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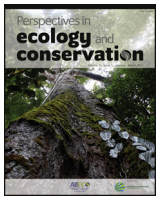

Essays and Perspectives

Where to release birds seized from illegal traffic? The value of vocal analyses and ecological niche modeling

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ABSTRACT

The principal strategy used to deal with animals recovered from trafficking operations is to release them back into nature. Our goal was to test the feasibility of using vocalizations to determine the origins of the recovered birds. We used ecological niche modeling to predict the potential distributions of four species: *Crypturellus soui*, *Diopsittaca nobilis, Sicalis flaveola*, and *Thamnophilus doliatus*. Modeling was performed with MaxEnt, which uses geographic coordinates from known specimens and local abiotic variables. To test the resulting model, we examined whether the vocalizations could be correctly classified into generated patches using a multinomial regression. An efficient call classification would support the niche models and indicate the existence of a spatial acoustic structure that could be used to determine a bird's geographic origin. The models adjusted well to our data, giving AUC values between 0.88 and 0.94. While *T. doliatus* calls showed a clear acoustical structure in which the majority of their calls were correctly classified among the model patches, the three remaining test species presented intermediate patterns in which only calls from a single patch were correctly classified. The method appears to be best applied to species not demonstrating vocal learning, despite the fact that the calls of *C. soui* showed intermediate effectiveness in classifying their origins. While vocal plasticity could lead to low classification efficiency, it also may aid the re-adaptation of reintroduced birds, making our methodology efficient when it matters the most, or when the cost of releasing individual birds outside of their original ranges would be high.

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Introduction

Wildlife trafficking is one of the largest and most profitable illegal activity in the world, ranking only behind illegal weapons and drugs. It is estimated that this commerce generates from 10 to 20 billion dollars annually (RENCTAS, 2002), with birds being among the main contraband items. Over 2600 bird species (27% of all existing species) were recorded in international trade documents between 1970 and 1990 (Gulx et al., 1997). In Brazil there are at least 295 bird species currently being traded as pets (Nobrega Alves et al., 2013), and 130 species in Peru (Daut et al., 2015). Wildlife commerce has largely contributed to the extinction of the Glaucous Macaw *Anodorhynchus glaucus* and Spix's Macaw *Cyanopsitta spixii* (Marini and Garcia, 2005), and certainly exerts negative pressures on wild populations of other bird species. In fact, habitat destruction and animal trafficking are two of the main factors influencing bird extinctions (Marini and Garcia, 2005).

Concerns about the impact of wildlife trade united 80 countries in 1973 in establishing rules to control and regulate the commerce of wildlife species, which resulted in the Convention on International Trade in Endangered Species of Wild Fauna and Flora – CITES. Many governments (including Brazil) have gone well beyond CITES, prohibiting all wild animal trade within their national territories. Governmental agencies in these countries (such as IBAMA in Brazil) invest human and monetary resources in surveillance to arrest illegal dealers and rescue animals, including birds. As a consequence of these actions, a single small facility designed to receive apprehended birds (CETAS) in Paraiba State receives 5000 animals annually! If, on the one hand, these measures have long-term inhibiting effects on the illegal trade in animals and can reduce negative impacts on the local fauna – they can also lead to short-term problems, such as what should IBAMA do with all the birds it seizes from wildlife traffickers?

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In light of the ethical issues involved, there are only three basic ways to handle recovered birds: (1) return them to their natural habitats; (2) keep them in captivity; or, (3) sacrifice them (IUCN, 2000). Returning them to nature is by far the most widely used strategy, and is most often adopted by wildlife regulatory and management agencies. When not carried out properly, however, this option brings little benefit to the birds involved – and can even harm local bird populations (Efe et al., 2006; Marini and Garcia, 2005). Side effects include high mortality rates of the released animals, the risk of invasive situations, the transmission of diseases and parasites, and the hybridization of otherwise genetically distinct races or subspecies (IUCN, 2000).

In spite of the difficulties involved in identifying the populations of origin (or subspecies) to which recovered individuals belong, returning seized birds to nature represents the most appropriate option, as it would allow them to fulfill their biological role. If, however, these birds are released outside of their original population ranges they may compromise native populations through the introduction of exotic genes. Evolution can be defined as a dynamic process in which the proportions of specific genes change within a population over time. Thus, although present in other populations of the same species, the introduction of geographically exotic genes may compromise the delicate evolutionary history of a local population and act against the conservation of unique historical evolutionary processes.

