

Approaches to Phylogenetic Inference Based on Morphological Data Applied to the Palaeontology of Geoemydid Turtles (Cryptodira: Testudinoidea)

Eduardo Ascarrunz

The clade Geoemydidae (Cryptodira: Testudinoidea) is comprised of ca. 70 species of living turtles and a rich fossil record that goes back to the Eocene. The phylogenetic relationships of the Paleogene species in this record remain unclear, as progress in their study has been hampered by the low amounts of phylogenetic information that could be gathered from the morphology of geoemydid shells. Here I present an exploration of different approaches to the collection and analysis of morphological characters that go beyond traditional practice in systematic palaeontology, and assess their reliability with comparisons against phylogenies inferred from molecular data. The approaches include character coding techniques that incorporate information about the frequencies of the observed states, and the use of continuous characters in various forms: the analysis of three-dimensional coordinates of homologous landmarks with different methods (linear parsimony, the new spatial parsimony, squared-change parsimony, maximum likelihood with a Brownian motion model, and neighbour-joining of Euclidean distances), and the analysis of ratios of measurements alone and in combination with discrete characters, also with diverse methods such as implied-weights linear parsimony, simple Brownian motion models with maximum likelihood and Bayesian inference. I also attempted to implement more complex Bayesian models that combine ratios with discrete characters, but this more ambitious project did not succeed.

None of the approaches sufficed for the reliable estimation of the phylogeny of all geoemydids, but better results can be obtained by using a reference tree with an approach called “phylogenetic placement”. In this approach, the morphological information is not used in the estimation of the entire tree. Instead, a reliable tree with extant species is used as a fixed base on which the phylogenetic positions of the fossils is estimated from the morphological characters. I used a procedure similar to leave-one-out cross-validation for quantifying the performance of this kind of analysis. Thus evaluated, phylogenetic placement with ratios and discrete characters yields good results.

Finally, I used ratios and discrete characters in the phylogenetic analysis of two morphotypes from the Eocene of Messel, Germany. I found middling support for a new hypothesis where the Messel geoemydids are sister to *Geoemyda* or a previous hypothesis where they fall in a clade formed by *Malayemys* and *Orlitia*. A close relationship with the turtles in the clade *Mauremys* is not well-supported, undermining the influential hypothesis of the “*Palaeochelys sensu lato* – *Mauremys*” group.

I conclude that the techniques used in this work are practical and useful, and will often be more appropriate than the traditional approaches for many phenotypes.

Jury:

Prof. Dr. Walter G. Joyce (thesis supervisor)
Prof. Dr. Julien Claude (external co-examiner)
Dr. Márton Rabi (external co-examiner)
Prof. Dr. Olivier Graefe (president of the jury)