-labeled tree, 80, 287, 289, 335
- multicomining node, 140
- multifurcating node, 8
- multiple crossover, 234
- multiple sequence alignment, 20
- MY-CLOSURE, software, 336

- naive algorithm, networks, 316
- nearest neighbor interchange, 38
- Needleman-Wunsch, 18
- neighbor-joining method, 54
- neighbor-net method, 254, 308, 332
- nested clusters, 130
- nested labels, 180, 288
- nested sets, 65
- nested-labels distance, 180
- nestedness, cluster networks, 135
- netting method, 249
- network alignment graph, 181
- network of life, 70
- Network, software, 75, 249, 333
- Newick format, network, 81, 334
- Newick format, tree, 66, 81, 334
- Nexus format, 332, 334
- NNI, 38
- NNI distance, 62
- node, 3
- nonparametric bootstrapping, 44
- normalized Hamming distance, 50
- Notung, software, 336
- NP-complete problem, 169

- observed p-distance, 50
- offset parameter, 325
- on \mathcal{X} , 11
- Optimal Consecutive Ones problem, 104
- ordinary least squares, 60
- out-edge, 4
- outdegree, 5
- outer-labeled planar, 104, 254
- outgroup, 89
- outgroup rooting, 26
- outgroup trick, 89
- overlap alignment, 18

- PADRE, software, 299, 336
- pairwise alignment, 14
- parametric bootstrapping, 44
- paraphyletic group, 12
- parent, 8
- parsimony index, 218
- parsimony score, 35
- parsimony splits, 111, 218
- partial order, 132
- partial split, 112, 268
- partial tree, 268

361 **Index**

- partially ordered set, 132
- path-multiplicity distance, 179
- path-multiplicity vector, 179
- patristic distance, 51
- PEGAS, software, 336
- phylogenetic network, 69
- phylogenetic tree, 25
- phylogeny, 11
- phylogram, 27, 323
- PhyloNet, software, 336
- planar, 190
- plane drawing, 317
- polyphyletic group, 12
- posterior probability, 45
- postorder traversal, DAG, 10
- postorder traversal, tree, 10
- preorder traversal, DAG, 10
- preorder traversal, tree, 10
- prior probability, 45
- prior probability distribution, 45
- probability of parsimony, 75, 334
- processing pipeline, SplitsTree, 332
- progressive alignment, 21
- projection of splits, 98
- properly contained, 156
- purines, 15
- pyrimidines, 15

- QNet method, 308
- QNet, software, 74, 336
- quartet distance, 62
- quartet topology, 108
- quartet-net method, 308
- quasi-median, 224
- quasi-median closure, 224
- quasi-median network, 224

- radial diagram, split network, 330
- radial diagram, tree, 329
- reassortment, 79
- reassortment network, 80
- Recodon, software, 336
- recombination network, 79, 233, 235
- recombination node, 235
- RecPars, software, 336
- rectangular cladogram, network, 322
- rectangular cladogram, tree, 315
- rectangular phylogram, network, 325
- rectangular phylogram, tree, 324
- reduced median network, 222, 333
- reducedness, cluster networks, 135
- refinement, 6
- related species, 11
- relaxed minimum spanning network, 230
- replacement, 14
- representation of a cluster, 129
- represented clusters, cluster network, 135
- represented tree, 144
- resolved tree, 8
- resolved, rooted phylogenetic network, 140
- restricted quasi-median, 232
- restriction, clusters, 129
- restriction, phylogenetic tree, 61, 275, 300
- restriction, splits, 88
- reticulate edge, 134, 139
- reticulate node, 134, 139
- reticulation, 134, 139
- reticulation-separation, 135, 159, 288
- reticulogram, 75, 261
- Robinson-Foulds distance, 61, 122
- root node, network, 139
- root node, tree, 7
- rooted \mathcal{X} -network, 139
- rooted phylogenetic network, 76, 138
- rooted SPR, 277
- rooted tree, 7
- rooted tree, phylogenetic, 26
- rooted triple, 300
- rooted triple distance, 62
- rooted triple encoding, 300
- rooting a tree, 7
- rSPR, 277
- rSPR distance, 62, 277

