

References

- Adams, E. N. 1986. N-trees as nestings: Complexity, similarity, and consensus. *J. Classif.* 3: 299-317.
- Anderberg, A., and A. Tehler. 1990. Consensus trees, a necessity in taxonomic practice. *Cladistics* 6: 399-402.
- Barrett, M., M. J. Donoghue, and E. Sober. 1991. Against consensus. *Syst. Zool.* 40: 486-493.
- Bledsoe, A. H., and R. J. Raikow. 1990. A quantitative assessment of congruence between molecular and non-molecular estimates of phylogeny. *J. Mol. Evol.* 30: 247-259.
- Boorman, S. A., and D. C. Olivier. 1973. Metrics on spaces of finite trees. *J. Math. Psych.* 10: 26-59.
- Bourque, M. 1978. Arbres de Steiner et réseaux dont varie l'emplacement de certains sommets. Ph.D. thesis, Département d'Informatique et de Recherche Opérationnelle, Université de Montréal, Quebec, Canada [not seen].
- Bremer, K. 1990. Combinable component consensus. *Cladistics* 6: 369-372.
- Brown, E. K., and W. H. E. Day. 1984. A computationally efficient approximation to the nearest neighbor interchange metric. *J. Classif.* 1:93-124.
- Day, W. H. E. 1985. Optimal algorithms for comparing trees with labeled leaves. *J. Classif.* 1:7-28.
- Day, W. H. E. 1986. Analysis of quartet dissimilarity measures between undirected phylogenetic trees. *Syst. Zool.* 35: 325-333.
- Douchette, C. R. 1985. An efficient algorithm to compute quartet dissimilarity measures. Unpubl. BSc(Hons) dissertation, Memorial Univ. Newfoundland, 58pp.
- Estabrook, G. F. 1992. Evaluating undirected positional incongruence of individual taxa between two estimates of the phylogenetic tree for a group of taxa. *Syst. Biol.* 41: 172-177.
- Estabrook, G. F., F. R. McMorris, and C. A. Meacham. 1985. Comparison of undirected phylogenetic trees based on subtrees of four evolutionary units. *Syst. Zool.* 34: 193-200.
- Felsenstein, J. 1989. PHYLIP - Phylogeny Inference Package (Version 3.2). *Cladistics* 5: 164- 166.

- Farris, J. S. 1988. Hennig86. Computer program and documentation. Port Jefferson Station, New York.
- Finden, C. R., and A. D. Gordon. 1985. Obtaining common pruned trees. *J. Classif.* 2: 255-276.
- Furnas, G. W. 1984. The generation of random, binary unordered trees. *J. Classif.* 1: 187-233.
- Goodman, M., J. Czelusniak, G. W. Moore, A. E. Romero-Herrera, and G. Matsuda. 1979. Fitting the gene lineage into its species lineage: A parsimony strategy illustrated by cladograms constructed from globin sequences. *Syst. Zool.* 28: 132-168.
- Guyer, C., and J. B. Slowinski. 1991. Comparisons of observed phylogenetic topologies with null expectations among three monophyletic lineages. *Evolution* 45: 340-350.
- Harding, E. F. 1972. The probabilities of rooted tree-shapes generated by random bifurcation. *Adv. Appl. Prob.* 3: 44-77.
- Hafner, M. S., and S. A. Nadler. 1988. Phylogenetic trees support the coevolution of parasites and their hosts. *Nature* 332: 258-259.
- Hendy, M. D., C. H. C. Little, and D. Penny. 1984. Comparing trees with pendant vertices labeled. *SIAM J. Appl. Math.* 44: 1054-1065.
- Hendy, M. D., and D. Penny. 1984. Cladograms should be called trees. *Syst. Zool.* 33: 245-247.
- Humphries, C. J., J. M. Cox, and E. S. Nielsen. 1986. *Nothofagus* and its parasites: A cladistic approach to coevolution. Pages 55-76 in: Coevolution and Systematics (A. R. Stone and D. L. Hawksworth, eds.). Clarendon Press, Oxford.
- Jarvis, J. P., J. K. Luedeman, and D. R. Shier. 1983. Comments on computing the similarity of binary trees. *J. theor. Biol.* 100: 427-433.
- Kluge, A. G. 1989. A concern for evidence and a phylogenetic hypothesis of relationships among *Epicrates* (Boidae, Serpentes). *Syst. Zool.* 38: 7-25.
- Krivánek, M. 1986. Computing the nearest neighbor interchange metric for unlabeled binary trees is NP-complete. *J. Classif.* 3: 55-60.
- Kubicka, E., G. Kubicki, and F. R. McMorris. 1992. An algorithm to find agreement subtrees. *J. Classif.* (in press).
- Lake, J. A. 1987. A rate-independent technique for analysis of nucleic acid sequences: Evolutionary parsimony. *Mol. Biol. Evol.* 4: 167-191.
- Lapointe, F.-J., and P. Legendre. 1991. The generation of random ultrametric matrices representing dendrograms. *J. Classif.* 8: 177-200.
- Livezey, B. C. 1986. A phylogenetic analysis of recent anseriform genera using morphological characters. *Auk* 103: 737-754.
- Maddison, W. P. 1989. Reconstructing character evolution on polytomous cladograms. *Cladistics* 5: 365-377.

