

# Index for Volume 57 (2008)

*Syst. Biol.* 57(6):957–986, 2008  
Copyright © Society of Systematic Biologists  
ISSN: 1063-5157 print / 1076-836X online  
DOI: 10.1080/10635150802630959

- 1*fin*, 922  
25*fin*, 922  
289*fin*, 922  
3*genes*, 930, 931  
6*fin*, 922  
A Bayesian Perspective on a Non-parsimonious Parsimony Model,  
John P. Huelsenbeck, Cécile Ané, Bret Larget, and Fredrik  
Ronquist, 406  
A Comparative Study in Ancestral Range Reconstruction Methods:  
Retracing the Uncertain Histories of Insular Lineages, John R.  
Clark, Richard H. Ree, Michael E. Alfaro, Matthew G. King,  
Warren L. Wagner, and Eric H. Roalson, 693  
A Justification for Reporting the Majority-Rule Consensus Tree in  
Bayesian Phylogenetics, Mark T. Holder, Jeet Sukumaran, and  
Paul O. Lewis, 814  
A Likelihood Framework for Estimating Phylogeographic History on  
a Continuous Landscape, Alan R. Lemmon and Emily  
Moriarty Lemmon, 544  
A Model-Based Approach to Study Nearest-Neighbor Influences  
Reveals Complex Substitution Patterns in Non-coding  
Sequences, Guy Baele, Yves Van de Peer, and Stijn  
Vansteelandt, 675  
A Novel Test for Host-Symbiont Codivergence Indicates Ancient  
Origin of Fungal Endophytes in Grasses, C. L. Schardl, K. D.  
Craven, S. Speakman, A. Stromberg, A. Lindstrom, and R.  
Yoshida, 483  
*A priori directionality test*, 554  
A Rapid Bootstrap Algorithm for the RAxML Web Servers,  
Alexandros Stamatakis, Paul Hoover, and Jacques Rougemont,  
758  
*A. aeolicus*, 855  
*A. altissima*, 798  
*A. angelinajoliae*, 646  
*A. atomarius*, 629, 632, 634, 639, 641, 642  
*A. australis*, 330  
*A. caesium*, 800  
*A. carpinifolium*, 800  
*A. catus*, 121  
*A. caudatum*, 805  
*A. circinatum*, 796, 804, 806  
*A. cissifolium*, 805  
*A. confucii*, 798  
*A. cotylalveus*, 23  
*A. crataegifolium*, 800  
*A. dawsoni*, 398, 403  
*A. distylum*, 800, 804  
*A. fabri*, 796  
*A. fumigatus*, 618  
*A. glabrum*, 796, 800, 804  
*A. haselbachense*, 805  
*A. heldreichii*, 805  
*A. henryi*, 805  
*A. kweilinense*, 796  
*A. laurinum*, 800, 804, 806  
*A. longicaulis*, 695  
*A. lyrata*, 481  
*A. macrophyllum*, 796, 800, 805, 806  
*A. macrophyllum/A. caesium*, 804  
*A. melas*, 119  
*A. nebulosus*, 119  
*A. negundo*, 796, 800, 804, 805  
*A. nidulans*, 618  
*A. nipponicum*, 800  
*A. oryzae*, 618, 624  
*A. osmontii*, 805  
*A. pennsylvanicum*, 796, 800, 806  
*A. pennsylvanicum/A. crataegifolium*, 804  
*A. petraea*, 478  
*A. pictum*, 280  
*A. pilosum*, 800, 804  
*A. polydentatus*, 22, 23  
*A. pseudoplatanus*, 800, 804, 805  
*A. rubrum*, 796, 800, 806  
*A. rubrum/A. saccharinum*, 804  
*A. saccharinum*, 796, 800, 807  
*A. saccharum*, 795, 796, 800, 804  
*A. spicatum*, 796, 800, 805  
*A. spicatum/A. carpinifolium*, 804  
*A. stellatus*, 912  
*A. tataricum*, 800  
*A. tegmentosum*, 800, 804  
*A. thaliana*, 469  
*A. trautvetteri*, 805  
*A. tricolor*, 695  
*A. vastus*, 403  
*A. wardii*, 796  
*A. weltoni*, 17, 22, 24, 27  
*Abacion magnum*, 922  
*Abalistes stellatus*, 907  
*Abalistes*, 906, 910–912, 916  
*Abbotii*, 880, 885, 886  
*Abronia*, 172  
*Acanthascus (Rhabdocalyptus)*, 391  
*Acanthascus dawsoni*, 390, 392, 398, 403  
*Acanthascus*, 395  
*Acanthaster planci*, 906, 918  
*Acanthocyclops vernalis*, 922  
*Acanthospartum*, 279  
Accounting for Phylogenetic Uncertainty in Biogeography: A  
Bayesian Approach to Dispersal-Vicariance Analysis  
of the Thrushes (Aves: *Turdus*), Johan A. A. Nylander, Urban  
Olsson, Per Alström, and Isabel Sanmartín, 257  
*Acer arcticum*, 806  
*Acer circinatum*, 800  
*Acer*, 795–808  
*Acer/Dipteronia*, 800, 804, 807

- Acheta veletis*, 889  
*Achimenes*, 706  
*Achnatherum inebrians*, 485  
*Acipenser*, 116  
*Acoelocalyx brucei*, 391, 395, 398, 402  
*Aconitum*, 58  
*Acontias*, 644  
*Acrochordus*, 421  
 ACT, 874  
 ACTB, 577  
 Actinobacteria, analysis of, 835  
 Actinopterygii, 519  
 Adaptive radiation, 562  
*Adelolecia pilati*, 143  
*Adenocarpus*, 748  
*adh1*, 478, 480  
 ADORA3, 500  
 ADRA2B, 500  
 ADRB2, 500  
*Aegilops*, 365  
*Aeonium*, 734, 744, 748  
*Aeschynanthus*, 694, 695  
*Aesculus*, 796, 798, 807, 808  
*Aetiocetus cotylalveus*, 17, 21, 27, 34  
*Aetiocetus polydentatus*, 17, 22, 34  
*Aetiocetus weltoni*, 16–18, 21, 23, 24, 27–30, 34  
*Aetiocetus*, 23, 27  
 AFLP, 347  
*Agathis australis*, 330  
*Agathis*, 330, 331  
*Aglaocetus patulus*, 34  
*Aglaocetus*, 23  
*Agorophius pygmaeus*, 31, 34  
*Agorophius*, 34  
*Agrostis hiemalis*, 485  
*Agrostis tenuis*, 485  
 Aguilera, G., Marthey, S., Chiapello, H., Lebrun, M.-H., Rodolphe, F., Fournier, E., Gendraul-Jacquemard, A., and Giraud, T., Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies, 613  
*Agus fran*, 735  
*Agus juba*, 735  
*Agus petr*, 735  
*Agustinii*, 741  
*Aichryson*, 744, 747  
*Ailanthus*, 798, 807  
*Ailuronyx seychellensis*, 564  
 Akaike information criterion (AIC), 42, 60, 76, 77, 84, 113  
*Akanthosuchus langstoni*, 181  
*Albatus*, 310  
*Albatarum pueri*, 282  
*Albifrons*, 537  
*Albula*, 537, 538  
*Alectoria*, 142  
 Alekseyenko, Alexander V., Lee, Christopher J. and Suchard, Marc A., Wagner and Dollo: A Stochastic Duet by Composing Two Parsimonious Solos, 772  
*Alfaro, Michael E.*, see Clark, John R., 693  
*Alfaro, Michael E.*, see Dornburg, Alex, 905  
*Ali, Farhan*, see Meier, Rudolf, 809  
 Alignment accuracy, 656  
*Alligator mississippiensis*, 173  
*Allodaposuchus precedens*, 181  
*Allognathosuchus*, 181  
*Allopauropus proximus*, 922  
*Allophana*, 143  
 Alpine, 58  
*Alpinobombus*, 59  
*Alström, Per*, see Nylander, Johan A. A., 257  
 Alternative phylogenies, 785  
 Alternative splicing evolution, 772  
*Altingia*, 43, 55  
*Ambiortus*, 188  
 AMBN, 15, 17, 18, 21, 25–27, 33, 34, 577, 579  
*Ambrosina bassii*, 269, 271, 272, 276, 277, 284  
*Ambrosina*, 271, 272, 276, 277, 279, 282  
*Ambystoma californiense*, 645  
*Ambystoma tigrinum melanostictum*, 561  
*Ameiurus brunneus*, 118  
*Ameiurus catus*, 118  
*Ameiurus melas*, 118  
*Ameiurus natalis*, 118  
*Ameiurus nebulosus*, 118  
*Ameiurus pectinatus*, 117, 119  
*Ameiurus platycephalus*, 118  
*Ameiurus sawrockensis*, 119  
*Ameiurus serracanthus*, 118  
*Ameiurus*, 116, 117, 121, 125–128  
 Ameloblastin (AMBN), 15  
*Amia*, 116, 519, 520, 527, 531, 532, 537  
 Amino acid model, 367  
     dimension reduction, 368  
     conversion to codon model, 368, 369  
     codon model equivalent to, 369, 370  
 Amniote, 179  
*Amorphophallus*, 272  
 Amplified fragment length polymorphism (AFLP), 347  
     DNA fingerprinting, 347  
     technique, 347, 348  
     automated scoring of, 350  
     Sampling Strategy for, 350, 351  
     Generation of Raw data, 351  
     optimal scoring parameters using AFLP, 352  
 An Integrative Method for Delimiting Cohesion Species: Finding the Population-Species Interface in a Group of Californian Trapdoor Spiders with Extreme Genetic Divergence and Geographic Structuring, Jason E. Bond and Amy K. Stockman, 628  
*Anadenobolus*, 644  
*Anartia*, 235  
*Anas*, 188, 481  
 Ancestral range reconstruction, 693  
     explicit methods, 698  
     analysis, 699–701  
 Ancestral state reconstruction, 141  
     of discrete morphological characters, 145, 146  
     for deep nodes with high support, 146  
     algorithm, 147  
     using maximum parsimony, 149  
     by SIMMAP, 152  
 Ancestral state reconstruction, 4  
*Amphidiscs*, 400  
*Andersen 17*, 34, 48, 91, 92, 143  
*Andersen, Heidi L.*, see Ekman, Stefan, 141  
*Androcymbium*, 745, 747  
*Aneides flavipunctatus*, 645  
*Anetia*, 235  
*Anguilla*, 537  
*Anidiops villosus*, 645  
 Annelida, 514  
*Anolis auratus*, 513  
*Anolis cristatellus*, 573

- Anolis extremus*, 328  
*Anolis*, 513, 571, 748, 889  
 Anomalous gene trees (AGTs), 131, 133, 134, 136, 139, 140  
*Anomalous gene trees*, 131  
*Anomalous*, 131, 132  
*Anomaly zone*, 131, 132  
*Anomochilus*, 430  
*Anopheles gambiae*, 780  
*Anopsobius neozelanicus*, 922  
*Anthoxanthum*, 748  
*Anthus*, 268  
*Anthyllis hermanniae*, 279, 282  
*Antilocapra americana*, 33  
*Antipathes galapagensis*, 392  
*Antrodiaetus riversi*, 645  
*Antrodiaetus unicolor*, 644  
*Anura*, 560  
*Ané, Cécile*, see Huelsenbeck, John P., 406  
*Aoraki denticulate*, 644  
*Apatornis*, 200, 514  
*Aphanopetalum*, 39, 43, 54  
*Apheliscus*, 313  
*Aphredoderus*, 538  
*Aphrocallistes vastus*, 390, 403  
*Aphrocallistes*, 391, 395, 396, 402  
*Aplysina fistularis*, 392, 396  
 APOB, 500, 501  
*Apomastus*, 644  
 Apomorphy, 903  
 APP, 500  
 Application of Phylogenetically Defined Names Does Not Require That Every Specifier Be Present on a Tree, Philip D. Cantino and Richard G. Olmstead, 157  
*Apsaravis*, 188, 189  
*Apteronotus*, 537  
*Aptostichus angelinajoliae*, 641, 646  
*Aptostichus atomarius*, 628–630, 634, 635, 639, 642, 643, 646  
*Aptostichus miwok*, 641, 646  
*Aptostichus simus*, 644  
*Aptostichus stanfordianus*, 641, 646  
*Aptostichus stephencolberti*, 628, 641, 646  
*Aptostichus stephencolberti*, 628  
*Aptostichus*, 629, 639, 641–644  
*Aptotichus angelinajoleae*, 646  
*Aquifex aeolicus*, 855  
*Arabidopsis halleri*, 481  
*Arabidopsis thaliana*, 469, 481, 780  
*Arabidopsis*, 341, 478, 844  
 Araceae, 269  
 Arachnida, 931  
*Arbutus*, 269  
 Archaea, 839  
*Archaeomycteris*, 502  
*Archaeopteryx lithographica*, 200  
*Archaeopteryx*, 174–176, 185–187, 200  
*Archeozetes longisetosus*, 711  
*Archeoziphius microglenoideus*, 873  
 Argentina, 537  
*Argulus*, 922  
*Argyranthemum*, 734, 744, 748  
*Arisarum probosciideum*, 283  
*Arisarum vulgare*, 276  
*Arisarum*, 271, 272, 276, 277, 282  
*Armadillidium vulgare*, 922  
*Artemia salina*, 922  
 Arthropoda, 920, 931  
*Arum maculatum*, 276  
*Arum pictum*, 269, 271, 272, 276, 277, 279–282  
*Arum*, 271, 272, 276, 279, 280, 282, 283  
 Ascomycetes, 141  
 Ascomycota, 613  
*Ashbya gossypii*, 615  
 Asher, Robert J., Geisler, Jonathan H., and Sánchez-Villagra, Marcelo R., Morphology, Paleontology, and Placental Mammal Phylogeny, 311  
*Asiatosuchus germanicus*, 180  
*Asiatosuchus*, 180, 181  
*Aspergillus fumigatus*, 615  
*Aspergillus nidulans*, 615  
*Aspergillus oryzae*, 615, 616, 625  
*Aspergillus*, 618, 624, 625  
*Aspidoscelis tigris*, 421  
 Assessing the Performance of Single-Copy Genes for Recovering Robust Phylogenies, G. Aguileta, S. Marthey, H. Chiapello, M.-H. Lebrun, F. Rodolphe, E. Fournier, A. Gendrault-Jacquemard, and T. Giraud, 613  
 Assignment, 750  
     graphic representation of, 753  
     flowchart of, 751  
     taxonomic, 752  
     probabilities, 753  
     false, 756  
*Astephus*, 116, 117, 119, 126–128  
*Astragalus*, 410, 414  
*Astrartes fulgurator*, 207, 210, 212–214  
*Astrocystis*, 155  
*Atolla vanhoffeni*, 392  
*atp1*, 41  
*ATP7A*, 17–19, 34, 500  
*AtpB*, 41, 55, 56, 410, 414  
*Aulaxyper*, 732, 733, 736, 740, 744, 745  
*Aulosaccus*, 391, 395, 398  
*Australosuchus clarkae*, 180  
 Automated scoring, 347  
     parameter settings, 348  
*AvG(G)*, 767  
*AVG(P)*, 767  
*AvG(P)*, 767  
*AvG(R)*, 767  
*AvG(S)*, 767  
 Avise, John C., and Robinson, Terence J., Hemipty: A New Term in the Lexicon of Phylogenetics, 503  
*Axestotrigona ferruginea*, 60  
*B. acutorostrata*, 24  
*B. alboanalis*, 72  
*B. appositus*, 72  
*B. ashtoni*, 73  
*B. atratus*, 58  
*B. beaticola*, 72  
*B. bimaculatus*, 72  
*B. bohemicus*, 73  
*B. borealis*, 25, 72  
*B. brydei*, 25, 34  
*B. californicus*, 72  
*B. caprisicus*, 912  
*B. cingulatus*, 72  
*B. conspicillum*, 910, 916  
*B. dahlbomii*, 68  
*B. davisii*, 281  
*B. dispar*, 281  
*B. distinguendus*, 72  
*B. edeni*, 34

- B. ephippiatus*, 58, 68  
*B. fernaldae*, 73  
*B. fervidus*, 72  
*B. flavidus*, 73  
*B. fuscus*, 912  
*B. gerstaeckeri*, 58  
*B. handlirschi*, 68  
*B. hypnorum*, 71, 72  
*B. impatiens*, 68  
*B. lapponicus*, 72  
*B. lucorum*, 71, 72  
*B. mexicanus*, 68  
*B. monticola*, 72  
*B. mori*, 233, 235, 240  
*B. morrisoni*, 58  
*B. musculus*, 25  
*B. ovalis*, 909  
*B. pennsylvanicus*, 72  
*B. perplexus*, 71, 72  
*B. physalus*, 25, 867, 873  
*B. polylepis*, 912  
*B. pratorum*, 71  
*B. pullatus*, 58  
*B. sandersoni*, 72  
*B. sitkensis*, 72  
*B. sonorus*, 58, 72  
*B. spinosus*, 398, 909  
*B. sylvicola*, 72  
*B. transversalis*, 58  
*B. vetula*, 912  
*B. volucelloides*, 68  
*Bacchetta*, Gianluigi, *see* Mansion, Guilhem, 269  
*Bacidia arceutina*, 146  
*Bacidia heterochroa*, 146  
*Bacidia rosella*, 143  
*Bacidia*, 145, 146, 150–154  
*Bacidina*, 154  
*Bacillus*, 840  
 Back-propagation, 202  
     rule, 206  
     neural network, 202, 203  
     DNA barcoding, 202, 207  
*Bacterial Code*, 507  
 Baele, Guy, Van de Peer, Yves and Vansteelandt, Stijn, A Model-Based Approach to Study Nearest-Neighbor Influences Reveals Complex Substitution Patterns in Non-coding Sequences, 675  
*Baker*, C. Scott, *see* Dalebout, Merel L., 857  
*Balaena mysticetus*, 23, 33, 34, 578  
*Balaena*, 29  
*Balaenoptera acutorostrata*, 16, 24, 30, 31, 33, 34, 574, 583  
*Balaenoptera bonaerensis*, 25, 33, 34  
*Balaenoptera borealis*, 33, 34  
*Balaenoptera brydei*, 34  
*Balaenoptera davidsonii*, 31  
*Balaenoptera edeni*, 33, 34  
*Balaenoptera gastaldii*, 34  
*Balaenoptera musculus*, 25, 27, 33, 34, 867, 873  
*Balaenoptera omurai*, 33, 874  
*Balaenoptera physalus*, 16, 25, 31, 33, 34  
*Balaenoptera siberi*, 32  
*Balaenoptera*, 23, 25, 31, 32, 34  
*Balearia*, 280  
 Baleen, 15  
*Balistapus undulates*, 907  
*Balistapus*, 906, 910, 912, 916  
*Balistes capricus*, 907  
*Balistes fuscus*, 916  
*Balistes polylepis*, 907  
*Balistes punctatus*, 907  
*Balistes vetula*, 907  
*Balistes*, 909–912, 916, 918  
 Balistidae, 905  
     phylogenetic relationships of, 916  
*Balistoides conspicillum*, 906, 907  
*Balistoides viridescens*, 906, 907, 910  
*Balistoides*, 905, 906, 910, 912, 916  
*Balistomorphus orbiculatus*, 909  
*Balistomorphus*, 906  
*Ball*, Bernard, *see* Regier, Jerome C., 920  
 Bandelt, Hans-Jürgen, and Fischer, Mareike, Perfectly Misleading Distances from Ternary Characters, 540  
*Baptornis*, 187, 188  
 Barcoding, 750  
*Barrett*, Paul M., *see* Wills, Matthew A., 891  
*Baru darrowi*, 180  
 Basal centrality, 245  
 Basidiomycota, 613  
*Basilosaurus cetooides*, 33  
*Basilosaurus*, 30  
*Bathydorus spinosus*, 398  
*Bathydorus*, 391, 395  
*Baumgartner*, Manuela, *see* Leigh, Jessica W., 104  
 Bayes factors (BFs), 120  
 Bayes factors, 388, 675, 795  
 Bayesian Analysis in Molecular Biology and Evolution (BAMBE), 87, 90  
 Bayesian analysis, 466  
 Bayesian Estimation of Species Trees (BEST), 299, 876  
 Bayesian genetic analyses, 732  
 Bayesian hierarchical model, 299  
 Bayesian inference, 86, 257, 693  
 Bayesian information criterion, 76  
 Bayesian methods, 905  
 Bayesian phylogenetic inference, 406, 772  
 Bayesian relaxed clock, 795  
 Bayesian, 708  
     MCMC, 710  
     constrained analysis, 714  
     test results, 716  
     unconstrained analysis, 713, 714, 716  
 Bayesian, 750  
     framework, 750  
     approach, 755, 756  
*BC*, 507–512  
*BDNF*, 17–19, 34, 500  
 Beiko, Robert G., Doolittle, W. Ford and Charlebois, Robert L., The Impact of Reticulate Evolution on Genome Phylogeny, 844  
 Belfiore, Natalia M., Liu, Liang, and Moritz, Craig, Multilocus Phylogenetics of a Rapid Radiation in the Genus *Thomomys* (Rodentia: Geomyidae), 294  
*Bell*, Charles D., *see* Jian, Shuguang, 38  
*Bellemera diamarta*, 142, 143  
*Belodon*, 177  
*Bencomia*, 748  
*Benton*, Michael J., *see* Martin, Jeremy E., 173  
 Beringian disjunctions, 795  
*Bernissartia fagesii*, 181  
*Berta*, Annalisa, *see* Deméré, Thomas A., 15  
 Betweenness, 432, 437  
     Intermediary species and, 436, 437  
     edge, 446  
*BF*, 713

