

Multiple ecological pathways to extinction in mammals

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As human population and resource demands continue to grow, biodiversity conservation has never been more critical. About one-quarter of all mammals are in danger of extinction, and more than half of all mammal populations are in decline. A major priority for conservation science is to understand the ecological traits that predict extinction risk and the interactions among those predictors that make certain species more vulnerable than others. Here, using a new database of nearly 4,500 mammal species, we use decision-tree models to quantify the multiple interacting factors associated with extinction risk. We show that the correlates of extinction risk vary widely across mammals and that there are unique pathways to extinction for species with different lifestyles and combinations of traits. We find that risk is relative and that all kinds of mammals, across all body sizes, can be at risk depending on their specific ecologies. Our results increase the understanding of extinction processes, generate simple rules of thumb that identify species at greatest risk, and highlight the potential of decision-tree analyses to inform conservation efforts.

conservation | biodiversity | body size | IUCN Red List | decision tree

Certain ecological traits, such as small geographic range, low population density, slow life history, and large body size are known to correlate strongly with extinction risk in mammals, and the importance of these traits can vary among different clades of mammals (1–5). Large body size, in particular, is a well-known predictor of both past and present human-related extinctions (4, 6, 7). Although the identification of these correlates of extinction has been an important first step in guiding conservation priorities, it is critical to understand how multiple ecological factors interact to predict risk across species that differ by orders of magnitude in body size, area of geographic range, abundance, life history, niche characteristics, and other traits. For example, it is not enough to know that species with small geographic ranges tend to be at greater risk; rather, we need to know how range size interacts with other ecological traits to make certain species with small ranges more vulnerable than others. By understanding how multiple key ecological predictors interact, we are able to identify the species at greatest risk and also to understand what makes them vulnerable. Additionally, to help avert the losses of populations and species of mammals (8–10), there is a real need for conservation scientists to provide results that are directly relevant and are easily interpretable for conservation practice. In this paper, we draw on a large dataset and methodological approach to build on current knowledge of extinction risk in mammals. Using a decision-tree modeling framework we (*i*) identify interactions among multiple ecological traits that lead to different pathways to extinction across mammals and (*ii*) use our model to codify simple rules of thumb that can be used to guide conservation.

Decision-Tree Modeling Approach. Although decision trees have been used previously in ecology, their application to conservation biology has been limited (11–15). The decision-tree approach is a powerful alternative to traditional linear models and

has documented advantages for extinction risk analyses, especially when the goal is predictive accuracy (14–16). Decision-tree models are designed to identify nonlinear, context-dependent associations among multiple correlated predictor variables (11, 14–17). They require fewer assumptions than correlational methods and do not assume a specific distribution of predictor variables. Further, they do not assume data independence, avoiding potential concerns about pseudoreplication and alleviating the need for explicit phylogenetic control (16, 18). In decision trees, the same predictor variables may reappear repeatedly in the model as necessary, a fundamental difference from the single-predictor variables of linear models. Consequently, the explanatory power of a predictor variable is not conflated by how many species share a particular trait value because of shared evolutionary history. Instead, the model quantifies the association of predictors and response variables on a species-by-species basis. Because decision trees predict outcomes of interest (i.e., extinction or survival) based on the nested internal structure of the predictor variables, they may provide a more accurate predictive framework for extinction risk than traditional parametric approaches. Whereas previous studies of mammalian extinction risk have addressed the interactions of variables in linear models (1, 4, 19), decision-tree analyses offer a major advance, because they reveal both how the interactions between predictors lead to the outcomes of interest and also how these interactions differ among subsets of the data (14). In contrast, linear models can indicate only whether a particular interaction is statistically significant over the entire dataset. This added insight into the context-dependence of interactions is a major advantage of decision-tree models. Finally, decision-tree analyses produce graphical outputs that quantify and summarize the interactions in a visual, easily interpretable format (14, 17). Because decision-tree models can be sensitive to small changes in the underlying data, we also used a random forest, a modeling technique that combines the predictions of many independent decision-tree models into a robust composite model (20).

Results and Discussion

The random forest model classified mammal threat status with 82% accuracy [percent correctly classified (PCC), Cohen's kappa = 0.44, $P < 0.001$; [supporting information \(SI\) Table S1](#)], based solely on ecological traits. It identified 8 major predictors of extinction risk: small geographic range, low population density, small group size, slow production rate, large home range, large body size, habitat mode, and activity period (Fig. 1). These predictors were intercorrelated ([Table S2](#)), and most have been

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