Dear editors,

I hope that you will consider this submission, Bartering accuracy and precision to obtain informative phylogenetic reconstructions, for publication as a Research Article in Biology Letters.

The effectiveness of morphological phylogenetic methods is a topic of great importance, and has recently attracted much attention. Most recent studies rate competing methods (notably probabilistic and parsimony-based approaches) based on Robinson-Foulds distances between trees, a measure of accuracy. Not only does the Robinson-Foulds metric have fundamental shortcomings, but it fails to reflect the implicit trade-off between precision and accuracy in phylogenetic reconstruction. Here I employ a quartet-based approach that identifies the relative contributions of accuracy and precision to the overall information content of a tree. Doing so provides an alternative perspective on analytical results. By re-analysing the results of two influential recent studies, I show a failure to account for both accuracy and precision has led to profoundly misleading conclusions, with important implications for phylogenetic practice.

The paper is not published or under consideration elsewhere, though an earlier draft has been posted as a preprint at BioRxiv [https://doi.org/10.1101/227942].

Thank you for considering this manuscript and I look forwards to hearing from you soon.

Martin Smith