- BGN, 874  
*Biarum dispar*, 269, 271, 272, 276, 277, 279, 281  
*Biarum*, 271, 272, 276, 279–281, 284  
*Biatora*, 145  
*Biblis*, 235  
*Bicirrhosum*, 538  
*Bicyclus anynana*, 232, 233, 241  
*Bicyclus*, 235  
*Bilimbia sabuletorum*, 143, 145  
*Bilimbia*, 150–152  
*Billia*, 796  
*Binary*, 253  
 Bioclimatic modeling, 328  
 Biodiversity conservation, 825  
 Biodiversity conservation, 825  
   applicability, 827  
   stability, 826, 827  
   bootstrapped, 849  
   problem specification, 827, 828  
 Biogeography, 269, 795  
*Bit score*, 219  
 BLAST database, 207  
 BLAST, 216  
*Boa*, 538  
*Bombias*, 68  
*Bombus gerstaeckeri*, 75  
*Bombus luanus*, 59  
*Bombus proavus*, 59  
*Bombus s.s.*, 68  
*Bombus vetustus*, 59  
*Bombus*, 58–60, 62, 63, 66–75, 946  
*Bombyx mori*, 231–233, 240–242  
*Bombyx*, 235, 240  
*Bond sp. nov.* (Figs. 1, 646  
 Bond, Jason E., and Stockman, Amy K., An Integrative Method for Delimiting Cohesion Species: Finding the Population-Species Interface in a Group of Californian Trapdoor Spiders with Extreme Genetic Divergence and Geographic Structuring, 628  
*Boomsma*, Wouter, *see* Munch, Kasper, 750  
 Bootstrap support, 602  
   survivor functions for, 608  
   limiting distribution of, 604  
 Bordewich, Magnus, Rodrigo, Allen G. and Semple, Charles, Selecting Taxa to Save or Sequence: Desirable Criteria and a Greedy Solution, 825  
*Borealis*, 25  
*Borealosuchus*, 181  
*Bos taurus*, 33, 574, 576–580  
*Bos*, 577–580, 582  
*Boss*, Darren, *see* Sanderson, Michael J., 335  
*Bothriopolys multidentatus*, 922  
*Botrytis cinerea*, 615  
*Bottae*, 310  
*Brachychampsia montana*, 179, 181  
*Brachychampsia sealeyi*, 180  
*Brachyelytrum erectum*, 485  
*Brachyphona*, 552, 560  
*Brachypodium sylvaticum*, 485  
*Brachyrhinodon*, 322  
 Branch Lengths, Support, and Congruence: Testing the Phylogenomic Approach with 20 Nuclear Loci in Snakes, John J. Wiens, Caitlin A. Kuczynski, Sarah A. Smith, Daniel G. Mulcahy, Jack W. Sites Jr., Ted M. Townsend, and Tod W. Reeder, 420  
 Branch length, 420  
   related to clade support, 420  
   estimation of, 421, 422  
   correlation between bootstrap and, 425  
   support/congruence and, 427  
   estimation of, 429  
   combined data, 429  
*Branchiopoda*, 931  
*Branchiostoma floridae*, 711  
*Brassica oleracea*, 481  
*Brassica rapa*, 481  
 BRCA, 500, 501  
 Breeding behavior, 474  
*Bridgeri*, 310  
*Brimleyi*, 552  
*Brintesia*, 235  
*Bromham*, Lindell, *see* Lanfear, Robert, 708  
*Bromus erectus*, 485  
*Bromus purgans*, 485  
*Bromus ramosus*, 485  
*Brotula*, 538  
*Brucei*, 391  
 Bruen, Trevor C., and Bryant, David, Parsimony via Consensus, 251  
 Brumfield, Robb T., Liu, Liang, Lum, David E. and Edwards, Scott V., Comparison of Species Tree Methods for Reconstructing the Phylogeny of Bearded Manakins (Aves: Pipridae, *Manacus*) from Multilocus Sequence Data, 719  
 Bryant, David, *see* Bruen, Trevor C., 251  
*Brydei*, 33, 34  
 BTN1A1, 577, 579, 588  
*Buchnera*, 463  
*Bulgaria inquinans*, 156  
 Bumblebees, 58  
 Burbrink, Frank T., and Pyron, R. Alexander, The Taming of the Skew: Estimating Proper Confidence Intervals for Divergence Dates, 317  
*Byssoloma leucoblepharum*, 143  
*C-mos*, 564  
*C. (L.) arboreus*, 210, 211, 213  
*C. (L.) hiurai*, 210, 211, 213  
*C. (L.) procerulus*, 210, 211, 213  
*C. albicans*, 790, 791  
*C. anthropophagorum*, 695  
*C. arcticus*, 398  
*C. aurantiicarpa*, 695  
*C. baileyi*, 465  
*C. californicus*, 465  
*C. calpidicarpa*, 695  
*C. coccinea*, 695  
*C. compressa*, 695  
*C. cordifolia*, 695  
*C. dryas*, 259  
*C. elegans*, 935  
*C. eremicus*, 465  
*C. feaniana*, 695  
*C. formosus*, 465  
*C. gracilirostris*, 259  
*C. grandiflora*, 695  
*C. grayana*, 695  
*C. grayi*, 695  
*C. hawaiiensis*, 695  
*C. hispidus*, 465  
*C. intermedius*, 465  
*C. jeffreyi*, 259  
*C. jonesii*, 695  
*C. kauaiensis*, 695  
*C. kaulantha*, 695  
*C. kealiae*, 695  
*C. kusaimontana*, 695

- C. laxiflora*, 695  
*C. leucantha*, 695  
*C. lherminieri dominicensis*, 259  
*C. lherminieri lawrencii*, 259  
*C. longifolia*, 695  
*C. meyeri*, 398  
*C. milnei*, 695  
*C. mollis*, 707  
*C. munroi*, 695  
*C. nukukivensis*, 695  
*C. occidentalis*, 259  
*C. occulta*, 695, 704  
*C. ootensis*, 695  
*C. pendula*, 695  
*C. picta*, 695  
*C. pogonantha*, 695  
*C. propinqua*, 695  
*C. pulchella*, 695  
*C. richii*, 695  
*C. samoensis*, 695, 698, 699  
*C. sandwicensis*, 695  
*C. spathulata*, 695  
*C. sulcata*, 695  
*C. thibaultii*, 695  
*C. tintinabula*, 695  
*C. urvillei*, 695  
*C. ustulatus*, 259  
*C. valdiviae*, 398  
*C. viridis*, 259  
*C. wagneri*, 695  
*C. wainihaensis*, 695  
*C. wawrae*, 695  
*C. weddelli*, 398  
*Cactophilus*, 310  
*Caenorhabditis elegans*, 780, 921, 926, 932  
*Caenorhabditis*, 109, 921, 922  
*Caerulea*, 470  
*Cairina moschata*, 387  
*Calabaria*, 429  
*Caladidosoma messelense*, 276  
*Caladium*, 272  
*Calamagras turkestanicus*, 322  
*Calamagras*, 327  
*Calamagrositis villosa*, 485  
Calculating gene tree probabilities (COAL), 133  
Calibrations, 909  
*Calinaga*, 237  
*Calla palustris*, 272, 276  
*Callicarpa japonica*, 707  
*Callithrix*, 590  
*Calopadia foliicola*, 143  
*Calycadenia*, 705  
*Calycidium*, 142, 156  
*Calymperaceae*, 514  
Cambrian explosion, 920  
*Camelus dromedarius*, 33  
Cameron, Sydney A., see Whitfield, James B., 939  
*Candida glabrata*, 615  
*Candida lusitanae*, 615  
*Canis familiaris*, 33, 574, 576  
*Canthidermis maculata*, 912  
*Canthidermis maculatus*, 907  
*Canthidermis*, 906, 909–912, 916  
Cantino, Philip D. and Olmstead, Richard G., Application of Phylogenetically Defined Names Does Not Require That Every Specifier Be Present on a Tree, 157  
Cantino, Philip D., see Dayrat, Benoît, 503  
*Caperea marginata*, 22, 23, 25, 26, 33, 34  
*Caperea*, 25  
*Capitella species*, 711  
*Carabus*, 207, 210, 211  
*Carboxydotherrmus hydrogenoformans*, 840  
*Carcinoscorpius rotundicauda*, 922  
*Cardamine*, 365  
*Carlia*, 308, 560  
*Carolinensis*, 391  
*Caryopteris*, 514  
*Casarea dussumieri*, 428  
CAT, 874  
Catalán, Pilar, see Díaz-Pérez, Antonio, 732  
*Catharus ustulatus*, 561  
*Catharus*, 259, 268  
*Cathayornis*, 192  
*Catinaria atropurpurea*, 143, 144  
*Catinaria*, 153  
*Caulophacella*, 391, 395, 398, 399, 402  
*Caulophacus (Caulodiscus)*, 391  
*Caulophacus (Caulophacus)*, 391  
*Caulophacus (Oxydiscus)*, 391  
*Caulophacus*, 395, 398, 402  
*Cavia*, 383  
CBest-RBS, 767  
CBest-SBS(GAMMA), 767  
CBest-SBS, 767  
CBest-SBS/CBest-RBS, 767  
Cdx, 708, 712, 714, 715  
*Cedrela*, 798  
Cenozoic freshwater fishes, 116  
*Centris*, 946  
*Cephaloleia*, 59  
*Cercidiphyllum*, 43  
Cetaceans, 574  
    OR subgenome of, 574  
    relationships among, 580  
Cetacean, 857  
*Cetotherium rathkii*, 34  
*Cetotherium*, 23  
*Cetradonia linearis*, 142  
*Cetradonia*, 156  
*Cetraria*, 145  
*Chaetodipus*, 449, 453, 454, 456, 457, 459, 465  
*Chaetomium globosum*, 615  
*Chaetopterus variopedatus*, 711  
*Chamaea fasciata*, 644  
*Changchengornis*, 188  
*Chanos*, 537  
Character evolution, 169  
Character state reconstruction, 694  
Character-state change, 195  
Character-state space, 938  
*Charina*, 429  
Charlebois, Robert L., see Beiko, Robert G., 844  
Chelicerata, 920  
*Chelonus*, 940, 942  
Chen, Duhong, see Sanderson, Michael J., 335  
Chiapello, H., see Aguilera, G., 613  
*Chihuahuae*, 310  
*Chilopoda*, 931  
*Chirocentrus*, 537  
*Chiroxiphia linearis*, 725  
*Chiroxiphia pareola*, 724  
*Chiroxiphia*, 727

- Chitoria*, 235  
*Chlamydochaera*, 259  
*Chlamydomonas*, 108  
*Choeropsis liberiensis*, 33  
*Chonecetus goedertorum*, 17, 21, 23, 27, 34  
*Chonecetus*, 23  
*Choneziphius*, 873  
*Choristylis*, 43  
*CHRNA1*, 874  
*Chrysochloris*, 315  
*Chrysops*, 538  
*Chthalamus fragilis*, 922  
*Cichlasoma*, 533, 538  
*Cichlerminia*, 263  
*Cichlherminia*, 258, 259, 264  
*Citrinopsithyrus*, 68  
 Clade asymmetry, 116  
*Cladistics*, 179  
*Cladonia digitata*, 143  
*Cladonia peziziformis*, 143  
*Cladonia*, 142  
*Clark, Clay*, see McGowen, Michael R., 574  
*Clark, John R., Ree, Richard H., Alfaro, Michael E., King, Matthew G., Wagner, Warren L. and Roalson, Eric H., A Comparative Study in Ancestral Range Reconstruction Methods: Retracing the Uncertain Histories of Insular Lineages*, 693  
*Clarke, Andrew C.*, see Holland, Barbara R., 347  
*Clarke, Julia A., and Middleton, Kevin M., Mosaicism, Modules, and the Evolution of Birds: Results from a Bayesian Approach to the Study of Morphological Evolution Using Discrete Character Data*, 185  
*Clarke, Julia A.*, see Dayrat, Benoît, 503  
*Clarkia*, 517  
*Clarkii*, 549  
*Clathrochone clathroclada*, 396, 402  
*Clathrochone*, 391, 395, 398  
*Clathroclada*, 391  
 Cluster analysis, 519  
   data partitioning approach, 526  
   parameter estimation, 522, 523  
*Cluster set*, 338  
 Cluster Sets, 343  
 Clustering coefficient, 432  
   units of co-occurrence and, 437, 438  
   of a node, 438  
*CNGC5*, 471, 473  
*CNR1*, 500  
 Coalescence, 131  
 Coalescence, 466  
   hybridization versus the sorting of ancestral polymorphisms tested by, 477–479  
*Coccidioides immitis*, 615  
*Cochoa*, 259  
 Coding Meristic Characters for Phylogenetic Analysis: A Comparison of Step-Matrix Gap-Weighting and Generalized Frequency Coding, A. Michelle Lawing, Jesse M. Meik, and Walter E. Schargel, 167  
 Codivergence in Heteromyid Rodents (Rodentia: Heteromyidae) and Their Sucking Lice of the Genus *Fahrenholzia* (Phthiraptera: Anoplura), Jessica E. Light and Mark S. Hafner, 449  
*Codon Model Equivalent to Amino Acid Model*, 369  
 Codon model, 367  
   conventional, 371–373  
*Coerulea*, 467  
 Coevolution, 483  
 Cohesion species, 628  
   concept, 629  
   methodological framework to, 632  
   topology-based evaluation of, 639–641  
*COI*, 292, 564, 809, 810  
*COII*, 292  
*Colias eurytheme*, 233  
*Collar, David C.*, see Revell, Liam J., 591  
*Collembola*, 220  
*Collins, Allen G.*, see Dohrmann, Martin, 388  
 Colonization of oceanic islands, 732  
 Colonization of South America, 264  
*Colossendeis*, 923  
 Combinability, 469  
*Combination*, 400  
 Commensalism, 840  
 Comparative method, 591  
 Comparison of Methods for Species-Tree Inference in the Sawfly Genus *Neodiprion* (Hymenoptera: Diprionidae), Catherine R. Linnen and Brian D. Farrell, 876  
 Comparison of Species Tree Methods for Reconstructing the Phylogeny of Bearded Manakins (Aves: Pipridae, *Manacus*) from Multilocus Sequence Data, Robb T. Brumfield, Liang Liu, David E. Lum, and Scott V. Edwards, 719  
 Compatibility, 251, 253  
 Concatenated analysis, 104  
 Concatenation with monophyly constraints (CMC), 876  
*Conchopetalum*, 796  
*Concornis*, 192  
*Condylostylus*, 707  
*Confuciusornis*, 189, 197  
 Congruence, 420  
   analyses of support and, 422, 423  
   gene tree, 428  
 Consensus method, 939  
 Consensus trees, 244, 785, 794  
*Conservation probability*, 648  
 Consistent Estimation of Divergence Times in Phylogenetic Trees with Local Molecular Clocks, Bodil Sennblad, 947  
 Context effect, 675  
 Context-dependent evolution, 675  
*Conti, Elena*, see Mansion, Guilhem, 269  
*Converged*, 94, 95  
*Convolutulus*, 747  
*Copepoda*, 931  
*Cophocetus oregonensis*, 34  
*Cophocetus*, 23  
 Cophylogenetic methods, 449  
   advantages and disadvantages, 450  
   component of, 450  
   data based, 452  
*Cophylogeny*, 449  
 Cophylogeny, 449  
   documentation of significant, 457  
   test of, 456, 457  
*Coprosma propinqua*, 280  
*Coptolabrus*, 207, 214  
*CorrAll*, 763  
*CorrBest*, 763, 764  
*Coryphaenoides*, 537  
 Cosmopolitan frog radiation, 327  
 Cospeciation, 449  
   testing for codivergence and, 449, 450  
   as contemporaneous speciation events, 460  
*Cotesia*, 940  
*Covering property*, 245  
*CP*, 438, 439

- CpG effect, 675  
 Craig, Timothy P., *Evolutionary Ecology of Parasites*, second edition, 182  
 Crambe, 734, 747  
*Cranoglanis boudierius*, 118–120  
*Cranoglanis*, 116, 126, 127  
 Cranston, Karen A., *see* Sanderson, Michael J., 335  
*Crassula*, 43  
*Crateromorpha* (*Crateromorpha*), 391  
*Crateromorpha meyeri*, 398  
*Crateromorpha*, 395, 402, 404  
*Cratogeomys merriami*, 463  
*Cratogeomys perotensis*, 450  
 Craven, K. D., *see* Schardl, C. L., 483  
 CREM, 500  
*Cretotrigona prisca*, 60  
*Cretotrigona*, 62  
 Crisp, Michael D., *Ghosts of Gondwana: The History of Life in New Zealand*, 329  
*Crocodylus niloticus*, 173, 176–178  
*Crocodylus*, 178, 181  
*Crocynia gossypina*, 143–146  
*Crocynia*, 150–152  
*Crotalus horridus*, 172  
 Crown Clades in Vertebrate Nomenclature: Correcting the Definition of Crocodylia, Jeremy E. Martin and Michael J. Benton, 173  
 Crown groups, 841  
*Cryptococcus neoformans*, 615  
*Cryptococcus*, 156  
*Crypturellus*, 192  
*Crysoleucas*, 537  
 CSN2, 17–20, 34  
*Ctenolepisma lineata*, 922  
 CTinter, 434  
 CTintra, 434  
 CTLA3, 874  
 Cuzzo, María Gabriela, *see* Santos, Daniel A. Dos, 432  
 Cummings, Michael P., *see* Regier, Jerome C., 920  
 Cunningham, Clifford W., *see* Regier, Jerome C., 920  
*Curimata aspera*, 443  
*Curimata cerasina*, 443  
*Curimata cisandina*, 443  
*Curimata cyprinoides*, 443  
*Curimata incompta*, 443  
*Curimata inornata*, 443  
*Curimata knerii*, 443  
*Curimata macrops*, 443  
*Curimata ocellata*, 443  
*Curimata roseni*, 443  
*Curimata vittata*, 443  
*Curimata*, 448  
*Curimatella dorsalis*, 443  
*Curimatella lepidura*, 442, 443  
*Curimatella meyeri*, 443  
*Curimatella*, 448  
*Curimatopsis crypticus*, 443  
*Curimatopsis microlepis*, 443  
*Curimatopsis myersi*, 443  
*Cyanophora paradoxa*, 686  
*Cyclamen balearicum*, 280  
*Cyclamen*, 283, 285  
 Cycles, 381, 383  
*Cylindrophis*, 429  
*Cynomorium coccineum*, 39  
*Cynomorium*, 56  
*Cyphocharax aspilos*, 442  
*Cyphocharax gangamon*, 443  
*Cyphocharax gilbert*, 442, 443  
*Cyphocharax gillii*, 443  
*Cyphocharax gouldingi*, 443  
*Cyphocharax laticlavus*, 443  
*Cyphocharax leucostictus*, 443  
*Cyphocharax meniscaprorus*, 443  
*Cyphocharax mestomyllon*, 443  
*Cyphocharax microcephalus*, 443  
*Cyphocharax modestus*, 443  
*Cyphocharax nagelii*, 443  
*Cyphocharax nigripinnis*, 443  
*Cyphocharax notatus*, 443  
*Cyphocharax oenas*, 443  
*Cyphocharax pantostictus*, 443  
*Cyphocharax platanus*, 443  
*Cyphocharax plumbeus*, 443  
*Cyphocharax saladensis*, 443  
*Cyphocharax spilolus*, 443  
*Cyphocharax spiluroopsis*, 443  
*Cyphocharax stilbolepis*, 443  
*Cyphocharax vanderi*, 443  
*Cyphocharax vexillapinnus*, 443  
*Cyphocharax voga*, 443  
*Cypridopsis vidua*, 922  
*Cypridopsis*, 925, 927, 929  
 Cyrestis, 237  
*Cyrtandra richii*, 707  
*Cyrtandra*, 693–699, 701–707  
*Cyrtandra*, 693  
*D. dyeriana*, 796, 800, 804  
*D. heermanni*, 450, 465  
*D. melanogaster*, 935  
*D. merriami*, 465  
*D. microps*, 465  
*D. nelsoni*, 465  
*D. ordii*, 465  
*D. panamintinus*, 465  
*D. persimilis*, 308, 479, 480, 560, 730, 889  
*D. phillipsii*, 465  
*D. rerio*, 521  
*D. santomea*, 481  
*D. simulans*, 669  
*D. sinensis*, 796, 800, 804  
*D. spectabilis*, 465  
*Dactylurina*, 60  
*Dakosaurus andiniensis*, 176  
 Dalebout, Merel L., Steel, Debbie and Baker, C. Scott, *Phylogeny of the Beaked Whale Genus Mesoplodon (Ziphiidae: Cetacea) Revealed by Nuclear Introns: Implications for the Evolution of Male Tusks*, 857  
*Danio rerio*, 791  
*Danio*, 537  
*Daphnia*, 220  
 Data for Evolution (DRIADE), 1  
 Data partitioning, 388, 519, 920  
   rate variation, 393  
     28S, 393  
     dinosaur, 902  
 Dataset, 711  
 Dayrat, Benoît, Cantino, Philip D., Clarke, Julia A., and de Queiroz, Kevin, *Species Names in the PhyloCode: The Approach Adopted by the International Society for Phylogenetic Nomenclature*, 507  
 de Queiroz, Kevin, *see* Dayrat, Benoît, 503  
*Debaryomyces hansenii*, 615