- Maddison, W. P., and D. R. Maddison. 1992. MacClade: Interactive analysis of phylogeny and character evolution. Version 3.0. Sinauer Associates, Sunderland.
- Madsen, C. S., K. P. McHigh, and S. R. de Kloet. 1988. A partial classification of waterfowl (Anatidae) based on single-copy DNA. *Auk* 105: 452-459.
- Margush, T., and F. R. McMorris. 1981. Consensus n -trees. *Bull. Math. Biol.* 43: 239-244.
- Mickevich, M. F., and N. I. Platnick. 1989. On the information content of classifications. *Cladistics* 5: 33-47.
- Mitter, C. abd D. R. Brooks. 1983. Phylogenetic aspects of coevolution. Pages 65-98 in: Coevolution (D. J. Futuyma and M. Slatkin, eds.). Sinauer Associates, Sunderland.
- Miyamoto, M. M. 1985. Consensus cladograms and general classifications. *Cladistics* 1: 186-189.
- Nelson, G. 1979. Cladistic analysis and synthesis: Principles and definitions, with a historical note on Adanson's *Famille des Plantes* (1763-1764). *Syst. Zool.* 28: 1-21.
- Nelson, G., and N. Platnick. 1981. Systematics and biogeography: Cladistics and vicariance. Columbia University Press, New York.
- Page, R. D. M., 1988. Quantitative cladistic biogeography: Constructing and comparing area cladograms. *Syst. Zool.* 37: 274-270.
- Page, R. D. M. 1989a. Comments on component-compatibility in historical biogeography. *Cladistics* 5: 167-182.
- Page, R. D. M. 1989b. COMPONENT User's manual (Release 1.5). University of Auckland, Auckland.
- Page, R. D. M. 1990a. Component analysis: A valiant failure? *Cladistics* 6: 119-136.
- Page, R. D. M. 1990b. Temporal congruence and cladistic analysis of biogeography and cospeciation. *Syst. Zool.* 39:205-226.
- Page, R. D. M. 1991. Random dendograms and null hypotheses in cladistic biogeography. *Syst. Zool.* 40: 54-62.
- Page, R. D. M. 1992. Comments on the information content of classifications. *Cladistics* 8: 87-95.
- Page, R. D. M. 1993a. Genes, organisms, and areas: The problem of multiple lineages. *Syst. Biol.* 42: 77-84.
- Page, R. D. M., 1993b. On islands of trees and the efficacy of different methods of branch swapping. *Syst. Biol.* 42: (in press).
- Page, R. D. M. 1993c. On describing the shape of rooted and unrooted trees. *Cladistics* 9: (in press)

- Penny, D., and M. D. Hendy. 1985. The use of tree comparison metrics. *Syst. Zool.* 34: 75-82.
- Penny, D., M. D. Hendy, and M. A. Steel. 1992. Progress with methods for constructing evolutionary trees. *Trends Ecol. and Evol.* 7: 73-79.
- Robinson, D. F. 1971. Comparison of labeled trees with valency three. *J. Comb. theor.* 11: 105-119.
- Robinson, D. F., and L. R. Foulds. 1981. Comparison of phylogenetic trees. *Math. Biosci* 53: 131-147.
- Rosen, D. E. 1979. Fishes from the uplands and intermontane basins of Guatemala: Revisionary studies and comparative geography. *Bull. Amer. Mus. Nat. Hist.* 162: 267-376.
- Rohlf, F. J. 1982. Consensus indices for comparing classifications. *Math. Biosci.* 59: 131-144.
- Rohlf, F. J. 1983. Numbering binary trees with labeled terminal vertices. *Bull. Math. Biol.* 45: 33-40.
- Sanderson, M. J. 1989. Confidence limits on phylogenies: The bootstrap revisited. *Cladistics* 5: 113-129.
- Savage, H. M. 1983. The shape of evolution. *Biol. J. Linn. Soc.* 20: 225-244.
- Schrage, L. 1979. A more portable FORTRAN random number generator. *ACM Trans. Math. Software.* 5: 132-138.
- Shao, K.-T., and R. R. Sokal. 1990. Tree balance. *Syst. Zool.* 39: 266-276.
- Sidow, A., and A. C. Wilson. 1990. Compositional statistics: An improvement of evolutionary parsimony and its application to deep branches in the tree of life. *J. Mol. Evol.* 31: 51-68.
- Simberloff, D., K. L. Heck, E. D. McCoy, and E. F. Connor. 1981. There have been no statistical tests of cladistic biogeographical hypotheses. Pages 40-63 in Vicariance biogeography: A critique (G. Nelson and D. E. Rosen, eds.). Columbia Univ. Press, New York.
- Slowinski, J. B., and C. Guyer. 1989. Testing the stochasticity of patterns of organismal diversity: An improved null model. *Am. Nat.* 134: 907-921.
- Sourdis, J. 1985. A method for numbering binary rooted and unrooted phylogenies and their hypothetical taxonomic units. *Bull. Math. Biol.* 47: 535-543.
- Sourdis, J., and C. Krimbas. 1987. Accuracy of phylogenetic trees estimated from DNA sequence data. *Mol. Biol. Evol.* 4: 159-166.
- Steel, M. 1992. The complexity of reconstructing trees from qualitative characters and subtrees. *J. Classif.* 9: 91-116.
- Swofford, D. L. 1990. PAUP: Phylogenetic Analysis Using Parsimony, version 3.0. Illinois Natural History Survey, Champaign.

- Swofford, D. L. 1991. When are phylogeny estimates from molecular and morphological data incongruent? Pages 295-333 in: Phylogenetic analysis of DNA sequences (M. M. Miyamoto and J. Cracraft, eds.). Academic Press, New York.
- Tolson, P. J. 1987. Phylogenetics of the boid snake genus *Epicrates* and Caribbean vicariance theory. *Occ. Papers Mus. Zool., Univ. Michigan* 715: 1-68.
- Waterman, M. S., and T. F. Smith. 1978. On the similarity of dendograms. *J. theor. Biol.* 73: 789-800.
- Zandee, M., and M. C. Roos. 1987. Component-compatibility in historical biogeography. *Cladistics* 3: 305-332.