Grandcolas, P. 2004. Abstracts of the 23rd Annual Meeting of the Willi Hennig Society. "Phylogenetics and Evolutionary Biology". Cladistics 20: 583-608.

"The 23rd annual meeting of the Willi Hennig Society took place in Paris with the support of Muséum national d'Histoire naturelle and CNRS (Centre National de la recherche Scientifique), from the 18th to the 23rd of July 2004."

p. 590:

Treatment of multiple trees in resampling analyses.
Jan De Laet, Steve Farris* and Pablo Goloboff. Koninklijk Belgisch Instituut voor Natuurwetenschappen, Vautierstraat 29, B-1000 Brussels, Belgium; Molekylärsytematiska laboratoriet, Naturhistoriska riksmuseet, Box 50007 SE-104 05 Stockholm, Sweden; Instituto Superior de Entomologia 'Dr Abraham Willink', Miguel Lillo 205, 4000 S.M. de Tucumán, Argentina
When Felsenstein first used bootstrapping in phylogenetic analyses he did not discuss how to treat multiple optimal trees that might be found for a single pseudoreplicate. He subsequently introduced a method in which all optimal trees found for a pseudoreplicate are passed to the majority-rule summary tree calculation, each tree being weighted by the inverse of the number of trees found for the pseudoreplicate. While this method is still use in both PHYLIP and PAUP, no justification has ever been offered for it, and in fact it seems to have been adopted originally simply because the old PHYLIP consensus program could not process multifurcating trees. We point out here that this method is defective in that it can yield high resampling frequencies for groups that are actually unsupported by the data, and this can occur in both parsimony and likelihood analyses.