- Decision theory (DT), 76, 77  
*Delphinapterus leucas*, 33  
 Delphinidae, 574  
*Delphinus delphis*, 576–578, 583, 588  
 Deméré, Thomas A., McGowen, Michael R., Berta, Annalisa and Gatesy, John, Morphological and Molecular Evidence for a Stepwise Evolutionary Transition from Teeth to Baleen in Mysticete Whales, 15  
*Dendrocrambe*, 747  
*Dendroscope*, 736  
*Denticrenatus*, 22  
*Depressaria*, 240  
*Deschampsia foliosa*, 746  
*Descurainia*, 267  
*Desmognathus fuscus conanti*, 172  
*Desmognathus fuscus fuscus*, 172  
 Developmental biology, 378  
   analysis of, 379, 380  
   evolution of, 380  
 Developmental sequences, 378  
*Deviacer wolfei*, 806  
 Dhingra, Amit, see Jian, Shuguang, 38  
 Diapsida, 179  
*Diaulula sandiegensis*, 513  
*Diaulula*, 513  
*Dicamptodon aterrimus*, 84, 560  
*Dicamptodon tenebrosus*, 561  
 Dinosaurs, 891  
   sample of, 899  
   avian, 892  
   nonavian, 899  
*Diorocetus hiatus*, 34  
*Diorocetus*, 23  
*Dioryctria*, 645  
*Diplocynodon muelleri*, 181  
*Diplocynodon ratelii*, 180  
*Diplocynodon*, 180  
*Dipodomys deserti*, 451  
*Dipodomys ordii*, 456  
*Dipodomys*, 449, 452–454, 456, 457, 459, 460, 465  
*Dipteronia dyerana*, 808  
*Dipteronia*, 795–808  
 Dirichlet process prior, 671  
*Discodoridae Diaulula sandiegensis*, 513  
*Discodoridae*, 511, 513, 514  
 Disconcordant trees, 540  
 Discordance of Species Trees with Their Most Likely Gene Trees: The Case of Five Taxa, Noah A. Rosenberg and Randa Tao, 131  
 Discrete gamma categories, 141  
 Dispersal models, 732  
   hypothesis testing of populations' IBD and, 742–744 and the PCT, 745  
   Bayesian approaches and, 746  
 Dispersal-extinction-cladogenesis (DEC), 6, 8, 11, 13  
*Dispersal-mediated allopatry*, 693  
 Dispersal-mediated allopatry, 693  
 Dispersal-vicariance analysis, 257  
 Dispersal, 4  
   explicit model of, 5  
   rates of, 6  
   between areas and rates of local extinction, 6, 7  
   estimated rates for, 7  
   history of the clade, 7  
   constraints, 11  
   unrealistic sequence of range evolution in, 13  
 DIVA, 269  
*Divergence of*, 729  
 Diversification rates, 905  
*Divisestylus*, 43, 52, 54, 55  
*DMP1*, 16–18, 21, 26, 27, 33, 34  
*Dmp1*, 33  
 DNA barcoding, 202, 216, 628  
*Dodonaea*, 796  
 Does Choice in Model Selection Affect Maximum Likelihood Analysis?, Jennifer Ripplinger and Jack Sullivan, 76  
 Dohrmann, Martin, Janussen, Dorte, Reitner, Joachim, Collins, Allen G., and Wörheide, Gert, Phylogeny and Evolution of Glass Sponges (Porifera, Hexactinellida), 388  
*Domínguez, Eduardo*, see Santos, Daniel A. Dos, 432  
*Doolittle, W. Ford*, see Beiko, Robert G., 844  
*Doridina*, 514  
 Dornburg, Alex, Santini, Francesco and Alfaro, Michael E., The Influence of Model Averaging on Clade Posteriors: An Example Using the Triggerfishes (Family Balistidae), 905  
*Dorosoma*, 537  
*Dorudon atrox*, 33  
*Dorudon*, 30  
 Dot maps, 432  
 Double-membrane, 835  
*Doyle, Jeff J.*, see Maureira-Butler, Iván J., 466  
*DQA*, 874  
*Dracophyllum*, 330  
*Dracunculus muscivorus*, 284  
*Dracunculus*, 271, 272, 276, 279, 280, 282  
*Dromiciops gliroides*, 315  
*Drosophila melanogaster*, 240, 674, 780, 921, 926, 932  
*Drosophila pseudoobscura*, 308, 479–482, 560, 730, 889  
*Drosophila simulans*, 155  
*Drosophila yakuba*, 481  
*Drosophila*, 241, 373, 374, 478, 481, 589, 626, 645, 669, 674, 731, 857, 921, 922, 932, 938  
*Drosophila/Homo*, 921  
*Dyeriana*, 796  
*Dysidea etheria*, 392  
*Dysidea*, 392, 396  
 Díaz-Pérez, Antonio, Sequeira, Miguel, Santos-Guerra, Arnoldo and Catalán, Pilar, Multiple Colonizations, In Situ Speciation, and Volcanism-Associated Stepping-Stone Dispersals Shaped the Phylogeography of the Macaronesian Red Fescues (*Festuca* L., Gramineae), 732  
*E. argentina*, 440, 441  
*E. australis*, 578  
*E. coli*, 214, 837  
*E. cryptomphala*, 440, 441  
*E. escoipensis*, 440, 441  
*E. glacialis*, 23  
*E. guevarai*, 440, 441  
*E. hemiclausa*, 440, 441  
*E. hieronymi*, 440, 441  
*E. jujuyensis*, 440, 441  
*E. parodizi*, 440, 441  
*E. puella*, 440, 441  
*E. puntana*, 440, 441  
*E. quirogai*, 440, 441  
*E. rhathymos*, 440, 441  
*E. saltana*, 440, 441  
*E. tomsici*, 440, 441  
*E. tranquelleonis*, 440, 441  
*E. trifasciata*, 440, 441  
*E. trigrammephora*, 440, 441  
*E. tucumanensis*, 440, 441  
*E. variegata*, 440, 441

- E. villavilensis*, 440, 441  
*E. walshi*, 440, 441  
*ear1*, 482  
*Echiniscus viridissimus*, 923  
*Echinopogon ovatus*, 485  
*Echium*, 734, 744, 747  
*Eco*, 351, 734  
 Ecological interchangeability, 628  
     second assessment of, 632  
     evaluation of, 641, 642  
*Ecology and Evolution of Flowers*, 516  
 Ecology and Evolution of Flowers, Jeff Ollerton, 516  
*Edeni*, 25  
*Edwards, Scott V.*, see Brumfield, Robb T., 719  
*EF-1 $\alpha$* , 920–923, 926, 931, 937  
*EF-2*, 920–923, 926, 931, 937  
 Efficiency of Markov Chain Monte Carlo Tree Proposals in Bayesian Phylogenetics, Clemens Lakner, Paul van der Mark, John P. Huelsenbeck, Bret Larget, and Fredrik Ronquist, 86  
 Efficient algorithm, 345  
*Effigia okeefeae*, 176  
*Eizirik, Eduardo*, see Springer, Mark S., 499  
 Ekman, Stefan, Andersen, Heidi L. and Wedin, Mats, The Limitations of Ancestral State Reconstruction and the Evolution of the Ascus in the Lecanorales (Lichenized Ascomycota), 141  
*Elaphe obsoleta*, 172  
*Elicodicerus muscivorus*, 280  
*Elongation factor-1 $\alpha$* , 878  
*Elops*, 537  
*Elymnias*, 240  
*Elymus canadensis*, 485  
*Eminium koenianum*, 283  
*Eminium*, 271, 272, 276, 279, 283, 284  
 ENAM, 15, 17, 18, 21, 23, 25–27, 32–34  
 Enamelin (ENAM), 15, 32  
*Endeis laevis*, 923  
 Endemism, 269  
     Hercynian, 270, 271  
     Mediterranean, 271  
     Corsican, 280  
     paleo-, 280  
 Endophytes, 483  
 Endosymbiotic gene transfer, 104  
*Eoalulavis*, 188  
 Eocene extinction, 116  
*Eocetus wardii*, 33  
*Eomysticetus whitmorei*, 23, 27, 30, 34  
*Eomysticetus*, 15  
*Eosuchus lerichei*, 181  
*Eosuchus minor*, 181  
*Epicephala*, 463  
*Epichloë amarillans*, 485  
*Epichloë baconii*, 485  
*Epichloë brachyelytri*, 485  
*Epichloë bromicola*, 485  
*Epichloë elymi*, 485  
*Epichloë festucae*, 485  
*Epichloë glyceriae*, 485  
*Epichloë sylvatica*, 485, 497  
*Epichloë typhina*, 485  
*Epichloë*, 485  
*Epicrates*, 32, 889  
*Epiperipatus biolleyi*, 939  
*Epiphragmophora*, 440, 441, 447  
 Equalrates Markov (ERM) model, 119, 161, 163, 165  
*Erebia*, 240  
*Eremita*, 263  
 Error rates, 347, 356  
 Error rates, 356  
*Eryx*, 429  
*Escherichia coli*, 826, 837  
*Eschrichtius robustus*, 23  
*Eschrichtius robustus*, 25, 26, 30, 33, 34  
*Eschrichtius*, 25, 29  
*Eshanosaurus*, 893, 901  
*Esox*, 537  
 Estimating Evolution of Temporal Sequence Changes: A Practical Approach to Inferring Ancestral Developmental Sequences and Sequence Heterochrony, Luke B. Harrison and Hans C. E. Larsson, 378  
*Eubalaena australis*, 33, 34  
*Eubalaena glacialis*, 23, 33, 34  
*Eubalaena japonica*, 33, 34, 576, 578, 583  
*Eubalaena*, 23, 29, 34, 583, 586, 588  
*Eublepharus turkmenicus*, 564, 566  
*Euchel:genes*, 930, 934, 936  
*Euchelicerata*, 931  
*Euglena*, 220  
*Eulemur*, 601  
*Eumesocampa fragilis*, 922  
*EuMyPan:genes*, 932, 934, 936  
*Euphorbia*, 748  
*Euphractus sexcinctus*, 317  
*Euplectella*, 389, 391, 395, 398, 402, 403  
*Euproctus*, 282  
*Eurycea*, 514  
*Eurypauropus spinosus*, 922  
*Eurytemora affinis*, 922  
*Euthyneura*, 514  
*Euxanthe*, 235  
 Event-pairs, 378  
     matrix, 378  
     tracing of, 379  
     cracking, 379  
     tree, 384  
 Evidence for a New Root of the Tree of Life, James A. Lake, Jacqueline A. Servin, Craig W. Herbold, and Ryan G. Skophammer, 835  
 Evolutionary developmental biology, 378  
*Evolutionary Ecology of Parasites*, 182  
*Evolutionary Ecology of Parasites*, second edition, Timothy P. Craig, 182  
 Evolutionary lability, 591  
*Evolutionary Pathways*, 184  
 Evolutionary simulation, 844  
 Evolution, 15  
     of nutrient foramina and baleen, 27  
     in Mysticeti, 21  
*Exiliboa*, 429  
 Exons, 231  
     finding and amplifying, 233, 234  
     assessing long, 235  
*Explicit ancestral range reconstruction*, 694  
 Extant phylogenetic bracket (EPB), 174  
 Extending subtree swapper (eSTS), 87, 91, 103  
 Extending tree bisection and reconnection (eTBR), 88, 91  
 Extinction, 4  
*F. agustinii*, 732–747  
*F. boleni*, 465  
*F. ehrlichi*, 465  
*F. fairchildi*, 450, 465  
*F. ferrisi*, 465

- F. francoi*, 732–740, 742–746  
*F. Francoi*, 738  
*F. hertigi*, 458, 465  
*F. jubata*, 732–742, 744, 745  
*F. microcephala*, 451, 465  
*F. occa*, 393, 394, 396  
*F. petraea*, 732–740, 742–747  
*F. pinnata*, 452, 465  
*F. reducta*, 452, 465  
*F. rivularis*, 732, 733, 744  
*F. rubra*, 733  
*F. texana*, 465  
*F. tribulosa*, 465  
*F. zacatecae*, 452, 465  
*Fagustinii*, 744  
Fabaceae, 466  
Fagales, 807  
*Fagonia*, 267, 917  
*Fahrenholzia*, 449, 451, 453–458, 460, 463, 465  
*Falcao*, 480  
*Farrea occa*, 390, 396, 404  
*Farrea*, 389, 391, 395  
*Farrell, Brian D.*, see Linnen, Catherine R., 876  
*Fellhanera bouteillei*, 143  
*Fellhanera subtilis*, 143  
*Female holotype*, 646  
*Female paratype*, 646  
*Fernández, Hugo R.*, see Santos, Daniel A. Dos, 432  
*Feroidobombus*, 62, 68–70, 72, 74  
*Festuca agustinii*, 733, 740  
*Festuca francoi*, 741  
*Festuca jubata*, 737, 739, 741  
*Festuca longifolia*, 485  
*Festuca petraea*, 741, 746  
*Festuca rubra*, 485  
*Festuca*, 732–738, 740–745, 747  
*Festuca* sect. *Aulaxyper*, 732  
*Ficus*, 463  
Filter-feeding, 15  
Filtered Z-Closure Supernetworks for Extracting and Visualizing  
  Recurrent Signal from Incongruent Gene Trees, James B.  
  Whitfield, Sydney A. Cameron, Daniel H. Huson, and Mike A.  
  Steel, 939  
Firmicutes, 835  
*Fischer, Mareike*, see Bandelt, Hans-Jürgen, 540  
*Flavipinnis*, 537  
*Forficula auricularia*, 922  
*Forficula*, 925, 927, 929  
Fossil calibration, 269  
Fossil record, 891  
  relationship between cladistic/stratigraphic congruence and the  
  completeness of, 899, 900  
*Fournier, E.*, see Aguilera, G., 613  
*Frutidella caesiaatra*, 143  
*Fugu*, 421  
Functional constraint, 591  
*Fundulus*, 537  
Fungi, 613  
FUNYBASE, 613  
*Fusarium graminearum*, 615  
*G. aculeatus*, 521  
*G3pdh*, 704  
*Gadus*, 537  
*Gallotia-Galloti*, 284  
*Gallus*, 421  
*Gambusia*, 537  
*Ganley, Austen R. D.*, see Regier, Jerome C., 920  
Gap excess ratio, 891  
GARLI program, 770  
*Gasterosteus*, 537  
Gastropoda, 514  
*Gatesy, John*, see Deméré, Thomas A., 15  
*Gatesy, John*, see McGowen, Michael R., 574  
*Gavialis gangeticus*, 173  
*Gavialis*, 178, 181  
GBSSI, 704  
*Geisler, Jonathan H.*, see Asher, Robert J., 311  
*Gekko gecko*, 421  
GenBank  
  data, 335  
  taxonomic diversity, 336  
  annotations, 336  
  tracking changes, 342  
  release 159, 342  
*Gendrault-Jacquemard, A.*, see Aguilera, G., 613  
Gene content tree, 844  
Gene Mapper, 358, 359  
Gene trees, 243, 249, 420, 719  
  congruence between, 723, 724  
  statistical consistency of ML species supertrees for, 246, 247  
  true, 247  
  estimation of, 294, 295  
  a posterior distribution of, 299  
  probability density function of, 299  
  topologies, 300  
  versus concatenated tree versus species trees, 304–306  
Gene-tree discordance, 876  
Gene-tree reconciliation, 574  
*General no-common-mechanisms*, 670  
Genetic distance, 219  
Genetic drift, 591  
  rate of phenotypic evolution by, 594  
  heterogeneous rate, 595, 597  
  constant-rate, 596  
  neutral, 600  
*Genista*, 279, 748  
Genome phylogeny, 844  
*Genome phylogeographic history*, 559  
*Genomes*, 855  
Genomic Outposts Serve the Phylogenomic Pioneers: Designing  
  Novel Nuclear Markers for Genomic DNA Extractions of  
  Lepidoptera, Niklas Wahlberg and Christopher West Wheat,  
  231  
*Gentiana*, 73  
*Geocarpa*, 475  
*Geodesic distance*, 436  
*Geomydoecus oregonus*, 464  
*Geomys breviceps*, 297  
Gesneriaceae, 693  
*Ghosts of Gondwana*, 329, 331  
*Ghosts of Gondwana: The History of Life in New Zealand*, Michael D.  
  Crisp, 329  
GHR, 500  
GI, 338  
*Giardia-Lamblia*, 840  
*Gilia*, 283  
Ginnala, 800  
*Giraud, T.*, see Aguilera, G., 613  
*Gitzendanner, Matthew A.*, see Jian, Shuguang, 38  
*Glesne*, 537  
*Glochidion*, 463  
*Glomerata*, 467