In order to truly safeguard the genetic lineages of birds, one must determine the origins of captured individuals before releasing them. With this in mind, the Brazilian Institute of the Environment and Renewable Natural Resources (IBAMA, 2008) determined that recovered specimens could only be reintroduced into the natural environment if the original capture site was known. Considering that evolutionary processes occur locally and result in local genetic differences, there is an urgent need for methodologies capable of efficiently and inexpensively determining the origins of birds recovered from illegal traders. Such methods would avoid the continued confinement or useless sacrifice of captured birds and promote their release back into the wild. The use of genetic markers is not currently feasible because of a lack of genetic data on most wild bird populations, the fact that genetic characterizations require invasive procedures, and because the genetic characterization of a species throughout its distribution range would be very expensive. For these reasons, it is not yet possible to use large-scale genetic information to determine the geographical origins of individual birds.

Although a genetic approach is not currently feasible for determining release locations, ecological considerations offer a promising option for determining the spatial distributions of many organisms. It has been known for some time that different species use different portions of any given environment because of habitat differences or past competition (Elton, 1927). These spaces are called niches, and can be defined as the multivariate space in which a given species persists (Hutchinson, 1957). Once it has been recognized that the environment in any geographic space is spatially heterogeneous, it is reasonable to conclude that different species will occupy different portions of it – being ultimately determined by biotic or abiotic environment characteristics (see a review in Soberón and Nakamura, 2009). If we can understand how habitats are used by a species, we may have a handle on potential areas to release recovered birds.

The distribution of a species can now be estimated based on environmental niche characteristics. Ecological Niche Modeling uses the locations of known occurrences of a target species to model its environmental niche – and then uses that model to project its potential geographical distribution (Costa et al., 2008; Costa and Schlupp, 2010; Marini et al., 2010; Pearson and Dawson, 2003; Peterson, 2003, 2001; Peterson et al., 2002, 2007; Peterson and Kluza, 2005). The areas of high probability pointed out by ENM represent places in which the climate is most favorable to the target species. The distribution of suitable habitats, as well as how those habitats are isolated from one another, are the cornerstones of evolutionary divergence (Schluter, 2000), as environmental isolation should produce morphological, genetic and/or acoustical differences among populations.

Although it is possible to use both genetic and morphological data to assess differences between isolated populations, the use of acoustical data may also represent a promising approach as: (1) there are large amounts of accumulated data currently available online (approximately 170,000 recordings of South American Birds; de Araújo and Marques, 2013) that can be easily accessed from the websites of the Macaulay Library, Fonoteca Neotropical Jacques Vielliard, Xenocanto, or Wikiaves; (2) acoustical methods are minimally intrusive, with no necessity of handling or capturing any bird (in the wild or in captivity); (3) acoustical analytical methods are easily implemented in software such as R or Raven; and, (4) the costs of recovering and storing bioacoustic data are much lower than the costs required for acquiring and holding specimens, skins, or genetic data.

Considering the Brazilian scenario, we propose here: (1) to use the geographical coordinates of known occurrences of target species to build hypothetical geographical population structures based on ENM; (2) use bioacoustics to test the validity of those ENM predictions; and, (3) determine if there is enough information contained in bird calls to allow the geographic identification of captured specimens. Although this paper restricts itself to Brazil, we believe many countries that prohibit illegal trading in birds face similar problems, so that this methodology may offer an inexpensive and efficient alternative to identifying the origins of recovered birds and allow their successful release to nature.

Materials and methods

Target species

Four species were chosen based on their phylogenies and call characteristics: *Diopsittaca nobilis* (non-Passeriformes) and *Sicalis flaveola* (oscines-Passeriformes), whose vocalizations show greater influences of learning components, and *Crypturellus soui* (non-Passeriformes) and *Thamnophilus doliatus* (Suboscines-Passeriformes), whose vocalizations show strong genetic components (*sensu* Marler, 2004). These species have wide distributions with favorable spatial structures for this type of investigation (several suitable habitat patches surrounded by unsuitable environments), and sound recordings are available for them.

C. soui belongs to the family Tinamidae. It inhabits both humid and dry environments, such as the edges of dense forests, dry forests, sandbanks, etc. It occurs from Mexico to Bolivia and Brazil (including the states of Espirito Santo, Rio de Janeiro, Minas Gerais, and Mato Grosso). These birds are adapted to terrestrial life, and their flights tend to be short and heavy. Their song is composed of a mild chirp with a tremulous tone with rising long sequences and descending whistles (Sick, 1997; Fig. 2). The learning component of the Tinamidae call is virtually nonexistent (Bertelli and Tubaro, 2002).

D. nobilis belongs to the family Psittacidae. It has a wide distribution that includes Venezuela, Suriname, Guyana, and Brazil (Mato Grosso State) to Bolivia, inhabiting savanna formations and forest borders (Collar, 1997; Sick, 1997). Most parrots have large vocal repertoires (de Araújo et al., 2011; de Moura et al., 2011), and we selected the flight call of this species (sensu Moura et al., 2011) for the study because it encodes species-specific information (de Araújo, 2011; de Araújo et al., 2011). The flight call of *D. nobilis*

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