- seed-growing algorithm, 203
- separated taxa, 129
- separation property, 163
- sequence-based methods, 33
- Serial NetEvolve, software, 336
- SHRUB, software, 337
- sibling nodes, 166
- simple graph, 4
- single crossover, 234
- Sliding MinPD, software, 337
- small parsimony problem, 34
- Smith-Waterman algorithm, 19
- softwired, 76
- softwired cluster distance, 174
- softwired clusters, 146
- softwired interpretation, 147
- softwired network, 148
- species phylogeny, 289
- Spectronet, software, 337
- split, 12, 44, 87, 88
- split decomposition, 111, 114, 332
- split encoding, 89
- split extension, 112
- split graph, 94, 329
- split metric, 116
- split network, 71, 96, 266, 329
- split network, embedding of, 329
- split part, 88
- split prime residue, 116
- split represented by e , 89
- split size, 88
- split weight, 88
- SplitsTree, software, 72, 75, 192, 249, 253, 259, 299, 331, 332
- SPR, 38, 335
- SPR distance, 40, 62
- stable ancestor, 142, 171, 175
- stable descendant, 175

Cambridge University Press

978-0-521-75596-2 - Phylogenetic Networks: Concepts, Algorithms and Applications

Daniel H. Huson, Regula Rupp and Celine Scornavacca

Index

[More information](#)**362** **Index**

- star decomposition heuristic, 37
- star tree, 37
- stationarity, 47
- statistical consistency, 32
- statistical parsimony, 75, 334
- stepwise-addition heuristic, 37
- strict consensus tree, 63, 265, 335
- strongly connected, 6
- sub-DAG rooted at v , 9
- subgraph, 5
- subnetwork, 178
- subnetwork isomorphism, 178
- substitution matrix, 15, 20
- subtree prune and regraft, 38, 277
- subtree reduction, 278
- subtree rooted at v , 8
- sum of pairs, 20
- super split network, 73, 271
- super tree, LSA, 143
- super tree, strict consensus, 271
- super-tree method, 143
- suppress a node, 5
- suppressible node, 5, 139, 197

- T-Rex algorithm, 261
- T-Rex, software, 75, 337
- T-theory, 122
- tangled clusters, 195, 199
- taxon labeling, 25
- TBR, 39
- TBR distance, 62
- TCS, software, 75, 249, 334
- temporal feasibility, 298
- three dimensional matching problem, 132
- three-point condition, 52
- tight span, 123
- time consistent, 167
- time reversible model, 40
- time stamp, 167
- top-down algorithm, 11
- topological embedding, rooted tree, 313
- topological embedding, split network, 190
- transfer edge, 81, 327
- transfer view, 81, 82, 327
- transitions, 15, 31, 217
- transversions, 15, 31, 217
- tree, 7
- tree bisection and reconnection, 39
- tree cycle, 162
- tree distance, 51
- tree edge, 134, 139
- tree length, 51
- tree node, 134, 139
- tree of life, 11
- tree traversals, 9
- tree, phylogenetic, 25
- tree, rooted phylogenetic, 26
- tree-child, 164
- tree-like distances, 51
- tree-sibling, 166
- Treemapper, software, 299, 337
- triangular cladogram, tree, 313
- tripartition, 175
- tripartition distance, 175
- trivial cluster, 128
- trivial split, 88

- ultra metric, 52
- UMP method, 335
- undirected graph, 3
- undirected path, 5
- uniqueness, cluster networks, 135
- unnormalized Hamming distance, 50
- unrooted phylogenetic network, 71
- unrooted tree, 7
- unrooted tree, phylogenetic, 25
- unstable ancestor, 175
- unstable descendant, 175
- unweighted split metric, 250

- vertex, 7
- virtual median, 226
- visibility property, 165

- weak compatibility, 106
- weakly connected, 6
- weight, cluster, 128
- weight, edge, 26
- weight, split, 88
- weighted least squares approach, 60
- weighted split metric, 250

- χ -tree, 25

- Z-closure, 269, 332, 335
- Z-relation, 268