- Glyceria striata*, 485  
*Glycine*, 480  
*Glyphopeltis ligustica*, 143  
*Glyphorhynchus spirurus*, 729, 731  
*Glypta*, 940  
*Glyptapanteles*, 940  
*gncm*, 670, 671, 673  
*Gnetum*, 808  
*Gobipteryx*, 192  
*Gorilla*, 505  
*Grabau*, 188  
*Grande Coupure*, 69, 74  
*Grantiopsis*, 392  
*Grasses*, 483  
   clades of, 489  
   cool season, 484, 489, 495  
   endophyte-infected, 484  
 Greedy algorithm, 825  
   for MAD, 832  
 GREEDYMMMD, 827, 830, 831, 833  
   HisA, 836, 838  
*Greta*, 237  
*Grimm, Guido W.*, see Renner, Susanne S., 795  
*Growth heterochrony*, 378  
*Gryllus firmus*, 172  
*Gryposuchus*, 180  
 GR, 575, 579, 580  
 GS, 478  
*Gsx*, 708, 712, 714, 715  
 GTR, 206–211, 213  
*Gymmoderma*, 156  
*Gymnotus*, 172  
*Gyrodactylus*, 463  
*H. annuus*, 466  
*H. anomalus*, 466  
*H. carolinensis*, 391  
*H. deserticola*, 466  
*H. desmarestianus*, 465  
*H. irroratus*, 465  
*H. muscivorus*, 279, 280  
*H. mustelina*, 259  
*H. paradoxus*, 466  
*H. petiolaris*, 466  
*H. pictus*, 465  
*H. salvini*, 465  
*Haasiophis terrasanctus*, 322  
*Haasiophis*, 322  
*Haematomma ochroleucum*, 143  
*Hafner, Mark S.*, see Light, Jessica E., 449  
*Halecania alpivaga*, 143, 144  
*Halecania*, 153  
*Halictus*, 889  
*Hallopus victor*, 179  
*Handeliodendron bodinieri*, 796  
*Handeliodendron*, 796, 798  
*Hanseniella*, 922  
 Haplotype trees, 639  
*Harbansus paucichelatus*, 922  
*Hardman, Lotta M.*, see Hardman, Michael, 116  
 Hardman, Michael and Hardman, Lotta M., The Relative Importance of Body Size and Paleoclimatic Change as Explanatory Variables Influencing Lineage Diversification Rate: An Evolutionary Analysis of Bullhead Catfishes (Siluriformes: Ictaluridae), 116  
 Harmon, Luke J., Melville, Jane, Larson, Allan, and Losos, Jonathan B., The Role of Geography and Ecological Opportunity in the Diversification of Day Geckos (*Phelsuma*), 562  
*Harmon, Luke J.*, see Revell, Liam J., 591  
 Harrison, Luke B., and Larsson, Hans C. E., Estimating Evolution of Temporal Sequence Changes: A Practical Approach to Inferring Ancestral Developmental Sequences and Sequence Heterochrony, 378  
*Hassianycteris*, 502  
 Hastings ratio, 86  
 Hawai'i, 4  
 Heath, Tracy A., Zwickl, Derrick J., Kim, Junhyong and Hillis, David M., Taxon Sampling Affects Inferences of Macroevolutionary Processes from Phylogenetic Trees, 160  
*Heathcote, Julia F.*, see Wills, Matthew A., 891  
 Heating parameter, 393  
*Helianthus deserticola*, 480  
*Helianthus*, 466, 481  
*Helichrysum frigidum*, 280  
*Helichrysum*, 283  
*Helicodiceros muscivorus*, 269, 271, 272, 277, 279, 281–283  
*Helicodiceros*, 271, 272, 276, 279, 280, 282  
*Heliconius melpomene*, 232, 241  
*Heliconius*, 233, 235, 237, 308, 730  
*Helobdella robusta*, 711  
*Helobdella triserialis*, 711  
*Helocarpon crassipes*, 143  
*Helocarpon*, 142, 153  
*Hemidactyliini*, 514  
 Hemiplasy: A New Term in the Lexicon of Phylogenetics, John C. Avise and Terence J. Robinson, 503  
*Hendry, Tory A.*, see Jian, Shuguang, 38  
*Hepialus*, 240  
 Herbert, Dai, Phylogeny and Evolution of the Mollusca, 955  
*Herbold, Craig W.*, see Lake, James A., 835  
*Herpetocetus*, 31  
*Herteliana taylorii*, 143  
*Hesionidae*, 514  
*Hesperornis*, 185, 187  
*Heterochone calyx*, 389  
*Heterochone*, 389, 391, 395, 396, 402  
 Heterochrony, 378  
   on a single phylogeny, 379, 380  
   debt, 385  
*Heteromys pictus*, 451  
*Heteromys*, 449, 453, 454, 456, 457, 465  
*Heteropodarke*, 514  
*Heuchera*, 56  
 Heuristics, 759  
*Hexasters*, 400  
*Hexactinella carolinensis*, 389  
*Hexactinella*, 391, 395, 396, 398  
 Hexactinellida, 388  
   taxonomy of, 394  
   molecular phylogeny of, 396, 399  
   phylogeny of, 400–402  
*Hexagenia limbata*, 922  
*Hexapoda*, 931  
 Hierarchical clustering, 104  
 Hierarchical likelihood-ratio test (hLRT), 76, 84  
*Hillebrandia sandwicensis*, 327  
*Hillis, David M.*, see Heath, Tracy A., 160  
 Hines, Heather M., Historical Biogeography, Divergence Times, and Diversification Patterns of Bumble Bees (Hymenoptera: Apidae: *Bombus*), 58  
*Hiodon*, 538  
*Hirudo medicinalis*, 711  
 Historical Biogeography, Divergence Times, and Diversification Patterns of Bumble Bees (Hymenoptera: Apidae: *Bombus*), Heather M. Hines, 58

- Historical biogeography, 4, 116, 257, 432  
 Quantitative statistical inference in, 4  
 methodological links between character evolution and, 11, 12  
 constraints on range evolution, 12
- Historis*, 237
- HKY, 208, 212
- HLRT, 76–79
- Holarctic, 58
- Holcus mollis*, 485
- Holder, Mark T., Sukumaran, Jeet and Lewis, Paul O., A Justification for Reporting the Majority-Rule Consensus Tree in Bayesian Phylogenetics, 814
- Holland, Barbara R., Clarke, Andrew C., and Meudt, Heidi M., Optimizing Automated AFLP Scoring Parameters to Improve Phylogenetic Resolution, 347
- Holostei, 519
- Homeobox, 708
- Homo sapiens*, 20, 33, 469, 521, 574, 576, 583, 620, 780, 921, 926, 932
- Homo*, 174, 175, 341, 421, 505, 537, 922
- Homoplasy, 503
- Homoplasy, 251
- Hoover, Paul, *see* Stamatakis, Alexandros, 758
- Hoplodactylus maculatus*, 285
- Hordelymus europaeus*, 485
- Hordeum brevisubulatum*, 485
- Hordeum marinum*, 283, 644
- Host, 449  
 multi host parasite, 460  
 vertebrate, 460  
 switching, 462  
 parasite relationship, 462
- Hox1*, 708, 712, 714, 715
- Hox10*, 712
- Hox14*, 708
- Hox2*, 708, 712, 714, 715
- Hox3*, 708, 712, 714, 715
- Hox4*, 708, 712, 714, 715
- Hox5*, 712, 714, 715
- Hox6*, 714, 715
- Hox7*, 715
- Hox8*, 708, 714, 715
- Hox9*, 708, 712, 714, 715
- Hoya*, 482
- Huelsenbeck, John P., Ané, Cécile, Larget, Bret, and Ronquist, Fredrik, A Bayesian Perspective on a Non-parsimonious Parsimony Model, 406
- Huelsenbeck, John P., *see* Lakner, Clemens, 86
- Huelsenbeck, John P., *see* Munch, Kasper, 750
- Huson, Daniel H., *see* Whitfield, James B., 939
- Hussey, April, *see* Regier, Jerome C., 920
- Hutchinsoniella macracantha*, 922
- Hyalonema*, 389, 391, 395, 396, 401
- Hybridization, 466  
 versus the sorting of ancestral polymorphisms tested by coalescence simulation, 477–479
- Hybridization, 876
- Hydra circumcincta*, 392
- Hydra littoralis*, 392
- Hydra*, 392
- Hydrozoa, 392
- Hylaeochampsia vectiana*, 181
- Hyllota*, 267
- Hylocichla*, 259
- Hypanartia*, 235
- Hypericum balearicum*, 280
- Hypericum*, 282
- Hyperoodon planifrons*, 862
- Hyperoodon rostratus*, 30
- Hypochaeris*, 366
- Hypochilus thorelli*, 644
- Hypochilus*, 644
- Hypogymnia physodes*, 143
- Hypothesis tests, 76  
 ML hypothesis test, 79  
 model-averaged, 81  
 outcome of, 83
- Hypotheticus*, 511
- Hypotrigona*, 60
- Hypsipetes*, 573
- Högnabba 101*, 143
- I. australis*, 117
- I. balsanus*, 117, 119
- I. batatas*, 351
- I. dugesi*, 116, 117, 119
- I. furcatus*, 117, 119
- I. lupus*, 119, 121, 125
- I. meridionalis*, 116, 117, 119
- I. mexicanus*, 117, 119
- I. naevia*, 259
- I. ochoterenai*, 116, 119
- I. panicea*, 396, 402
- I. pricei*, 117, 119
- I. punctatus*, 119, 121, 125–127
- I. tiliacea*, 351, 355
- Iaceornis*, 188
- Iberomesornis*, 188
- Icaronycteris*, 502
- ICBN, 507–512
- Ichthyornis*, 185, 200, 514
- ICPN, 507
- Ictalurus furcatus*, 118, 121, 122, 126, 127
- Ictalurus lupus*, 118
- Ictalurus punctatus*, 117–119, 791
- Ictalurus rhaea*, 119
- Ictalurus*, 116, 117, 119, 121, 125, 126, 538
- ICZN, 507–513
- Immigration-mutation-death process, 772
- Importance sampling, 294
- In silico*, 365
- Incertae sedis*, 390, 391, 396, 402, 405
- Incomplete lineage sorting, 202, 294  
 of daughter species, 295  
 demographic scenarios of, 305
- Incomplete lineage sorting, 719
- Incongruence length difference (ILD) test, 104
- Incongruence, 466  
 test of, 472  
 various causes of, 474–477  
 among data sets, 479
- Incongruence, 613
- Indels, 835
- Independent contrasts, 129
- Indian Ocean, 562
- Indopacetus pacificus*, 873
- Indostomus paradoxus*, 315
- Inferring Species Membership Using DNA Sequences with Back-Propagation Neural Networks, A. B. Zhang, D. S. Sikes, C. Muster, and S. Q. Li, 202
- Inocybe*, 155
- Insecta*, 752–755
- Institutional abbreviations*:, 34
- Intercept*, 763, 767

- Intermediary species, 432  
 and betweenness measure, 436, 437  
 removal of, 438  
 clustering value of, 438
- Internal nodes*, 338
- International Code of Botanical Nomenclature*, 507
- International Code of Phylogenetic Nomenclature*, 507
- International Code of Zoological Nomenclature*, 507
- Interpenetrate*, 435
- Intertextae*, 474, 475, 481
- Introgression, 876
- Intron conservation, 772  
 inference based on, 779–781  
 phyla representatives used in, 780  
 parameter estimates for, 781
- Iphiteon panicea*, 394, 396, 399, 401
- Iphiteon*, 391, 395, 398, 401
- Ipomoea batatas*, 349, 350
- Ipomoea*, 351, 353–364
- IRBP, 501
- Isanacetes laticephalus*, 34
- Isanacetes*, 23
- Ischyrochampsia meridionalis*, 180
- Isisfordia duncani*, 177
- Isohypsibius elegans*, 923
- Ithomia*, 232, 242
- Ixoreus*, 259
- Janjucetus hunderi*, 17, 23, 34
- Janussen, Dorte*, see Dohrmann, Martin, 388
- Jian, Shuguang, Soltis, Pamela S., Gitzendanner, Matthew A., Moore, Michael J., Li, Ruiqi, Hendry, Tory A., Qiu, Yin-Long, Dhiragra, Amit, Bell, Charles D. and Soltis, Douglas E., Resolving an Ancient, Rapid Radiation in Saxifragales, 38
- Kalanchoe*, 42
- Kelneriapis*, 60
- Keratoperma allenbyense*, 284
- KH test, 450
- Kim, Junhyong and Sanderson, Michael J., Penalized Likelihood Phylogenetic Inference: Bridging the Parsimony-Likelihood Gap, 665
- Kim, Junhyong, see Heath, Tracy A., 160
- Kimura two-parameter (K2P) model, 77, 78, 81, 84
- King, Matthew G., see Clark, John R., 693
- Kishino, Hirohisa, see Seo, Tae-Kun, 367
- KITLG, 17–19, 34
- Kluyveromyces lactis*, 615
- Koeleria cristata*, 485
- Koelreuteria*, 796
- Kogia breviceps*, 33, 578
- Kogia sima*, 574, 583
- Kogia*, 23
- Krog & Timdal MAU61/08*, 143
- Kuczynski, Caitlin A., see Wiens, John J., 420
- L. atrosanguinea*, 149
- L. fuscoatra*, 149
- L. kurilensis*, 214
- L. silacea*, 142
- Labidesthes*, 537
- Lacantunia enigmatica*, 128
- Lachnum*, 156
- Lactuca*, 748
- Lake, James A., Servin, Jacqueline A., Herbold, Craig W. and Skophammer, Ryan G., Evidence for a New Root of the Tree of Life, 835
- Lakner, Clemens, van der Mark, Paul, Huelsenbeck, John P., Larget, Bret and Ronquist, Fredrik, Efficiency of Markov Chain Monte Carlo Tree Proposals in Bayesian Phylogenetics, 86
- LALBA*, 577, 579, 588
- Lama guanicoe*, 33
- Lamium purpureum*, 158
- Landscape, 544
- Lanfear, Robert and Bromham, Lindell, Statistical Tests between Competing Hypotheses of Hox Cluster Evolution, 708
- Lapparentophis defrennei*, 320
- Large data sets, 38
- Larget, Bret, see Huelsenbeck, John P., 406
- Larget, Bret, see Lakner, Clemens, 86
- Larson, Allan, see Harmon, Luke J., 562
- Larsson, Hans C. E., see Harrison, Luke B., 378
- Lateral gene transfer (LGT), 104, 113
- Lateral gene transfer, 104
- Lateral genetic transfer (LGT), 844, 845, 847, 848, 849, 852
- Lateral genetic transfer, 844
- Laudakia caucasia*, 572
- Lavatera*, 269, 748
- Lawing, A. Michelle, Meik, Jesse M. and Schargel, Walter E., Coding Meristic Characters for Phylogenetic Analysis: A Comparison of Step-Matrix Gap-Weighting and Generalized Frequency Coding, 167
- Lebrun, M.-H., see Aguilera, G., 613
- Lecania atrynoides*, 143
- Lecanora intumescens*, 143
- Lecanora*, 141, 143, 145, 146, 150–154, 156
- Lecanorales, 141
- Lecidea atrosanguinea*, 143
- Lecidea fuscoatra*, 142, 143
- Lecidea silacea*, 143
- Lecidea turgidula*, 143, 149
- Lecidea*, 149, 153, 154
- Lecidella meiococca*, 143
- Lecontei*, 876–878, 880, 886, 888
- Lecontei*, 885
- Lee, Christopher J., see Alekseyenko, Alexander V., 772
- Lehtonen, Samuli, Phylogeny Estimation and Alignment via POY versus Clustal + PAUP\*: A Response to Ogden and Rosenberg (2007), 653
- Leidyosuchus canadensis*, 181
- Leidyosuchus*, 181
- Leigh, Jessica W., Susko, Edward, Baumgartner, Manuela and Roger, Andrew J., Testing Congruence in Phylogenomic Analysis, 104
- Lemmon, Alan R., and Lemmon, Emily Moriarty, A Likelihood Framework for Estimating Phylogeographic History on a Continuous Landscape, 544
- Lemmon, Emily Moriarty, see Lemmon, Alan R., 544
- Leotia lubrica*, 156
- Lepas anserifera*, 922
- Lepidoptera, 231
- Lepidothrix coronata*, 730
- Lepidothrix coronta*, 729
- Lepisosteidae*, 531, 532
- Lepisosteus*, 116, 519, 520, 527, 532, 537
- Lepraria bergensis*, 143
- Lepraria lobificans*, 143
- Lepraria*, 150
- Leptocarabus*, 207, 210, 214, 215
- Leptopogon*, 267
- Leptospirae*, 474
- Lethe*, 240
- Leucascus*, 392
- Leuckarti*, 391
- Leucophanella*, 514
- Leucopsacus*, 391, 395
- Lewis, Paul O., see Holder, Mark T., 814

- Li, Chenhong, Lu, Guoqing, and Ortí, Guillermo, Optimal Data Partitioning and a Test Case for Ray-Finned Fishes (Actinopterygii) Based on Ten Nuclear Loci, 519
- Li, Guoliang, Steel, Mike, and Zhang, Louxin, More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States, 647
- Li, Ruiqi*, see Jian, Shuguang, 38
- Li, S. Q.*, see Zhang, A. B., 202
- Li, Wai Lok Sibon*, see Ross, Howard A., 216
- Libinia emarginata*, 922
- Libythea*, 237
- Libytheana*, 235
- Lichanura*, 429
- Lichens, 141
- Light, Jessica E., and Hafner, Mark S., Codivergence in Heteromyid Rodents (Rodentia: Heteromyidae) and Their Sucking Lice of the Genus *Fahrenholzia* (Phthiraptera: Anoplura), 449
- Likelihood function, 675
- Likelihood methods, 693
- Likelihood ratio testing, 104
- Likelihood-ratio test (LRT), 43, 76, 105, 367
- Liliopsida*, 752–755
- Limenavis*, 188
- Limnadia lenticularis*, 922
- Limulus polyphemus*, 922, 923
- Limulus*, 925, 927
- Lindstrom, A.*, see Schardl, C. L., 483
- Lineage sorting, 307
- Lineage sorting, 131, 466, 876
- Lineage-through-time (LTT), 58
- Lingula anatina*, 711
- Linnen, Catherine R. and Farrell, Brian D., Comparison of Methods for Species-Tree Inference in the Sawfly Genus *Neodiprion* (Hymenoptera: Diprionidae), 876
- Liomys*, 449, 454, 465
- Liotrigona*, 60
- Liotrionopsis*, 60
- Liotyphlops*, 428
- Liquidambar*, 43, 55, 56
- Lissodelphis borealis*, 33
- Lithobius forficatus*, 922
- Lithobius*, 925, 927
- Lithornis*, 192
- Liu, Liang*, see Belfiore, Natalia M., 294
- Liu, Liang*, see Brumfield, Robb T., 719
- Llanocetus denticrenatus*, 30
- Llanocetus*, 22, 31
- Lobodon carcinophagus*, 15
- Lolium arundinaceum*, 485
- Lolium edwardii*, 485
- Lolium multiflorum*, 485
- Lolium perenne*, 485
- Lolium*, 485
- Long branch attraction, 38
- Lopadium disciforme*, 143
- Lopadium*, 153
- Lophius*, 538
- Lophocalyx*, 391, 395, 398, 402
- Losos, Jonathan B.*, see Harmon, Luke J., 562
- Lotus*, 748
- Low copy nuclear genes, 466
- Loxocemus*, 429
- Loxothylacus texanus*, 922
- LR1+nt3*, 929
- LR1*, 923, 925–929, 935, 937, 938
- Lu, Guoqing*, see Li, Chenhong, 519
- Lucius*, 537
- Lum, David E.*, see Brumfield, Robb T., 719
- Lupularia*, 474
- Lutjanus*, 533, 538
- Lycodes*, 533, 538
- Lycopersicon*, 365
- Lygodactylus*, 564, 566
- Lynceus*, 922
- Lysichiton*, 283
- M. rhodopea*, 473
- M. arabica*, 467, 473
- M. arborea*, 467, 468, 475
- M. astroides*, 468
- M. aurantiacus*, 719–723, 725, 728
- M. auranticaus*, 727
- M. bahamondi*, 874
- M. bidens*, 864, 865
- M. biflora*, 468, 482
- M. blancheana*, 467
- M. bowdoini*, 864, 871
- M. brachycarpa*, 468
- M. cancellata*, 481
- M. candei*, 719–723, 725, 727–729
- M. carlhubbisi*, 864, 865, 871
- M. carstiensis*, 467
- M. ciliaris*, 467, 473
- M. constricta*, 467
- M. coronata*, 467, 479
- M. crassipes*, 468
- M. cretacea*, 468, 475
- M. densirostris*, 861, 864–866, 871
- M. disciformis*, 467, 479
- M. doliata*, 467
- M. edgeworthii*, 466, 467
- M. europaeus*, 32, 864, 865
- M. europeus*, 871
- M. falcata*, 480
- M. fischeriana*, 468
- M. ginkgodens*, 864, 865, 868
- M. granadensis*, 467, 473
- M. grayi*, 864, 865
- M. hectori*, 864, 865, 871, 872
- M. heymaniana*, 467, 479, 482
- M. huberi*, 468, 482
- M. hybrida*, 480, 481
- M. intertexta*, 467, 473
- M. italica*, 467, 482
- M. laciniata*, 467
- M. lanigera*, 467, 482
- M. laxispira*, 467, 482
- M. layardii*, 859, 864, 868, 871
- M. lesinsii*, 467, 475, 482
- M. littoralis*, 467, 481
- M. lupulina*, 467, 474, 479, 482
- M. manacus*, 719–723, 725, 727–729
- M. marina*, 467, 473
- M. micrococca*, 149
- M. minima*, 467, 479
- M. mirus*, 32, 864, 865, 871
- M. monspeliaca*, 468
- M. murex*, 467
- M. muricolepsis*, 467, 473
- M. noeana*, 467
- M. novaeangliae*, 25
- M. orbicularis*, 467, 482
- M. perrini*, 864, 865, 870–872

