

Assessment of mode of extinction and recovery based on changes in morphospace and species-abundance relationship

UBUKATA, Takao^{1*}

¹Kyoto University

Morphological disparity has been attracting attention as a clue for understanding mode of mass extinction because selective extinctions readily reduce the disparity than do random extinctions. In recent years, changes in morphospace occupation are also used to assess selectivity of extinction and subsequent recovery. However, hitherto approaches to this subject have been based on among-species variation and have omitted abundance of each species. Recent developments of database systems such as the Paleobiology Database allow us to utilize data of collection-based occurrences as a proxy of abundance of each species. Here I would propose a method to determine which model of extinction and recovery best explains the observed data on species-abundance relationship as well as on the patterns of morphospace occupation. In the present method, the mode of mass extinction and subsequent recovery is categorized into three models: 1) random extinction and random recovery, 2) selective extinction and random recovery and 3) selective extinction and selective recovery. The method is based on a statistical model selection in which each model is rated in terms of congruence with observed data according to an information criterion. Likelihood functions are computed for various model conditions through simulations of extinction and origination. Prior to the simulations, the morphological values and the number of fossil occurrences are provided for each species through measurements and tabulation of database information. In the simulation of mass extinction, a given percentage of actual occurrences are stochastically removed from the morphospace. In the case of selective extinction, fitness is defined as a function of a morphological variable to determine the probability of removal for each occurrence with a value of the variable. The recovery process is simulated by adding new hypothetical occurrences to the morphospace such that the total number of species is same as the actual data. An addition of new occurrence originates a new species or just increases abundance of a preexisting species randomly chosen. In the former case, morphological values of the new species are stochastically determined so that the new species is located in the neighborhood of the ancestral species in the morphospace. In the selective recovery model, the fitness function defined above also determines where a new occurrence is likely to be introduced in the morphospace. Maximum-likelihood estimation of model parameters requires vast number of simulations with various conditions for each model. In order to select the best model among the three scenarios, the present method refers to the Akaike Information Criterion and its modified version for a small sample sizes.

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