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SÉMINAIRE

Dating phylogenies with incompletely preserved fossils

Fredrik Ronquist

Department of Biodiversity Informatics, Swedish Museum of Natural History, Stockholm, Sweden

In recent years, evolutionary biologists have become increasingly interested in dating phylogenies. This is usually accomplished by calibrating interior nodes in the tree against the fossil record, an ad hoc approach with a considerable risk of misrepresenting the fossil information. I discuss an alternative approach, in which fossils are included along with extant taxa in a Bayesian total-evidence analysis. By coding morphological characters for both extant and extinct taxa, it is possible to explicitly integrate over the uncertainty in the placement of individual fossils, while using their ages to date the tree. In such a total-evidence analysis of the early radiation of the Hymenoptera (wasps, ants and bees), we showed that fossils contributed significantly to the estimation of divergence times, despite considerable uncertainty in their placement. The posterior distributions on divergence times were less sensitive to prior assumptions and tended to be more precise than in standard node dating. The total-evidence analysis also showed that four of the seven Hymenoptera calibration points used in node dating were based on erroneous or doubtful assumptions about fossil placement. One of the most important advantages of total-evidence dating over node dating is that it provides a better platform for further modeling of important aspects, such as the fossilization process and the sampling of extinct and extant taxa. We are currently exploring such extensions of the basic model.