- M. peruvianus*, 859, 864, 865, 870, 872  
*M. phrygia*, 468  
*M. pironae*, 467  
*M. platicarpa*, 482  
*M. platycarpa*, 466, 467, 473, 481  
*M. plicata*, 467, 482  
*M. polymorpha*, 467  
*M. popovii*, 467, 473  
*M. praecox*, 467, 479  
*M. prasina*, 149  
*M. prostrata*, 467  
*M. radiata*, 467, 482  
*M. ralloides*, 259  
*M. rhodopea*, 467, 481  
*M. rigidula*, 467, 481  
*M. rotata*, 467, 482  
*M. ruthenica*, 467, 473  
*M. sativa*, 466–471, 473, 478–481  
*M. sauvagei*, 467  
*M. secundiflora*, 467, 482  
*M. shepardii*, 467, 482  
*M. soleirolii*, 467, 482  
*M. stejnegeri*, 864, 865, 871  
*M. suavei*, 482  
*M. suffruticosa*, 467, 480, 481  
*M. tenoreana*, 467, 474, 479, 482  
*M. tornata*, 481  
*M. traversii*, 859, 860, 871  
*M. truncatula*, 466, 467, 469, 471–473, 479, 481, 482  
*M. turbinata*, 467  
*M. v. milleri*, 728  
*M. vitellinus*, 719–722, 725, 727–729  
*M. vitellinus/M. manacus*, 727  
M13(–21), 922  
M13, 922  
M13REV, 922  
*Mabuya*, 572  
Macaronesia, 732  
*Machiloides banksi*, 922  
*Macrantha*, 806  
*Macrobiotus islandicus*, 923  
Macroevolution, 905  
*Macrolepidotus*, 538  
*Macrothele calpeiana*, 643  
*Maculata/clarkii*, 552  
*Maf\_order*, 681  
*Magnaporthe grisea*, 615  
*Mahogoni*, 538  
*Malacosaccus coatsi*, 398  
*Malacosaccus*, 391, 395, 398, 402  
*Malacostraca*, 931  
*Male holotype*, 646  
*Male paratype*, 646  
*Mammalodon colliveri*, 17, 23, 34  
*Manacus manacus*, 720  
*Manacus*, 719–721, 723–725, 727–730  
*Manakin*, 719  
Mandibulata, 920  
*manE*, 723  
Mansion, Guilhem, Rosenbaum, Gideon, Schoenenberger, Nicola, Bacchetta, Gianluigi, Rosselló, Josep A., and Conti, Elena, Phylogenetic Analysis Informed by Geological History Supports Multiple, Sequential Invasions of the Mediterranean Basin by the Angiosperm Family Araceae, 269  
*manW*, 723  
*Maoricicada*, 480, 730  
Markov chain Monte Carlo, 86, 406, 675  
*Marpesia*, 235  
*Marthey, S.*, see Aguilera, G., 613  
Martin, Jeremy E. and Benton, Michael J., Crown Clades in Vertebrate Nomenclature: Correcting the Definition of Crocodylia, 173  
*Martin, Joel W.*, see Regier, Jerome C., 920  
*Martini*, 188  
*mask1*, 923  
*mask2*, 923, 926  
*Mastigoproctus giganteus*, 923  
*Mastigoproctus*, 925, 927  
*mat*, 272, 274, 276, 283, 807  
*matK*, 41, 43, 55, 470  
*matR*, 39, 41, 43  
*Matthiola bolleana*, 749  
*Mauicetus*, 15  
Maureira-Butler, Iván J., Pfeil, Bernard E., Muangprom, Amorntip, Osborn, Thomas C., and Doyle, Jeff J., The Reticulate History of *Medicago* (Fabaceae), 466  
Maximum likelihood (ML) estimate, 249  
Maximum likelihood (ML), 797  
Maximum Likelihood Inference of Geographic Range Evolution by Dispersal, Local Extinction, and Cladogenesis, Richard H. Ree and Stephen A. Smith, 4  
Maximum Likelihood Supertrees, Mike Steel and Allen Rodrigo, 243  
Maximum likelihood, 76, 104, 243, 406, 544, 708, 758  
  approach to supertree, 247  
  framework, 246  
  statistical consistency, 248  
  of the no-common-mechanism model, 415  
  use of, 408  
  estimation of ?, 547  
  compared with other data, 551  
Maximum parsimony, 251  
  tree, 253  
  score, 253  
*Mayoa*, 274  
McGowen, Michael R., Clark, Clay, and Gatesy, John, The Vestigial Olfactory Receptor Subgenome of Odontocete Whales: Phylogenetic Congruence between Gene-Tree Reconciliation and Supermatrix Methods, 574  
*McGowen, Michael R.*, see Deméré, Thomas A., 15  
MCMC approaches, 86, 118  
MCMC model, 409  
*Meade, Andrew*, see Venditti, Chris, 286  
Median tree, 785  
*Medicago hypogaea*, 475  
*Medicago lupulina*, 479  
*Medicago rigiduloides*, 481  
*Medicago ruthenica*, 481  
*Medicago sativa*, 480, 481  
*Medicago saxatilis*, 481  
*Medicago sinkiae*, 481  
*Medicago syriaca*, 481  
*Medicago truncatula*, 469, 480  
*Medicago*, 466–471, 473–482  
*Medicago*, 466  
Mediterranean Basin, 269  
*Megachile rotundata*, 479  
*Megalaria grossa*, 143  
*Megalaria*, 153  
*Megaptera hubachi*, 34  
*Megaptera longimana*, 33  
*Megaptera mioaena*, 34  
*Megaptera novaeangliae*, 23, 25, 33, 34, 872  
*Megaptera*, 25, 32



- Megascapheus*, 295–298, 300, 302, 305–307  
 Meier, Rudolf, Zhang, Guanyang and Ali, Farhan, The Use of Mean Instead of Smallest Interspecific Distances Exaggerates the Size of the “Barcoding Gap” and Leads to Misidentification, 809  
 Meik, Jesse M., *see* Lawing, A. Michelle, 167  
*Melanitis*, 237  
*Melanobombus*, 68  
*Melanoplus*, 365, 730, 889  
*Melanopus*, 506  
*Melanosaurus*, 904  
*Melichthys niger*, 906, 907, 916  
*Melichthys vidua*, 907  
*Melichthys*, 906, 910, 912, 916  
*Melilotus*, 466  
*Melipona grandis*, 60  
*Meliponula bocandei*, 60  
*Melitaea cinxia*, 232, 233  
*Melitaea*, 237  
 Melville, Jane, *see* Harmon, Luke J., 562  
*Mendacibombus*, 59, 69, 71  
*Menidia*, 172  
 Meredith, Robert W., *see* Springer, Mark S., 499  
*Merlia normani*, 405  
*Mertensiella luschani*, 573  
*Mesocetus argillarius*, 32  
*Mesocyclops edax*, 922  
*Mesocyclops*, 925, 927, 929, 935, 936  
*Mesoplodon bahamondi*, 874  
*Mesoplodon bidens*, 33, 34  
*Mesoplodon bowdoini*, 872, 873  
*Mesoplodon carlhubbsi*, 873  
*Mesoplodon densirostris*, 30, 873  
*Mesoplodon gervaisi*, 873  
*Mesoplodon grayi*, 30, 858  
*Mesoplodon hectori*, 873  
*Mesoplodon layardii*, 874  
*Mesoplodon mirus*, 873  
*Mesoplodon perrini*, 873  
*Mesoplodon peruvianus*, 33, 34  
*Mesoplodon traversii*, 874  
*Mesoplodon*, 22, 31, 32, 857–860, 862–868, 870–874  
*Metajapyx subterraneus*, 922  
 Metazoan phylogeny, 388  
*Methanopyrus kandleri*, 855  
*Methona*, 235  
 Meudt, Heidi M., *see* Holland, Barbara R., 347  
*Micarea alabastrites*, 143  
*Micarea erratica*, 143, 146  
*Micarea intrusa*, 146  
*Micarea micrococca*, 143, 146  
*Micarea sylvicola*, 143, 146, 149  
*Micarea*, 143, 145, 146, 149–153  
*Microdipodops*, 449  
*Micromysticetus rothauseni*, 32  
*Micromysticetus*, 15  
*Microplitis*, 940  
*Microraptor zhauianus*, 200  
 Middleton, Kevin M., *see* Clarke, Julia A., 185  
*Migratorius*, 263, 264  
*Milnesium tardigradum*, 923  
*Mimulus*, 696, 705  
 Minimize deep coalescences (MDC), 876, 877, 879, 880  
*Minimum extension*, 256  
*Minuta*, 391  
*Miriquidica garovaglii*, 143  
*Mitsukurii*, 391, 398  
*Mitsukurii/R. nodastrella*, 398  
*Mixocetus elysius*, 34  
*Mixocetus*, 23  
 Mixture models, 286  
 ML bootstrap pseudoreplicates (MLBPs), 121  
 Model averaging, 905  
 Model comparison, 367, 388  
     of codon and amino acid model, 368  
     61-dimensional SK-P0 and amino acid model, 369  
     of paired-sites models, 393, 394  
     of single-gene analyses, 394  
     Tree topologies and PPs, 394  
 Model of Diversity, 828, 829  
*Model organism*, 338  
 Model selection, 76, 665  
     standard, 83  
     relationship between model-fit and, 84  
 Molecular clock, 905  
 Molecular dating, 58, 269  
 Molecular evolution, 286  
 Molecular phylogeny, 562  
 Molecular rates, 449  
*Molissima*, 695  
*Mollissima*, 695  
*Mollusca*, 514  
*Monanthes*, 744  
*Monodelphis breviceaudata*, 317  
*Monodelphis domestica*, 521  
*Monodelphis*, 537  
*Monopterus*, 538  
*Monosiga brevicollis*, 390, 392  
*Montastraea franksi*, 392  
*Monticola*, 261  
 Moore, Michael J., *see* Jian, Shuguang, 38  
*Morawanocetus*, 22  
 More Taxa Are Not Necessarily Better for the Reconstruction of Ancestral Character States, Guoliang Li, Mike Steel, and Louxin Zhang, 647  
 Moritz, Craig, *see* Belfiore, Natalia M., 294  
*Morone*, 533, 538  
 Morphological and Molecular Evidence for a Stepwise Evolutionary Transition from Teeth to Baleen in Mysticete Whales, Thomas A. Deméré, Michael R. McGowen, Annalisa Berta, and John Gatesy, 15  
 Morphology and Placental Mammal Phylogeny, Mark S. Springer, Robert W. Meredith, Eduardo Eizirik, Emma Teeling, and William J. Murphy, 499  
 Morphology, Paleontology, and Placental Mammal Phylogeny, Robert J. Asher, Jonathan H. Geisler, and Marcelo R. Sánchez-Villagra, 311  
 Morphometrics, 316  
 Morrison, David A., *Phylogenetic Trees Made Easy: A How-to Manual*, third edition, 658  
 Morrison, David A., *The Cambridge Companion to the Philosophy of Biology*, 822  
*Mos*, 320, 322  
*Mosaic evolution*, 185  
 Mosaicism, Modules, and the Evolution of Birds: Results from a Bayesian Approach to the Study of Morphological Evolution Using Discrete Character Data, Julia A. Clarke and Kevin M. Middleton, 185  
*Motacilla*, 268  
*MPeLT*, 815  
 MRCA, 498  
*Mse*, 351, 734  
*MT-CO2*, 577–579

- MT-CYB, 577–579, 586  
 MtDNA, 38  
*Muangprom*, *Amorntip*, see Maureira-Butler, Iván J., 466  
*Mugil*, 538  
*Mulcahy*, Daniel G., see Wiens, John J., 420  
*Multibarbata*, 538  
*Multidivtime*, 798, 800  
*Multidivtime*, 798  
 Multigene phylogenies, 613  
 Multilocus Phylogenetics of a Rapid Radiation in the Genus  
     *Thomomys* (Rodentia: Geomyidae), Natalia M. Belfiore, Liang  
     Liu, and Craig Moritz, 294  
 Multilocus phylogeny, 294  
 Multiple Colonizations, In Situ Speciation, and Volcanism-Associated  
     Stepping-Stone Dispersals Shaped the Phylogeography of the  
     Macaronesian Red Fescues (*Festuca* L., Gramineae), Antonio  
     Díaz-Pérez, Miguel Sequeira, Arnoldo Santos-Guerra, and  
     Pilar Catalán, 732  
 Munch, Kasper, Boomsma, Wouter, Huelsenbeck, John P., Willerslev,  
     Eske and Nielsen, Rasmus, Statistical Assignment of DNA  
     Sequences Using Bayesian Phylogenetics, 750  
*Murex*, 475  
*Murphy*, William J., see Springer, Mark S., 499  
*Murugan*, Sumathi, see Ross, Howard A., 216  
*Mus musculus*, 20, 33, 469, 521, 574, 711  
*Mus*, 537  
*Muscivorus*, 279  
*Musculus*, 537  
*Museum abbreviations*, 260  
*Muster*, C., see Zhang, A. B., 202  
*Myadestes*, 259  
*Mycale fibrexilis*, 392, 396  
*Mycoblastus sanguinarius*, 143  
 Mygalomorphae, 628  
*Mykiss*, 538  
*Myophonous*, 261  
*Myosotis*, 285  
*Myria:genes*, 930, 934, 936  
*Myriapoda*, 931  
*Myriapoda*, 920  
     nonavian, 900  
*Myriophyllum*, 42  
*Myripristis*, 537  
*Mystacina*, 329  
*Mysticetes*, 574  
*Mysticeti*, 15  
*N. abbotii*, 883, 886, 888  
*N. autumnalis*, 878, 879  
*N. baileyi*, 119  
*N. compar*, 883, 888  
*N. crypticus*, 117  
*N. cubensis*, 878  
*N. dubiosus*, 889  
*N. elegans*, 119  
*N. eremita*, 259  
*N. exilis*, 125  
*N. fasciatus*, 119  
*N. gladiator*, 117, 119  
*N. gyrinus*, 127  
*N. hildebrandi*, 119  
*N. insignis*, 127  
*N. insularis*, 878  
*N. maurus*, 886  
*N. merkei maestrensis*, 878  
*N. merkei*, 888  
*N. miurus*, 127  
*N. nigroscutum*, 883, 886, 888  
*N. pratti*, 886  
*N. stanauli*, 117, 119  
*N. stigmosus*, 119, 127  
*N. taedae taedae*, 878  
*N. taedae*, 883  
*nad5*, 41, 43  
*Naegleria gruberi*, 108  
*Naegleria*, 109  
*Nananthea perpusilla*, 280  
*Nananthea*, 281  
*Narceus americanus*, 922  
*Narceus*, 925, 927  
*Narcissus*, 517  
*Naso*, 918  
 National Evolutionary Synthesis Center (NESCent), 1  
*Natural History*, 184  
*Nature*, 179  
*Naufraga balearica*, 283  
*Naufraga*, 280  
*ND2*, 564, 566  
*ndhB*, 41  
*ndhF*, 41, 55  
 NDNA, 466  
 Nearest-neighbor influences, 675  
*Nebalia hessleri*, 922  
*Nebalia*, 925, 927, 929, 935, 936  
*Nectarinia*, 573  
*Negundo*, 806  
*Nematostella vectensis*, 708  
*Neobulgaria pura*, 156  
*Neochlamisus*, 889  
*Neodiprion abietis*, 889  
*Neodiprion fulviceps*, 890  
*Neodiprion nigroscutum*, 889  
*Neodiprion pratti*, 889, 890  
*Neodiprion rugifrons*, 889  
*Neodiprion virginianus*, 889  
*Neodiprion*, 876–878, 880, 881, 885–890  
*Neogonodactylus oerstedii*, 922  
*Neopsacas*, 404  
*Neoscopelus*, 538  
*Neotoma fuscipes*, 645  
*Neotyphodium aotearoae*, 485  
*Neotyphodium coenophialum*, 485  
*Neotyphodium gansuense*, 485  
*Neotyphodium lolii*, 485  
*Neotyphodium occultans*, 485  
*Neotyphodium typhinum*, 485  
*Neotyphodium*, 485  
*Nepeta cataria*, 158  
*Nereis virens*, 711  
*Nesocichla*, 258, 259, 263  
*Neuquenornis*, 192  
 Neural networks, 202  
     memory of, 203  
     output of, 203  
     definition of, 203  
*Neurospora crassa*, 613, 615  
*New Systematics*, 661  
 Niche conservatism, 591  
 Niche-based distribution modeling, 628  
*Nicoletia meinerti*, 922  
*Nielsen*, Rasmus, see Munch, Kasper, 750  
*Nipponopsalis abei*, 923  
*Nitophyllites zaisanicus*, 276

