



Making biodiversity discovery more efficient: An exploratory test using Mexican birds

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Abstract

Recent studies have explored the possible utility of ecological niche modeling as a tool for species discovery, with promising initial results, but no detailed test has as-yet evaluated the success or failure rates of the method. We use a comprehensive distributional summary for the birds of Mexico to develop a test, in which well-known and broadly-distributed species are used to predict the distributional areas of poorly-known congener species. The results indicated that all of the ‘unknown’ species chosen for testing were predicted significantly better than random expectations by the ecological characteristics of at least one well-known congener species. These results bode well for broader applications of using biodiversity informatics tools to guide species discovery, but further testing and development of protocols is still needed.

Key words: ecological niche models, model predictivity, species discovery, distribution, Aves

Introduction

The challenges remaining for discovering and describing biological diversity are considerable (Wilson, 1988). Although some taxonomic groups remain largely undescribed (Erwin, 1991), others, such as birds, mammals, diurnal butterflies, reptiles, and amphibians, are now mostly documented (Kelly, 2000; Peterson, 1998)—what remains are generally rare or isolated local endemics, or are forms that are only subtly different from known species. As such, the challenge for ‘finishing’ the global inventory of species in such groups consists of survey and inventory efforts in the most remote and inaccessible areas, and of detailed taxonomic study of what specimen material is available.

One publication (Raxworthy, et al., 2003) explored the use of ecological niche models as a predictive guide for searches for unknown elements of biodiversity, using niche profiles of known chameleon species to anticipate the distributional characteristics of 7 unknown chameleon species. The idea underlying this work is the observation that ecological niches are conserved across evolutionary time periods (Peterson, et al., 1999); this initial result has seen both support (Kozak & Wiens, 2006; Peterson, 2003) and non-support (Graham, et al., 2004; Knouft, et al., 2006; Peterson & Holt, 2003) in subsequent analyses. Nonetheless, at least when niche conservatism exists, ecological niche models can be developed for known species, and their predictions of apparently suitable—but uninhabited—areas can be flagged as areas of particular interest for surveys. Such suitable areas may be inhabited by an unknown sister species (or other close relative) or an unknown population of the same species (Bourg, et al., 2005; Jarvis, et al., 2005), or may be uninhabited for reasons of history (i.e., dispersal limitation) or species’ interactions or extinction (Kambhampati & Peterson, 2007). Similarly, niche models offer the opportunity to discover cryptic species that may be geographically isolated and/or ecologically differentiated from other populations of the same ‘species’ (Raxworthy, et al., 2007; Wiens, 2007; Wiens & Graham, 2005).