

# COMPARISON OF WEIGHTING STRATEGIES FOR SPECIMEN-LEVEL PHYLOGENY BASED ON SKELETAL MATERIAL OF LIZARDS (SQUAMATA)

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Weighting strategies in phylogenetic analysis have been a controversial topic throughout the last few decades. Tests have been performed using both simulations and real datasets, comparing parsimony to model-based approaches with discrete morphological characters. Here, we provide a first test case of a number of weighting strategies that use a real dataset composed of morphological characters and specimen-level operational taxonomic units represented by skeletons of lacertilians, with the genus *Lacerta* as the ingroup. We compare the results from analyses under equal weighting, implied weighting with different k-values, and extended implied weighting with the same k-values as used with traditional implied weighting. Tree accuracy was tested based on the number of specimens of a known biological species that actually formed a monophyletic clade and relative length increase to constrained trees. Our results show that the analyses run under both extended and traditional implied weighting recovered better-resolved trees than the analysis under equal weighting. Also, tree accuracy was generally higher when the characters were weighted, especially when using higher k-values (between 10 and 50), representing a weaker downweighting of homoplastic characters. Our data highlight the advantages of implied weighting over equal weights for the specimen-level phylogeny in terms of tree resolution and recognition of species clades. Considering that many fossil vertebrate species are represented by single specimens, extended or traditional implied weighting (with a high k-value) appear to be the best strategies to find the more accurate trees when using parsimony.