- Nodastrella*, 391  
*Node clusters*, 338  
*Node-density effect*, 286  
   magnitude of the reduction in, 289  
   degree of, 287  
*Noguerornis*, 188  
*noLR1+nt2*, 923, 925–929, 931, 933, 935–938  
*noLR1*, 923, 926, 927  
*noLR1nt2*, 926  
*Noninformative ternary characters*, 540  
*Nonparametric bootstrap*, 76  
*Normania*, 747  
*Norops auratus*, 513  
*Norops*, 513  
*North American ichthyofauna*, 116  
*Notemigonus*, 537  
*Nothofagus*, 330, 331  
*Notocetus vanbenedeni*, 32  
*Noturus albater*, 118  
*Noturus baileyi*, 118  
*Noturus crypticus*, 119, 129  
*Noturus elegans*, 118  
*Noturus eleutherus*, 118, 127  
*Noturus exilis*, 118, 125  
*Noturus fasciatus*, 118  
*Noturus flavater*, 118  
*Noturus flavipinnis*, 118  
*Noturus flavus*, 118, 127  
*Noturus funebris*, 118  
*Noturus furiosus*, 118  
*Noturus gilberti*, 118  
*Noturus gladiator*, 129  
*Noturus gyrimus*, 118  
*Noturus hildebrandi*, 118  
*Noturus insignis*, 118  
*Noturus lachneri*, 118  
*Noturus leptacanthus*, 118  
*Noturus maydeni*, 116, 118  
*Noturus miurus*, 118  
*Noturus munitus*, 118  
*Noturus nocturnus*, 118  
*Noturus phaeus*, 118  
*Noturus placidus*, 118  
*Noturus stanauli*, 129  
*Noturus stigmatosus*, 118  
*Noturus taylori*, 118  
*Noturus*, 116–119, 121, 125–129  
*Novaeangliae*, 25  
*NRinter*, 434  
*NRintra*, 434  
*nt1*, 923, 937  
*nt12 and nt3*, 925  
*nt12*, 923, 925, 927, 928, 930, 931, 935, 937, 938  
*nt123*, 923, 925–929, 935  
*nt123-*, 929  
*nt2*, 923, 925–927  
*nt3*, 923, 926–929, 935, 937  
*ntLR1+nt2*, 928  
*Nuclear genes*, 920  
*Nuclear introns*, 857  
   amplification of, 860, 862t  
   analysis of, 871  
   nuclear, 860  
   observed level of, 894  
*Nuclear loci*, 519  
*Nuclear ribosomal DNA*, 38  
*Nuclear ribosomal RNA gene (nrLSU)*, 142, 144, 145, 147  
*Nucleotide composition*, 927  
*Nudibranchia*, 514  
*Nye, Tom M. W.*, *Trees of Trees: An Approach to Comparing Multiple Alternative Phylogenies*, 785  
*Nylander, Johan A. A., Olsson, Urban, Alström, Per, and Sanmartín, Isabel*, *Accounting for Phylogenetic Uncertainty in Biogeography: A Bayesian Approach to Dispersal-Vicariance Analysis of the Thrushes (Aves: Turdus)*, 257  
*Nymphalidae*, 231  
*Nymphalis*, 242  
*O. glandulosa*, 366  
*O. latipes*, 521  
*O. macrophylla*, 366  
*O. modesta*, 366  
*O. moesta*, 259  
*O. oenanthe*, 259  
*O. pleschanka*, 259  
*O. simpsonii*, 366  
*OCP*, 439, 441, 448  
*Odontocetes*, 574  
   database for, 575  
   degradation of olfaction in, 580  
*Odontotrizona haematoptera*, 60  
*Odonus niger*, 907  
*Odonus*, 906, 910, 912, 916  
*Oenanthe*, 259, 261  
*Olea europaea*, 746, 748  
*Olfactory receptors*, 574  
*Oligobalistes robustus*, 909  
*Oligobalistes*, 906  
*Ollerton, Jeff*, *Ecology and Evolution of Flowers*, 516  
*Olmstead, Richard G.*, see *Cantino, Philip D.*, 157  
*Olsson, Urban*, see *Nylander, Johan A. A.*, 257  
*Ombrophila violacea*, 156  
*On Evolution*, Danny Yee, 184  
*On Growth and Form*, 185  
*On the Distributions of Bootstrap Support and Posterior Distributions for a Star Tree*, Edward Susko, 602  
*Oncorhynchus mykiss*, 791  
*Oncorhynchus*, 538  
*One-interval data set*, 288  
*Onthophagus*, 873  
*Oopsacas minuta*, 390, 404  
*Oopsacas*, 391, 395  
*Oopsacas/Leucopsacus*, 396  
*Optimal Data Partitioning and a Test Case for Ray-Finned Fishes (Actinopterygii) Based on Ten Nuclear Loci*, Chenhong Li, Guoqing Lu, and Guillermo Ortí, 519  
*Optimizing Automated AFLP Scoring Parameters to Improve Phylogenetic Resolution*, Barbara R. Holland, Andrew C. Clarke, and Heidi M. Meudt, 347  
*OR10A1*, 579  
*OR10AB1*, 579, 583, 584  
*OR10AB2*, 584  
*OR10J1*, 579, 583, 588  
*OR10J2*, 579, 583  
*OR10K1*, 579  
*OR10K3*, 579  
*OR13F1*, 579, 583  
*OR13J1*, 579, 580, 583, 586  
*OR13J1B*, 579  
*OR11I*, 579, 580, 583, 584, 588  
*OR2AT1*, 579  
*OR6M1*, 579, 583, 584

- Orchesella imitari*, 922  
*Orcinus orca*, 576–578, 583, 588  
*Oreochromis*, 533, 538  
*Origin and Evolutionary Radiation of the Mollusca*, 955  
 Origin of life, 840  
*Ornithorhynchus*, 175  
*Orontium*, 283  
*Orthogeomys grandis*, 450  
*Orthogeomys heterodus*, 297  
 Orthology, 503  
 Ortí, Guillermo, *see* Li, Chenhong, 519  
*Orycteropus afer*, 316  
*Oryza sativa*, 338  
*Oryzias*, 533, 537  
 Osborn, Thomas C., *see* Maureira-Butler, Iván J., 466  
*Oscarella tuberculata*, 392  
*Osteoglossum*, 538  
*Ourisia crosbyi*, 366  
*Ourisia*, 350, 351, 353–366  
*Overall directionality test*, 552  
*Ovis dalli*, 33  
*Ovophis okinavensis*, 431  
 p-Median, 832, 833  
*P. borbonica borbonica*, 564  
*P. borbonica mater*, 564  
*P. borbonica*, 566  
*P. brachyphona*, 549  
*P. brimleyi*, 549  
*P. cepediana* A, 564  
*P. comorensis*, 566, 568  
*P. comoroensis*, 571  
*P. crassidens*, 588  
*P. edwardnewtonii*, 571  
*P. feriarum*, 549, 551, 552, 554–556  
*P. flavipes polionota*, 259  
*P. flavus*, 465  
*P. fouquettei*, 549  
*P. fuscus*, 909  
*P. g. rosagularis*, 563  
*P. gigas*, 571  
*P. guimbeau guimbeau*, 563  
*P. hathewayi*, 11  
*P. hawaiiensis*, 8  
*P. kaduana*, 8, 9, 11  
*P. kalmi*, 549  
*P. leucops*, 259  
*P. litsipsirupa*, 259  
*P. longimembris*, 465  
*P. m. kochi*, 563  
*P. maculata*, 549, 551, 556  
*P. maculata/clarkii*, 549, 551  
*P. madagascarensis grandis*, 563  
*P. mariniana*, 8  
*P. mauiensis*, 8  
*P. merriami*, 465  
*P. nigrita*, 549  
*P. o. inexpectata*, 564  
*P. olivaris*, 125, 127  
*P. ornata ornata*, 564  
*P. parkeri*, 564  
*P. pasteurii*, 568  
*P. sundbergi longinsulae*, 564  
*P. sundbergi sundbergi*, 564  
*P. triseriata*, 549, 556  
*P. v-nigra anjouanensis*, 564  
*P. v-nigra comoraegrandensis*, 564  
*P. v-nigra v-nigra*, 564  
*Pachycladae*, 748  
*Pachydactylus*, 564, 566  
*Pachyspirae*, 474, 475  
*Pacificus*, 538  
*Paeonia*, 39, 42, 46, 53, 284  
 Page, Roderic D. M. and Sullivan, Jack, *The Expanding Contributions of Systematic Biology*, 1  
 Pagel, Mark, *see* Venditti, Chris, 286  
*Palaeochiropteryx*, 502  
 Paleomap, 269  
*Pallimnarchus*, 180  
*Palmata*, 796, 800, 804, 806  
*Pan*, 505  
*Pancrust:genes*, 930, 934, 936  
*Pancrustacea*, 931  
*Pancrustacea*, 920  
*Papilio glaucus*, 234  
*Papilio*, 242  
 Papilionoidea, 344  
*Pappogeomys bulleri*, 450  
*Parabalaenoptera baulinensis*, 34  
*Paradoris dubia*, 511  
*Paradoris*, 511  
*Paradoxopoda*, 920  
 ParaHox, 708  
*Paralamyctes grayi*, 922  
*Paranephrops*, 331  
 Paraphyletic, 640  
*Parapliosaccomys*, 297  
*Pararge*, 235  
*Parasite phylogeny mirrors host phylogeny*, 462  
 Parasite, 449  
     host and, 450, 451  
     tree, 452, 453, 455  
     COI gene, 453  
     speciation, 462  
     topologies, 462  
     phylogenies, 454  
*Parastacoides*, 331  
*Parasuchus*, 177  
*Pareas*, 430  
 Parent cluster, 338  
 Parent, 338  
*Parietobalaena palmeri*, 32, 34  
*Parietobalaena*, 23  
*Parmelia*, 142  
*Parsimony length*, 251  
 Parsimony model, 406  
 Parsimony via Consensus, Trevor C. Bruen and David Bryant, 251  
 Parsimony-based analyses, 39  
 Parsimony, 785  
     bootstrapping in PAUP, 797  
     with the Robinson-Foulds metric, 787  
     meta-trees and, 787, 788  
*Passer*, 174  
*Patagopteryx deferrariisi*, 199  
*Pauropoda*, 931  
 PCR, 231  
*PD*, 831  
*Pectinopygus*, 463  
*Pedetontus saltator*, 922  
*Pedicularis*, 73, 74  
*Pelagosaurus*, 176  
*Pellona*, 537  
*Pelocetus calvertensis*, 34

- Pelocetus*, 23  
*Peltandra*, 271, 277  
*Peltigera*, 154  
 Penalized Likelihood Phylogenetic Inference: Bridging the Parsimony-Likelihood Gap, Junhyong Kim and Michael J. Sanderson, 665  
 Penalized likelihood, 665  
   estimator for phylogeny, 666, 667  
   maximum estimate of the tree, 668  
   estimator, 670  
   in tree inference, 671  
*Penthorum*, 42  
*Per-generation*, 546  
 Perfect phylogeny, 540  
 Perfectly Misleading Distances from Ternary Characters, Hans-Jürgen Bandelt and Mareike Fischer, 540  
*Pericallis*, 748  
*Peridiscus*, 43  
*Period*, 242  
 Peripatric model, 595  
*Periplaneta americana*, 922  
*Perognathus flavus*, 452  
*Perognathus*, 449, 453, 454, 456, 457, 459, 465  
*Peromyscus aztecus*, 85, 536  
*Peromyscus maniculatus*, 333  
*Pfeil, Bernard E.*, see *Maureira-Butler, Iván J.*, 466  
*Phanerochaete chrysosporium*, 615  
*Phascolion strombi*, 711  
*Phelsuma andamanensis*, 564  
*Phelsuma comorensis*, 568  
*Phelsuma guentheri*, 571  
*Phelsuma nigristrata*, 568  
*Phelsuma robertmertensi*, 568  
*Phelsuma*, 562–567, 570–573  
*Pheronema carpenteri*, 405  
*Pheronema*, 391, 395, 396  
 Philippine endemic rodents, 292  
*Philoceanus*, 464  
*Phocoena phocoena*, 576, 578, 588  
*Phocoenoides dalli*, 574, 583  
*Phryma*, 705  
*Phylloscopus*, 730  
*PhyloCode*, 507–514  
*Phylogen*, 162  
 Phylogenetic Analysis Informed by Geological History Supports Multiple, Sequential Invasions of the Mediterranean Basin by the Angiosperm Family Araceae, Guilhem Mansion, Gideon Rosenbaum, Nicola Schoenenberger, Gianluigi Bacchetta, Josep A. Rosselló, and Elena Conti, 269  
 Phylogenetic congruence, 104  
 Phylogenetic database, 335  
 Phylogenetic diversity, 825  
 Phylogenetic inference, 758  
 Phylogenetic informativeness, 613  
 Phylogenetic Mixture Models Can Reduce Node-Density Artifacts, Chris Venditti, Andrew Meade, and Mark Pagel, 286  
 Phylogenetic mixture models, 286  
 Phylogenetic nomenclature (PN), 173  
 Phylogenetic resolution, 347, 354, 355  
 Phylogenetic Signal, Evolutionary Process, and Rate, Liam J. Revell, Luke J. Harmon, and David C. Collar, 591  
 Phylogenetic supertree, 243  
   estimates of, 243  
   ML, 244  
   triplet-based, 247  
   likelihood-based, 247, 248  
   subtree-to, 247  
 Phylogenetic Trees Made Easy: A How-to Manual, third edition, David A. Morrison, 658  
 Phylogenetic trees, 483  
 Phylogenetic variation, 419  
*Phylogenetically informative cluster*, 338  
 Phylogenetics, 216, 378, 519, 591, 708, 750  
   tree, 217, 220  
   circumstances, 217  
   scenario, 218  
   software library of, 219  
   model-based, 519  
   risk of, 520  
   pattern of relationships, 520  
   topology, 378, 379, 381  
   analysis in R, 383  
   signal, 385  
 Phylogenomics, 104, 231, 335  
   newly designed genes for, 233  
   concept, 232  
   goals of, 231  
   analyses, 336  
   GeneTrees, 339  
 Phylogeny and Evolution of Glass Sponges (Porifera, Hexactinellida), Martin Dohrmann, Dorte Janussen, Joachim Reitner, Allen G. Collins, and Gert Wörheide, 388  
*Phylogeny and Evolution of the Mollusca*, 955  
 Phylogeny and Evolution of the Mollusca, Dai Herbert, 955  
 Phylogeny Estimation and Alignment via POY versus Clustal + PAUP\*: A Response to Ogden and Rosenberg (2007), Samuli Lehtonen, 653  
 Phylogeny estimation, 665  
 Phylogeny inference, 85  
 Phylogeny of the Beaked Whale Genus *Mesoplodon* (Ziphiidae: Cetacea) Revealed by Nuclear Introns: Implications for the Evolution of Male Tusks, Merel L. Dalebout, Debbie Steel, and C. Scott Baker, 857  
 Phylogeny reconstruction, 286  
   using Bayesian mixture, 288  
   using Markov chains, 289  
   making ancestral, 292  
 Phylogeny: phylogenomics, 420  
   higher-level, 422  
   methods, 428  
   snake, 420, 421  
   implication of, 429, 430  
 Phylogeny, 141, 347, 449, 574, 719, 857, 891  
   of the order Lecanorales, 142  
   Bayesian analyses of, 147  
   53-taxon,  
   and classification, 153, 154  
   to changes in parameter settings, 359  
   additional independent evidence for, 364  
   simulated, 849  
   multi-gene, 864  
   p-median, 832, 833  
   molecular, 870, 872  
   robust, 859  
 Phylogeography, 544, 732  
 Phyloinformatics, 335  
 PhyloMapper, 544  
*PHYML(hrs)/GARLI(hrs)*, 767  
*Physeter macrocephalus*, 30–34, 576, 578, 583  
*Physeter*, 23, 586, 588  
*PI*, 439, 440, 442, 444, 445, 448  
*Pieris rapae*, 232, 233  
*Pinus*, 478, 482  
*Pinusrigidae*, 885

- Pionopsitta*, 731  
*Piscobalaena nana*, 31  
*Pistia*, 284  
 PKDREJ, 17–19, 34  
 PL, 666, 667, 670–672  
*Plakortis simplex*, 392  
*Plasmodium*, 108  
 Plastid inverted repeat, 38  
*Platanthera leucophaea*, 748  
*Platanus*, 39, 41  
*Platismatia glauca*, 143  
*Platycichla*, 258, 259  
 PLCB4, 500  
*Plebeia*, 60  
*Plectrodon*, 537  
*Plectroninia neocaledoniense*, 392  
*Plethodon vandykei*, 84  
*Plethodontidae*, 514  
*Pleuronectes*, 538  
*PLoS Biology*, 1  
*PLoS One*, 1  
 Pocket gopher, 294  
*Podarcis lilfordi*, 284  
*Podarcis lilfordii*, 279  
*Podarcis*, 283  
*Podura aquatica*, 922  
*Podura*, 925, 927, 929  
*Poephila*, 730  
*Pol II*, 920–923, 926, 930, 931, 936, 937  
*Polychaeta*, 514  
*Polygona*, 242  
 Polymerase chain reaction (PCR), 348  
*Polymixia*, 533, 538  
*Polyodon*, 116, 527, 537  
*Polypterus*, 527, 532, 538  
*Polyxenus fasciculatus*, 922  
*Porichthys*, 537  
*Porifera*, 388  
*Porphyra*, 111  
*Porpidia*, 889  
 Posterior probability, 602  
     limiting distribution of, 603, 604  
     limiting survivor function of, 608  
*Potamorhina laticeps*, 442  
*Potamorhina latior*, 443  
*Potamorhina pristigaster*, 443  
*Potamorhina squamoralevis*, 443  
*Potamorhina*, 448  
*Potential*, 344  
*Pratti*, 880, 885, 886  
*Prietella*, 117  
 Primers, 231  
     cDNA-based, 232  
     PCR, 232  
     test, 233  
*Pristichampsus rollinatti*, 180  
*PRM1*, 17–19, 34, 577, 579  
 Probability, 131  
     gene tree, 133  
     general model, 131, 132  
     overall, 132  
     distribution, 132  
*Proctoporus*, 172  
*Produces anomalies*, 132  
*Progeomys*, 297  
*Prokaryotes*, 835  
*Proplebeia dominicana*, 74  
*Proplebeia*, 60  
*Proterochampsia*, 179  
*Protoblastenia rupestris*, 143  
*Protocalliphora*, 214, 230  
 ProtoHox, 708  
*Protomicarea limosa*, 143, 146  
*Protosuchus richardsoni*, 176–178  
*Protosuchus*, 179  
*Proxapertites*, 285  
*psaI-accD*, 704  
*psbA-trnH*, 695–697, 699, 700, 796  
*psbB*, 41  
*psbB-psbH*, 704  
*psbB/T/N/H*, 41  
*psbH*, 41  
*psbM-trnD*, 796  
*psbN*, 41, 42  
*psbT*, 41  
*Psectrogaster amazonica*, 443  
*Psectrogaster essequibensis*, 443  
*Psectrogaster falcata*, 443  
*Psectrogaster rhomboides*, 443  
*Psectrogaster rutiloides*, 443  
*Psectrogaster saguiru*, 443  
*Pseudacris brachyphona*, 556, 560  
*Pseudacris feriarum*, 544, 548–556, 558  
*Pseudacris kalmi*, 549, 551  
*Pseudacris triseriata triseriata*, 560  
*Pseudacris*, 544, 548, 551, 560, 561  
*Pseudacris*, 544  
*Pseudergolis*, 235  
*Pseudobalistes flavimarginatus*, 907, 910  
*Pseudobalistes fuscus*, 910, 916  
*Pseudobalistes fuscus*, 907, 909, 910, 916  
*Pseudobalistes viridescens*, 916  
*Pseudobalistes*, 905, 910, 912, 916  
*Pseudocurimata patiae*, 442  
*Pseudocurimata*, 442, 448  
*Pseudogenes*, 574  
     phylogenetic utility of, 574  
     OR, 575  
     and optimization of nonsense mutations, 576, 577  
     Percentage of, 583  
*Pseudorca crassidens*, 33, 576, 578, 588  
*Pseudoryx nghetinhensis*, 31  
*Psilolechia leprosa*, 143  
*Psilolechia lucida*, 143  
*Psithyrus*, 59, 62, 68–70, 73–75  
*Psittacula*, 572  
*Psophocichla*, 258, 259, 263  
*Psora decipiens*, 143  
*Psora rubiformis*, 143  
*Psora*, 145, 146, 150–153  
*Psorula rufonigra*, 143  
*Psorula*, 145  
*Psychotria*, 4, 6, 8, 9, 11–13, 704, 706  
*Psychotria*, 4  
*Pteropus*, 315  
*Pterostemon*, 43  
*Puccinia graminis*, 620  
*Purussaurus*, 180, 181  
*Pycnogonida*, 931  
*Pycnogonida*, 920  
*Pygmaeus*, 310  
*Pygocentrus*, 537

