Index

D-split, 112
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
bifurcating 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
clad, 11
cladogram, 312
clique, 131
cluster, 11, 128, 129
cluster containment problem, 168
cluster distance, trees, 62
cluster network, 79, 190, 254, 259, 310, 330, 332
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

358
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
duplication, 291
edge, 3
degradation, 151
edge coloring, 93
degree, 159
degrect length, 323
degrect weight, 323
degrect-weighted tree, 27
dependence 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
genealogy, 13, 20
geodesically pruned quasi-median network, 232
geodesically pruned median network, 232
global alignment, 17
guide tree, 21, 316
Hamming distance, 33, 50
haplotype, 75, 216
haplotype network, 75
hardwired, 76, 193
hardwired clusters, 173
hardwired interpretation, 147
hardwired network, 148
Hasegawa–Kishino–Yano model, 31
Hasse diagram, 133, 243
homologous, 13
horizontal gene transfer, 289
HybridInterleave, software, 336
hybridization network, 77, 275, 335
identifiable models, 32
identifiability, 172
immediate dominator, 142
incident, 3
incompatible, 292
incompatible edges, 9
incompatible 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
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
MC7, 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
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 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
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
retricate edge, 134, 139
retricate node, 134, 139
retrication, 134, 139
retrication-separation, 135, 159, 288
reticulogram, 75, 261
Robinson-Foulds distance, 61, 122
root node, network, 139
root node, tree, 7
rooted, 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