

Retraction: Measures of Clade Confidence Do Not Correlate with Accuracy of Phylogenetic Trees

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As a result of a bug in the Perl script used to compare estimated trees with true trees, the clade confidence measures were sometimes associated with the incorrect clades. The error was detected by the sharp eye of Professor Sarah P. Otto of the University of British Columbia. She noticed a discrepancy between the example tree in Figure 1B and the results reported for the gene *nuoK* in Table 1, and requested that she be sent all ten *nuoK* Bayesian trees. She painstakingly did a manual comparison of those trees with the true trees, concluded that for that dataset there was a strong correlation between clade confidence and the probability of a clade being true, and suggested the possibility of a bug in the Perl script. Dr. Otto put in considerable effort, and we want to acknowledge the generosity of that effort.

The major conclusion of our paper, as given in its title, is therefore invalid, and the paper must be retracted. It is important to stress that the responsibility for the necessity of retracting our paper is entirely mine (Barry Hall), and that my coauthor Stephen J. Salipante bears none of the responsibility. I wrote the Perl script and failed to check its accuracy sufficiently.

We have now corrected the script and reanalyzed the trees in Tables 1–6. The results show that there are strong correlations between clade confidence and the probability that a clade is valid for Bayesian posterior probabilities and for Maximum Likelihood bootstrap percentages and weaker correlations for Maximum Likelihood aLRT values. We have prepared a new paper describing this reanalysis and the results achieved and have submitted it for publication.

This retraction may be found online at doi:10.1371/journal.pcbi.0030158.

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