- Pylodictis olivaris*, 117–119, 121, 126, 127  
*Pylodictis*, 119, 121, 125–127  
*Pyrobombus*, 62, 68–70, 74  
*Pyrococcus*, 855  
 Pyron, R. Alexander, *see* Burbrink, Frank T. 317  
*Pyrrhospora quernea*, 143  
 Qiu, Yin-Long, *see* Jian, Shuguang, 38  
 Quantitative characters, 591  
 Quartet puzzling, 771  
*Quercus*, 795  
*Quinkana*, 181  
*R. aculeatus*, 912  
*R. assasi*, 912  
*R. lunula*, 910, 912  
*R. nodastrella*, 398, 402  
*R. nuda*, 398  
*R. pinicola*, 259  
*R. racovitzae*, 398  
*R. rectangularis*, 910, 912  
*R. tintinnus*, 391, 398  
*R. verrucosus*, 910, 912  
 RA, 648, 649  
*Rabida*, 125  
*Racovitzae*, 391  
*Radiation of the Genus*, 866  
 RAG, 501  
*rag1*, 129  
*RAG1*, 17–19, 34, 577, 579, 588  
*Rag2*, 117, 118, 129  
*RAG2*, 577  
*Rahonavis*, 188  
*Ramalina fastigiata*, 143  
*Ramalina*, 142  
 Random exchanges, effects of directed versus, 854, 855  
 Random subtree pruning and regrafting (rSPR), 87, 89, 91  
 Random walk, 544  
 Randomization, 891  
 Ranidae, 327  
 Rapid bootstrap(RBS), 758  
   heuristics in RAxML, 758, 759  
   search, 760, 762  
   Outline of, 761  
 Rapid radiation, 38  
*Rattus norvegicus*, 20, 33, 469  
 RAxML program, 765  
 RAxML, 758  
 Ray-finned fish, 519  
   diversity, 521  
   characteristics of the ten nuclear loci amplified in, 523  
   phylogenetic relationships among, 527  
   Strict consensus tree of, 530  
*rbc*, 56, 272, 274, 276, 807  
*rbcL*, 41, 54–56, 160, 328, 410, 414, 796–798, 800, 801, 807, 808  
*RBS(Bips)*, 763, 765  
*RBS(hrs)*, 762  
 Real time, 925  
 Reconciled trees, 590  
 Ree, Richard H. and Smith, Stephen A., Maximum Likelihood  
   Inference of Geographic Range Evolution by Dispersal, Local  
   Extinction, and Cladogenesis, 4  
 Ree, Richard H., *see* Clark, John R., 693  
 Reeder, Tod W., *see* Wiens, John J., 420  
*Regalecus*, 537  
 Regier, Jerome C., Shultz, Jeffrey W., Ganley, Austen R. D., Hussey,  
   April, Shi, Diane, Ball, Bernard, Zwick, Andreas, Stajich, Jason  
   E., Cummings, Michael P., Martin, Joel W. and Cunningham,  
   Clifford W., Resolving Arthropod Phylogeny: Exploring  
   Phylogenetic Signal within 41 kb of Protein-Coding Nuclear  
   Gene Sequence, 920  
 Reitner, Joachim, *see* Dohrmann, Martin, 388  
 Relative proximity, 435  
 Relaxed clock, 116  
   MCMC approach, 118  
   UCLN modelling, 119  
*Relictus*, 310  
 Renner, Susanne S., Grimm, Guido W., Schneeweiss, Gerald M.,  
   Stuessy, Tod F. and Ricklefs, Robert E., Rooting and Dating  
   Maples (*Acer*) with an Uncorrelated-Rates Molecular Clock:  
   Implications for North American/Asian Disjunctions, 795  
 Resolving an Ancient, Rapid Radiation in Saxifragales, Shuguang  
 Jian, Pamela S. Soltis, Matthew A. Gitzendanner, Michael J.  
 Moore, Ruiqi Li, Tory A. Hendry, Yin-Long Qiu,  
 Amit Dhingra, Charles D. Bell, and Douglas E. Soltis, 38  
 Resolving Arthropod Phylogeny: Exploring Phylogenetic Signal  
 within 41 kb of Protein-Coding Nuclear Gene Sequence,  
 Jerome C. Regier, Jeffrey W. Shultz, Austen R. D. Ganley, April  
 Hussey, Diane Shi, Bernard Ball, Andreas Zwick, Jason E.  
 Stajich, Michael P. Cummings, Joel W. Martin, and Clifford W.  
 Cunningham, 920  
 Retrotransposon, 499  
 Revell, Liam J., Harmon, Luke J., and Collar, David C., Phylogenetic  
 Signal, Evolutionary Process, and Rate, 591  
*RF*, 763, 764  
*RF-SBS/RF-RBS*, 767  
*Rhabdocalyptus dawsoni*, 404  
*Rhabdopectella tintinnus*, 389, 398  
*Rhabdopectella*, 391, 395, 398, 402  
*Rhinecanthus aculeatus*, 907  
*Rhinecanthus assasi*, 907  
*Rhinecanthus lunula*, 907  
*Rhinecanthus rectangularis*, 907  
*Rhinecanthus verrucosus*, 907, 912  
*Rhinecanthus*, 906, 910–912, 916  
*Rhinecantus*, 906  
*Rhinotus purpureus*, 922  
*Rhizocarpon*, 154  
*Rhizopus oryzae*, 615, 616  
*RHO*, 874  
*Rhododendron*, 73  
*Rhoptropella ocellata*, 564, 566  
*Rhoptropus boultoni*, 564  
*Rhoptropus*, 573  
*Rhymphoctona*, 947  
 Ribosomal DNA, 388  
*Richii*, 695  
*Richtersius coronifer*, 923  
 Ricklefs, Robert E., *see* Renner, Susanne S., 795  
*Ridgwayia*, 259  
 Ripplinger, Jennifer and Sullivan, Jack, Does Choice in Model  
 Selection Affect Maximum Likelihood Analysis?, 76  
*RLH(hrs)*, 766  
*RLH*, 766  
 RNA secondary structure, 388  
 Roalson, Eric H., *see* Clark, John R., 693  
 Robinson, Terence J., *see* Avise, John C., 503  
*Robustus*, 25  
 Rodolphe, F., *see* Aguileta, G., 613  
 Rodrigo, Allen G., *see* Bordewich, Magnus, 825  
 Rodrigo, Allen, *see* Steel, Mike, 243  
 Roger, Andrew J., *see* Leigh, Jessica W., 104  
*Rolfidium coccocarpioides*, 143  
 Ronquist, Fredrik, *see* Huelsenbeck, John P., 406

- Ronquist, Fredrik, *see* Lakner, Clemens, 86
- Rooted, 251
- Rooting and Dating Maples (*Acer*) with an Uncorrelated-Rates Molecular Clock: Implications for North American/Asian Disjunctions, Susanne S. Renner, Guido W. Grimm, Gerald M. Schneeweiss, Tod F. Stuessy, and Robert E. Ricklefs, 795
- Rooting of phylogenies, 795
- Root, 835
- Rosellinia, 155
- Rosenbaum, Gideon, *see* Mansion, Guilhem, 269
- Rosenberg, Noah A. and Tao, Randa, Discordance of Species Trees with Their Most Likely Gene Trees: The Case of Five Taxa, 131
- Ross, Howard A., Murugan, Sumathi, and Li, Wai Lok Sibon, Testing the Reliability of Genetic Methods of Species Identification via Simulation, 216
- Rossella nodastrella, 402, 405
- Rossella, 391, 395, 398, 402
- Rosselló, Josep A., *see* Mansion, Guilhem, 269
- Rotatae, 474, 475
- Rougemont, Jacques, *see* Stamatakis, Alexandros, 758
- Rozeni, 60
- rp, 466, 469, 470, 472, 473
- rpl16, 796
- rpl2, 41
- rpl23, 41
- rpoC1, 480
- rpoC2, 41–43
- rps, 272, 274, 276, 284
- rps12, 41
- rps16, 87
- rps3, 41, 43
- rps4, 41–43
- rps4-cob, 471
- rps4/trnV, 41
- rps7, 41
- rrn16, 41
- rrn23, 41
- rrn4.5, 41
- rrn5, 41
- Rubra, 804, 806
- Rubra-Hyptiocarpa, 804
- Rubus, 73
- S. albicaudatum*, 912
- S. bayanus*, 790, 791
- S. bolanderi*, 158
- S. bredanensis*, 588
- S. bursa*, 912
- S. castellii*, 790, 791
- S. cerevisiae*, 623, 790
- S. chrysopterum*, 912
- S. coeruleoalba*, 580
- S. galericulata*, 158
- S. granosus*, 445
- S. kluyveri*, 790, 791
- S. kudriavzevii*, 790, 791
- S. lidii*, 749
- S. marshalli*, 444, 445
- S. mikatae*, 790
- S. nodorum*, 618, 624, 625
- S. paradoxus*, 790
- S. pombe*, 623
- S. pullus*, 444, 445
- S. sialis*, 259
- S. str.*, 400
- S. thompsoni*, 445
- S. vulgaris*, 259
- Saccharomyces bayanus*, 615
- Saccharomyces castellii*, 615
- Saccharomyces cerevisiae*, 613, 615, 621
- Saccharomyces kluyveri*, 615
- Saccharomyces kudriavzevi*, 615
- Saccharomyces mikatae*, 615
- Saccharomyces paradoxus*, 615
- Saghatarium antiquum*, 315
- Sanderson, Michael J., Boss, Darren, Chen, Duhong, Cranston, Karen A., and Wehe, Andre, The PhyLoTA Browser: Processing GenBank for Molecular Phylogenetics Research, 335
- Sanderson, Michael J., *see* Kim, Junhyong, 665
- Sandiegensis, 513
- Sanmartín, Isabel, *see* Nylander, Johan A. A., 257
- Santalum, 702, 706
- Santini, Francesco, *see* Dornburg, Alex, 905
- Santos, Daniel A. Dos, Fernández, Hugo R., Cuezso, María Gabriela, and Domínguez, Eduardo, Sympatry Inference and Network Analysis in Biogeography, 432
- Santos-Guerra, Arnoldo, *see* Díaz-Pérez, Antonio, 732
- Sapeornis, 188
- Sarcosuchus imperator, 176
- Sarcosuchus, 179
- Sarga, 514
- Satan eurytomus, 117
- Sauromatum guttatum, 279
- Sauromatum, 272, 276
- Saxifraga flagellaris, 57
- Saxifraga integrifolia, 43
- Saxifraga, 749
- Saxifragales, 38
- SBS(Bips), 763, 765
- SBS(hrs), 762
- Sceloporus undulatus, 463
- Sceloporus, 645
- Schadonia fecunda, 143, 146
- Schardl, C. L., Craven, K. D., Speakman, S., Stromberg, A., Lindstrom, A., and Yoshida, R., A Novel Test for Host-Symbiont Codivergence Indicates Ancient Origin of Fungal Endophytes in Grasses, 483
- Schargel, Walter E., *see* Lawing, A. Michelle, 167
- Schilbeodes, 125
- Schismatoglottis, 282
- Schizosaccharomyces pombe, 615
- Schmidly, David J., Terry Lamont Yates, 333
- Schneeweiss, Gerald M., *see* Renner, Susanne S., 795
- Schoenenberger, Nicola, *see* Mansion, Guilhem, 269
- Sciobius, 443–446, 448
- Scleromochlus taylori, 178
- Sclerotinia sclerotiorum, 615
- Scoliciosporum intrusum, 143
- Scoliciosporum umbrinum, 143
- Scolopendra polymorpha, 922
- Scoring parameters, 347
- automated, 364
- of AFLP, 364
- Scutellaria bolanderi, 158
- Scutellaria galericulata, 158
- Scutellaria, 73, 158
- Scutigera, 922
- Scyphozoa, 392
- Sebastes, 538
- Securidaca, 808
- Selecting Taxa to Save or Sequence: Desirable Criteria and a Greedy Solution, Magnus Bordewich, Allen G. Rodrigo, and Charles Semple, 825



- Semi-parametric, 665  
*Semibalanus balanoides*, 922  
*Semotilus atromaculatus*, 791  
*Semotilus*, 537  
*Semperella schulzei*, 396  
*Semperella*, 391, 395  
*Semple, Charles*, see Bordewich, Magnus, 825  
*Senecio jacobaea*, 365  
*Senecio*, 282  
 Seo, Tae-Kun, and Kishino, Hirohisa, Synonymous Substitutions Substantially Improve Evolutionary Inference from Highly Diverged Proteins, 367  
 Separate analysis, 104  
   advantage of, 105  
   lowers bootstrap support, 111  
*Sequeira, Miguel*, see Diaz-Pérez, Antonio, 732  
*Sequence heterochrony*, 378  
 Sequence heterochrony, 378  
   identification of, 379, 380  
   hypothetical, 380  
 Sequencing protocol, 907  
*Sericolophus hawaiiicus*, 396  
*Sericolophus*, 391, 395  
*Serjania*, 796  
*Sertifer*, 877–879, 890  
*Servin, Jacqueline A.*, see Lake, James A., 835  
 Sexual selection, 857  
*SF(hrs)*, 766  
 Shallowest divergences (SD), 876  
*Shi, Diane*, see Regier, Jerome C., 920  
*Shultz, Jeffrey W.*, see Regier, Jerome C., 920  
*Sialia*, 259  
*Sikes, D. S.*, see Zhang, A. B., 202  
 Simulation, 286  
 Site-specific rates, 670  
*Sites Jr., Jack W.*, see Wiens, John J., 420  
*Skogsbergia lernerii*, 922  
*Skophammer, Ryan G.*, see Lake, James A., 835  
*SLH*, 766  
 Slowly evolving genes, 38  
*Smith, Sarah A.*, see Wiens, John J., 420  
*Smith, Stephen A.*, see Ree, Richard H., 4  
*Smith, Vincent S.*, The New Taxonomy, 660  
*Smithi*, 263  
*Smyrna*, 240  
*Solanum vespertilio*, 749  
*Solanum*, 365  
*Soleneiscus stolonifer*, 392  
*Soltis, Douglas E.*, see Jian, Shuguang, 38  
*Soltis, Pamela S.*, see Jian, Shuguang, 38  
*Sonchus gandogeri*, 748  
*Sonchus*, 734, 744, 748  
*Songlingornis linghensis*, 188  
*Songlingornis*, 188, 189, 192, 193  
*Sorghum*, 514  
*Sotalia*, 589  
*Spatial expression*, 439  
*Speakman, S.*, see Schardl, C. L., 483  
*Speciation in Birds*, 515  
*Speciation in Birds*, Glenn-Peter Sætre, 515  
 Speciation rate of evolution, 562  
 Speciation, 4, 116  
 Species choice, 833  
 Species delineation, 628  
 Species identification, 202  
   success rate of, 207  
   BP-based, 208, 209  
 Species identification, 216  
   testing methods of  
     discussion, 222, 226  
     paraphyly and, 228  
 Species Names in the *PhyloCode*: The Approach Adopted by the International Society for Phylogenetic Nomenclature, Benoît Dayrat, Philip D. Cantino, Julia A. Clarke, and Kevin de Queiroz, 507  
 Species tree, 243, 294  
   gene trees versus concatenated tree versus, 304, 306  
   species tree analysis, 300  
   distribution of, 299  
 Species tree, 719  
   Bayesian estimation of, 724  
   congruence between gene trees and, 725  
   reconstruction, 725  
   phylogenetic methods, 729  
*SpeedupF*, 766  
*Speleonectes tulumensis*, 922  
*Speleonectes*, 925, 927, 929  
*Sphaerophorus globosus*, 143  
*Sphaerophorus*, 142, 150  
*Sphenodon guntheri*, 330  
*Sphenodon*, 175, 331  
*Sphenopholis obtusata*, 485  
*Sphenosuchus acutus*, 179  
 Spiders, 628  
*Spirocarpos*, 474, 481  
 Split, 785  
   definition, 787  
   consensus of sets of, 788  
   tree-like sets of, 789  
*Spongilla lacustris*, 392, 396  
*SPR distance*, 251  
 SPR distance, 251  
*SPR median tree*, 253  
*SPR*, 250  
 Springer, Mark S., Meredith, Robert W., Eizirik, Eduardo, Teeling, Emma, and Murphy, William J., Morphology and Placental Mammal Phylogeny, 499  
*SPTBN1*, 577, 579  
*Squalodon calvertensis*, 34  
*Squamarina lentigera*, 143  
*Squamarina scopulorum*, 154  
*SRY*, 577  
*Stagonolepis Robertsoni*, 179  
*Stagonolepis*, 177  
*Stagonospora nodorum*, 615, 616  
*Stajich, Jason E.*, see Regier, Jerome C., 920  
 Stamatakis, Alexandros, Hoover, Paul and Rougemont, Jacques, A Rapid Bootstrap Algorithm for the RAxML Web Servers, 758  
 Star tree, 602  
   paradox, 602, 607  
   simulation, 605  
 Starting tree, 578  
*STAT5A*, 17–19, 34  
 Statistical Assignment of DNA Sequences Using Bayesian Phylogenetics, Kasper Munch, Wouter Boomsma, John P. Huelsenbeck, Eske Willerslev, and Rasmus Nielsen, 750  
 Statistical consistency, 243  
   of ML supertree, 245, 247  
   of MRP, 246  
   for maximum likelihood, 248  
 Statistical phylogeography, 544  
   primary aim of, 544  
   coalescent-based approaches in, 556

- to test for simultaneous vicariance in, 558  
future of, 559, 560
- Statistical Tests between Competing Hypotheses of Hox Cluster  
Evolution, Robert Lanfear and Lindell Bromham, 708
- Statistically consistent, 249
- Steel, Debbie, *see* Dalebout, Merel L., 857
- Steel, Mike A., *see* Whitfield, James B., 939
- Steel, Mike, and Rodrigo, Allen, Maximum Likelihood Supertrees, 243
- Steel, Mike, *see* Li, Guoliang, 628
- Steindachnerina argentea, 443
- Steindachnerina atratoensis, 442
- Steindachnerina biornata, 443
- Steindachnerina brevipinna, 443
- Steindachnerina conspersa, 443
- Steindachnerina dobula, 443
- Steindachnerina elegans, 442, 443
- Steindachnerina fasciata, 443
- Steindachnerina hypostoma, 443
- Steindachnerina insculpta, 443
- Steindachnerina leucisca, 443
- Steindachnerina notonota, 443
- Steindachnerina pupula, 443
- Steindachnerina quasimodoi, 443
- Steindachnerina runa, 443
- Steindachnerina, 448
- Stenella coeruleoalba, 580
- Stenella coeruleoalba, 574, 576, 578, 579, 583, 586, 588
- Steneosaurus, 175
- Steno bredanensis, 576, 578, 588
- Steno, 588, 589
- Stereocaulon pileatum, 143
- Stereocaulon tomentosum, 143
- Stochastic Dollo, 772  
multi-state model, 776, 778  
binary model, 773–775
- Stochastic mapping (SIMMAP), 141
- Stochastic mapping, dispersal, 693
- Stochastic nearest neighbor interchange (stNNDI), 87
- Stockman, Amy K., *see* Bond, Jason E., 628
- Stomias, 538
- Storeria dekayi, 379
- Stratigraphic congruence, 891  
choose between trees for the same taxa, 901, 902  
and the completeness of the fossil record, 899, 900  
existing indices of, 894  
for dinosaurs, 902
- Stratigraphic fit, 903
- Streptocephalus seali, 922
- Stricto, 388
- Strobus, 482
- Stromberg, A., *see* Schardl, C. L., 483
- Strong, 929
- Structure, 748
- Struthio, 174
- Stuessy, Tod F., *see* Renner, Susanne S., 795
- Sturnus, 259, 261
- Suberites ficus, 392, 396
- Substitution rates, 539
- Substitution rates, 795
- Subterraneobombus, 68
- Subtree clusters, 338
- Subtree, 338, 344
- Subtree-prune and regraft, 251
- Suchard, Marc A., *see* Alekseyenko, Alexander V., 772
- Sufflamen albicaudatum, 907
- Sufflamen bursa, 907
- Sufflamen chrysopterum, 907
- Sufflamen fraenatum, 907, 911
- Sufflamen, 906, 910–912, 916
- Sukumaran, Jeet, *see* Holder, Mark T., 814
- Sulfolobus, 844, 854
- Sullivan, Jack, *see* Page, Roderic D. M., 1
- Sullivan, Jack, *see* Ripplinger, Jennifer, 76
- Sump, 234, 631
- Sumt, 631
- Superkingdom, 104
- Supermatrix analysis, 104
- Supermatrix, 574  
and GR analyses, 575, 588  
advantages of, 575  
combined, 579  
of OR genes and independent DNA data, 584
- Supernetworks, 939
- Supertree construction, 248
- Supertree methods, 940
- Supertree, 243
- Supertrees, 243
- Support values, 758
- Sus scrofa, 26, 33
- Susko, Edward, *see* Leigh, Jessica W., 104
- Susko, Edward, On the Distributions of Bootstrap Support and Posterior Distributions for a Star Tree, 602
- Svenblad, Bodil, Consistent Estimation of Divergence Times in Phylogenetic Trees with Local Molecular Clocks, 947
- Symbiobacterium thermophilum, 840
- Symbiosis, 449
- Sympatry Inference and Network Analysis in Biogeography, Daniel A. Dos Santos, Hugo R. Fernández, María Gabriela Cuezco, and Eduardo Domínguez, 432
- Symphyla, 931
- Symplocarpus, 283
- Synapomorphy, 503
- Synodus, 537
- Synonymous saturation, 367  
and Evolutionary Distance, 370, 371  
effect of ignoring, 371
- Synonymous Substitutions Substantially Improve Evolutionary Inference from Highly Diverged Proteins, Tae-Kun Seo and Hirohisa Kishino, 367
- Systematic Biology, 1, 2, 43, 335, 440, 512, 822, 872, A-1
- Syzygium, 403
- Sánchez-Villagra, Marcelo R., *see* Asher, Robert J., 311
- Sætre, Glenn-Peter, Speciation in Birds, 515
- T. albicollis paraguayensis, 259
- T. albicollis, 264
- T. albocinctus, 259
- T. amaurochalinus, 259
- T. ambiguum, 468
- T. anguina, 468
- T. arabica, 468
- T. assimilis dague, 259
- T. aurantius, 259
- T. b. awahmee, 305
- T. balansae, 468
- T. bewsheri, 259
- T. bottae awahmee, 297, 300
- T. bottae, 295, 297–300, 302, 304–307
- T. bouboul, 259
- T. bulbivorus, 295, 297, 300, 302, 304
- T. caerulea, 468
- T. calliceras, 468
- T. cardis, 259, 265

- T. celaenops*, 259  
*T. chiguanco chiguanco*, 259  
*T. chiguanco*, 264  
*T. chrysolaus*, 259  
*T. clusius*, 295, 297, 306  
*T. corniculata*, 468  
*T. cretica*, 468  
*T. dissimilis*, 259  
*T. falcklandii magellanicus*, 259  
*T. feae*, 265  
*T. foenum-graecum*, 468  
*T. fulvoventris*, 259, 264  
*T. fumigatus*, 259  
*T. fuscater fuscater*, 259  
*T. fuscater*, 264  
*T. glabra*, 468  
*T. grayi*, 259, 261  
*T. haplochrous*, 259  
*T. hauxwelli*, 259  
*T. hortulorum*, 259  
*T. idahoensis*, 295, 297, 300, 302, 306  
*T. ignobilis debilis*, 259  
*T. iliacus iliacus*, 259  
*T. iliacus*, 264  
*T. infuscatus*, 259  
*T. jamaicensis*, 259  
*T. kessleri*, 259  
*T. lawrencii*, 259  
*T. leucomelas leucomelas*, 259  
*T. libonyanus peripheris*, 259  
*T. m. merula/T. m. intermedius*, 264  
*T. macrorrhynca*, 468  
*T. maculirostris*, 259  
*T. maranonicus*, 259  
*T. maritima*, 855  
*T. mazama*, 295, 297, 300  
*T. merula intermedius*, 260  
*T. merula mandarinus*, 259  
*T. merula maximus*, 260  
*T. merula merula*, 260  
*T. merula simillimus*, 260  
*T. mesopotamica*, 468  
*T. migratorius migratorius*, 260  
*T. migratorius*, 266  
*T. monticola*, 295, 297, 300, 302  
*T. mupinensis*, 260, 261  
*T. naumanni eunomus*, 260  
*T. naumanni naumanni*, 260  
*T. nigrescens*, 260  
*T. nigriceps*, 260  
*T. nudigenis*, 260  
*T. obscurus*, 260  
*T. obsoletus parambanus*, 260  
*T. olivaceofuscus*, 263, 265  
*T. olivaceofuscus*, 260  
*T. olivaceus abyssinicus*, 260  
*T. olivaceus helleri*, 260  
*T. olivaceus ludovicicae*, 260  
*T. olivaceus nyikae*, 260  
*T. olivaceus olivaceus*, 260  
*T. olivaceus roehli*, 260  
*T. olivaceus smithi*, 260  
*T. olivater*, 260  
*T. pallidus*, 260  
*T. pelios centralis*, 260  
*T. pelios saturatus*, 260  
*T. pelios*, 260, 263, 265  
*T. philomelos philomelos*, 260  
*T. philomelos*, 261  
*T. pilaris*, 260, 264  
*T. plebejus*, 260  
*T. plumbeus ardosiaceus*, 260  
*T. plumbeus plumbeus*, 260  
*T. poliocephalus hygroskopus*, 260  
*T. poliocephalus kulambangrae*, 260  
*T. poliocephalus niveiceps*, 260  
*T. poliocephalus poliocephalus*, 260  
*T. poliocephalus rennellianus*, 260  
*T. poliocephalus thomassoni*, 260  
*T. pratenses*, 468  
*T. r. atrogularis*, 266  
*T. r. ruficollis*, 266  
*T. reevei*, 260  
*T. rubripes*, 521  
*T. rubrocanus gouldi*, 260  
*T. rubrocanus rubrocanus*, 260  
*T. ruficollis atrogularis (AB)–T. ruficollis ruficollis (B)*, 266  
*T. ruficollis atrogularis*, 260  
*T. ruficollis ruficollis*, 260  
*T. rufitorques*, 260, 264  
*T. rufiventris*, 260, 264  
*T. rufopalliatius*, 258  
*T. serranus serranus*, 260  
*T. serranus*, 264  
*T. spicata*, 468  
*T. spruneriana*, 468  
*T. stellata*, 468  
*T. suavissima*, 468  
*T. swalesi swalesi*, 260  
*T. talpoides*, 295, 297, 300, 302, 306  
*T. tephronotus*, 260, 263  
*T. torqatus torqatus*, 260  
*T. torquatus–T. ruficollis*, 265  
*T. townsendii*, 295, 297, 300, 302, 304  
*T. tubulosum*, 391  
*T. umbrinus*, 295, 297, 302, 307  
*T. unicolor*, 260, 265  
*T. viscivorus viscivorus*, 260  
*Tachyglossus*, 175  
*Takifugu*, 538  
*Talpa europaea*, 314, 315  
*Tamias amoenus*, 84  
*Tamura-Nei model*, 678  
*Tamystylum orbiculare*, 923  
*Tamystylum*, 925, 927, 929  
*Tao, Randa, see Rosenberg, Noah A.*, 131  
*Tapirus indicus*, 33  
*Taq*, 17, 469, 576  
*Tarsius bancanus*, 316  
*Tasmacetus sheperdi*, 22  
*Tasmacetus shepherdii*, 34, 860, 874  
*Taxon ID*, 338  
*Taxon names*, 336  
*Taxon Sampling Affects Inferences of Macroevolutionary Processes from Phylogenetic Trees*, Tracy A. Heath, Derrick J. Zwickl, Junhyong Kim, and David M. Hillis, 160  
*Taxon selection*, 835  
*Taxon Selection*, 835  
*Taxonomic distinctness (TD)*, 831, 832  
*taxonomic distinctness*, 831, 832  
*Taxonomic distinctness*, 831  
*Taxonomy tree*, 335

- Taxus mairei*, 681  
*Tayassu tajacu*, 33  
 TBR, 250  
 TBX4, 577  
 Teeling, Emma, see Springer, Mark S., 499  
 Teeth, 857  
   medial, 906, 916  
   tusk-like, 857  
   strap-like, 868  
*tefA*, 489  
*Tegeticula yuccasella*, 84  
*Tektin*, 242  
*Teleosaurus*, 175  
*Teline*, 748  
*Teloschistes*, 154  
 Temporal diversification, 905  
 Tenrecs, 316  
*Tenuis*, 391, 398  
*Tephromela atra*, 143  
*Terraenovae*, 538  
 Terry Lamon Yates, David J. Schmidly, 333  
 Testing Congruence in Phylogenomic Analysis, Jessica W. Leigh, Edward Susko, Manuela Baumgartner, and Andrew J. Roger, 104  
 Testing the Reliability of Genetic Methods of Species Identification via Simulation, Howard A. Ross, Sumathi Murugan, and Wai Lok Sibon Li, 216  
*Tetracarpaea*, 43  
*Tetragnatha*, 562  
*Tetragonisca angustula*, 60  
*Tetragonula fuscobalteata*, 60  
*Tetramorium*, 645  
*Tetraodon*, 538  
 Tetraodontiformes, 905  
 Tetrapoda, 175  
*Texasophis galbreathi*, 322  
*Thaleichthys*, 538  
*Thamnophilus*, 267  
*Thamnophis*, 29  
 The Cambridge Companion to the Philosophy of Biology, David A. Morrison, 822  
 The Expanding Contributions of *Systematic Biology*, Roderic D. M. Page and Jack Sullivan, 1  
*The Florida Naturalist*, 184  
 The Impact of Reticulate Evolution on Genome Phylogeny, Robert G. Beiko, W. Ford Doolittle, and Robert L. Charlebois, 844  
 The Influence of Model Averaging on Clade Posteriors: An Example Using the Triggerfishes (Family Balistidae), Alex Dornburg, Francesco Santini, and Michael E. Alfaro, 905  
 The Limitations of Ancestral State Reconstruction and the Evolution of the Ascus in the Lecanorales (Lichenized Ascomycota), Stefan Ekman, Heidi L. Andersen and Mats Wedin, 141  
 The Modified Gap Excess Ratio (GER\*) and the Stratigraphic Congruence of Dinosaur Phylogenies, Matthew A. Wills, Paul M. Barrett, and Julia F. Heathcote, 891  
*The New Systematics*, 661  
*The New Taxonomy*, 660, 662, 663  
 The New Taxonomy, Vincent S. Smith, 660  
 The PhyLoTA Browser: Processing GenBank for Molecular Phylogenetics Research, Michael J. Sanderson, Darren Boss, Duhong Chen, Karen A. Cranston, and Andre Wehe, 335  
 The Relative Importance of Body Size and Paleoclimatic Change as Explanatory Variables Influencing Lineage Diversification Rate: An Evolutionary Analysis of Bullhead Catfishes (Siluriformes: Ictaluridae), Michael Hardman and Lotta M. Hardman, 116  
 The Reticulate History of *Medicago* (Fabaceae), Iván J. Maureira-Butler, Bernard E. Pfeil, Amorntip Muangprom, Thomas C. Osborn, and Jeff J. Doyle, 466  
 The Role of Geography and Ecological Opportunity in the Diversification of Day Geckos (*Phelsuma*), Luke J. Harmon, Jane Melville, Allan Larson, and Jonathan B. Losos, 562  
 The Taming of the Skew: Estimating Proper Confidence Intervals for Divergence Dates, Frank T. Burbrink and R. Alexander Pyron, 317  
 The Use of Mean Instead of Smallest Interspecific Distances Exaggerates the Size of the “Barcoding Gap” and Leads to Misidentification, Rudolf Meier, Guanyang Zhang, and Farhan Ali, 809  
 The Vestigial Olfactory Receptor Subgenome of Odontocete Whales: Phylogenetic Congruence between Gene-Tree Reconciliation and Supermatrix Methods, Michael R. McGowen, Clay Clark, and John Gatesy, 574  
*Thecadactylus rapicauda*, 644  
*Thecostraca*, 931  
*Thereuonema*, 922  
 Thermodynamic integration, 190  
 Thermodynamic integration, 675  
*Thermoplasma*, 844, 854  
*Thermotoga maritima*, 855  
*Theromyzon trizonare*, 711  
*Thomomys bottae*, 308–310, 464  
*Thomomys bulbivorus*, 310  
*Thomomys idahoensis*, 310  
*Thomomys mazama*, 310  
*Thomomys monticola*, 310  
*Thomomys talpoides*, 309, 310  
*Thomomys townsendii*, 300, 307, 309, 310  
*Thomomys umbrinus*, 300, 308, 310  
*Thomomys*, 294–298, 300, 302, 305–310, 518, 886, 889  
*Thomomys*. Geomyidae, 294  
*Thoracobombus*, 68  
*Thoracosaurus*, 181  
*Thouinia*, 796  
*Thouinopsis*, 796  
*Three-interval data set*, 288  
*Thul*, 934  
*Thuliana:genes*, 930, 936  
*Thulina stephaniae*, 923  
*Thulina*, 934  
*Thulinia stephaniae*, 922  
*Thulinia*, 925, 927, 930, 934  
*Thulinia:genes*, 934  
*Tigriopus californicus*, 644  
 Time dependency, 730  
*tk3*, 274  
*tn*, 672  
 TNT, 234  
*Tolpis*, 744, 745, 747, 748  
*Tomocerus*, 922  
*Toninia cinereovirens*, 143  
*Toona*, 798  
 Topological score, 613  
   as a function of the Robinson-Foulds, 618, 619  
   relationship between the Kuhner-Felsenstein distance, 618  
   distribution of, 619, 620  
   as a function of gene size for the 246 individual gene phylogenies, 622  
 Topology proposals, 86  
 Topology, 785  
   result for the star, 788  
   frequency of, 789

- Townsend, Ted M., *see* Wiens, John J., 420
- Townsendii, 310
- Toxoneuron, 940
- Trachyboa, 429
- Trachyiulus nordquisti, 922
- Tragopogon, 56
- Tragulus napu, 33
- Trebouxia, 156
- Tree bisection reconnection (TBR), 20, 42, 60, 78, 90
- Tree of life, 613, 835
- Tree-based methods, 450
- Trees of Trees: An Approach to Comparing Multiple Alternative Phylogenies, Tom M. W. Nye, 785
- Tretodictyum, 391, 395, 396, 398
- Trichoderma reesei, 615
- Trichopeziza, 156
- Trichoplax, 392, 396
- Trifolium, 467, 468, 472, 473
- Triggerfish  
     global diversification rate of, 909  
     age and evolutionary history of, 906
- Trigona, 60, 74, 75, 947
- Trigonella, 466–470, 473, 476, 480
- Triguera, 747
- Trilophosuchus rackhami, 180
- Triops longicaudatus, 922
- Triops, 925, 927, 929
- Tripleurospermum, 280
- Triseriata, 552
- trn, 272, 274, 276, 283, 284, 733, 808
- trnA, 41
- trnC-ycf6, 704
- trnD-trnT, 796
- trnL, 41
- trnL, 41, 796
- trnL-F, 55, 796
- trnL-trnF, 704
- trnN, 41
- trnR, 41
- trnT-trnD, 704
- trnT-trnF, 55
- trnV, 41
- Trochodendron, 39
- Trogloglanis pattersoni, 117, 128
- Tropicalis, 537
- Tropidophis, 429
- tubB, 489
- Tubulosum, 391
- Turdus feae, 258
- Turdus iliacus, 264
- Turdus, 257–259, 261, 263–266, 268
- Turdus, 257
- Tursiops truncatus, 588
- Tursiops, 30, 589
- Two-interval data set, 288
- Typhlomolge, 514
- Typhonium giganteum, 279
- Typhonium, 272, 276
- Typhonodorum, 277
- Tyrrhenoleuctra, 283
- UA, 648, 649
- Ukurunduense, 805
- Ultrametric, 828
- Ultrametric, 540
- Ungaliophis, 429
- Units of co-occurrence, 432  
     and clustering coefficient, 437, 438  
     extracting, 438, 439
- Uroleucon, 463
- Uropeltis melanogaster, 429
- Uropeltis, 424, 429
- Urosaurus, 172
- Ursus arctos, 509
- Usnea, 142
- Ustilago maydis, 615
- V-nigra, 568
- Vacoparis, 514
- Vagrans, 235
- Valdiviae, 391
- Van de Peer, Yves, *see* Baele, Guy, 675
- Van der Mark, Paul, *see* Lakner, Clemens, 86
- Vansteelandt, Stijn, *see* Baele, Guy, 675
- Variation distance, 249
- Venditti, Chris, Meade, Andrew, and Pagel, Mark, Phylogenetic Mixture Models Can Reduce Node-Density Artifacts, 286
- Veronica cymbalaria, 365
- Veronica, 329
- Vicariance, 4, 693  
     basic rationale of, 12  
     pattern of, 5
- Vidua, 464
- Vincelestes neuquenianus, 316
- Viola palmensis, 747
- Virginianus, 880, 886
- Virginianus, 885
- Viscivorous, 261
- Vitellinus, 720, 721, 724, 728
- Vitis, 39, 41, 55
- Vorona, 195, 196
- Vultur gryphus, 512
- VWF, 500, 501
- W. leuckarti, 398
- Wagner and Dollo: A Stochastic Duet by Composing Two Parsimonious Solos, Alexander V. Alekseyenko, Christopher J. Lee, and Marc A. Suchard, 772
- Wagner, Warren L., *see* Clark, John R., 693
- Wahlberg, Niklas, and Wheat, Christopher West, Genomic Outposts Serve the Phylogenomic Pioneers: Designing Novel Nuclear Markers for Genomic DNA Extractions of Lepidoptera, 231
- Walking legs, 646
- Walteria leuckarti, 398
- Walteria, 391, 395, 398, 402
- Wardiana, 796
- Weapons, 857
- Web site, 613
- Web-based taxonomy, 661
- Wedin, Mats, *see* Ekman, Stefan, 141
- Wehe, Andre, *see* Sanderson, Michael J., 335
- Whale, 15
- Wheat, Christopher West, *see* Wahlberg, Niklas, 231
- Whitfield, James B., Cameron, Sydney A., Huson, Daniel H. and Steel, Mike A., Filtered Z-Closure Supernetworks for Extracting and Visualizing Recurrent Signal from Incongruent Gene Trees, 939
- Wiens, John J., Kuczynski, Caitlin A., Smith, Sarah A., Mulcahy, Daniel G., Sites Jr., Jack W., Townsend, Ted M., and Reeder, Tod W., Branch Lengths, Support, and Congruence: Testing the Phylogenomic Approach with 20 Nuclear Loci in Snakes, 420
- Wikipedia, 822
- Willerslev, Eske, *see* Munch, Kasper, 750
- Wills, Matthew A., Barrett, Paul M. and Heathcote, Julia F., The Modified Gap Excess Ratio (GER\*) and the Stratigraphic Congruence of Dinosaur Phylogenies, 891

- WIN, 404  
 Wingless, 87, 241, 289  
 Withania aristata, 280  
 Wolseley 18/2/98, 143  
 Woody clade, 53  
 WRF, 763, 764  
 WRF-SBS/WRF-RBS, 767  
 Wörheide, Gert, *see* Dohrmann, Martin, 388  
 X. auromarginatus, 912  
 X. ringens, 912  
 Xanthichthys auromarginatus, 906, 907  
 Xanthichthys mento, 907  
 Xanthichthys ringens, 907  
 Xanthichthys, 906, 912, 916  
 Xanthosoma, 272  
 Xantusia vigilis, 421  
 Xantusia, 645  
 Xenobalistes, 907  
 Xenodermus, 430  
 Xenopeltis, 429  
 Xenophidion schaeferi, 430  
 Xenopus leavis, 342  
 Xenopus tropicalis, 521  
 Xenopus, 537  
 Xerophilus, 310  
 Xiphosura, 931  
 Xlox, 708, 712, 714, 715  
 Xvaria, 468  
 Yanornis, 188, 189, 192, 193  
 Yarrowia lipolytica, 615  
 ycf1, 41, 42  
 ycf15, 41  
 ycf2, 41  
 ycf6-psbM, 704  
 Yee, Danny, On Evolution, 184  
 Yixianornis grabau, 200  
 Yixianornis, 187–189, 192, 193, 198  
 Yoshida, R., *see* Schardl, C. L., 483  
 Yucca moths, 84  
 Yule tree, 654  
 Z. cameronensis graueri, 260  
 Z. citrina innotata, 260  
 Z. crossleyi, 260  
 Z. dauma aurea, 260  
 Z. dixon, 260  
 Z. erythronota mendeni, 260  
 Z. monticola, 260  
 Z. princei batesi, 260  
 Z. schistacea, 260  
 Z. sibirica davisoni, 260  
 Zaglossus, 175  
 Zea maize, 478  
 Zea mays, 747  
 Zea, 480, 482  
 Zeus, 533, 538  
 Zhang, A. B., Sikes, D. S., Muster, C., and Li, S. Q., Inferring Species Membership Using DNA Sequences with Back-Propagation Neural Networks, 202  
 Zhang, Guanyang, *see* Meier, Rudolf, 809  
 Zhang, Louxin, *see* Li, Guoliang, 628  
 Ziphrostrum, 873  
 Ziphius cavirostris, 34, 860, 863, 873, 874  
 Ziphius, 864, 872  
 ZooTaxa, 663  
 Zoothera, 260  
 Zwick, Andreas, *see* Regier, Jerome C., 920  
 Zwickl, Derrick J., *see* Heath, Tracy A., 160  
 Zygogeomys trichopus, 450  
 Zygorhiza kochii, 20, 34  
 Zygorhiza, 22