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Generalizing and transferring spatial models: A case study to predict Eurasian badger abundance in Atlantic Spain

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ABSTRACT

Even when spatially explicit models are published in accessible international journals, they are rarely reused by the scientific community. This is unfortunate, as these models contain useful information to develop further research and to support decision-making policies. In the absence of a major study on Eurasian badger (*Meles meles*) abundance in Atlantic Spain, and given the potential role of this species in *Mycobacterium bovis* epidemiology, we aimed to predict broad-scale badger abundance by generalizing published models for sett suitability within the UK (one calibrated for Northern Ireland and another one for England and Wales). The UK models used fine-resolution environmental predictors that were not available for Spain. Thus, we generalized the models using the outputs of the published models as response variables and calibrated new models using broad-scale environmental predictors. The new model derived from that for Northern Ireland accurately predicted the badger abundance (field data for 48 1 km × 1 km squares in 12 localities) in Atlantic Spain, and indicated a high potential for the species in lowland pastoral areas. The mean density of badgers in the study area was 3.81 adults/km^2 (3.0 ± 1.3 adults/group), which is higher than in Mediterranean areas in Spain, but lower than in some areas in England where badgers contribute to *M. bovis* maintenance. We provide the first example of generalization of published spatial models, and confirm that this procedure allows for more efficient use of research funding, by generating new information of relevance, in this case study, for badger management and for understanding *M. bovis* epidemiology in Atlantic Spain.

1. Introduction

Spatially explicit statistical models have helped to understand the patterns of biodiversity, and are a particularly useful framework upon which conservation and management strategies can be developed. The key factors regulating a given ecological pattern can be quantified and parameterized using inductive and deductive procedures. Then, by applying the models in geographical space, predictions of species distributions and population abundances can be cartographically represented (Guisan and Zimmerman, 2000). These kind of models are now relevant tools for biodiversity conservation and management (Barbosa et al., 2010; Guisan et al., 2013), and substantial efforts are being devoted to establish both the conceptual framework and the analytical procedures behind the spatial modelling (Jiménez-Valverde et al., 2008; Elith et al., 2010; Acevedo et al., 2012).

Spatial models can be transferred in space and/or time (Randin et al., 2006; Barbosa et al., 2009). This is typically done to assess the effects of simulated environmental changes on species distribution (Peterson et al., 2002; Acevedo et al., 2011). However, the creation of a model and its transference are usually included in the same study system. Even when models are clearly reported in scientific publications, they are rarely exploited by other research groups. This is unfortunate, as these models contain useful information that could be used to develop further research and to support decision-making policies in new scenarios. This is currently a particularly important topic given the social context of severe cuts in budget for research in European countries such as Spain (Pain, 2012). Under these conditions, the reuse of previously published models in a critical way (involving the model's assessment), is an economical way to develop further research by using previous investments.

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An example of a situation in which the transference of a spatial model would be helpful, is in the management of the Eurasian badger (*Meles meles*) and bovine tuberculosis (bTB) in Spain. The badger is considered the most relevant wild reservoir of *Mycobacterium bovis*, the main causal agent for bTB, in the United Kingdom (UK) (Bourne et al., 2007) and the Republic of Ireland (Griffin et al., 2005). Infection of cattle by bTB is a major concern and causes severe economic loss to the livestock industry in many countries (Zinsstag et al., 2006). The effectiveness of national disease eradication programmes partially depends on the wildlife host' ecology (Gortázar et al., 2012), but also on other factors related to livestock (Gilbert et al., 2005). Given the relevance of badgers for bTB epidemiology in the UK, a significant body of scientific research exists on badgers and bTB (Bourne et al., 2007). Under this epidemiological framework, reliable estimates for badger population abundance were demanded in order to establish the basis on which management schemes for both species and potential diseases could be sustained. Thus, in the UK relevant funding was invested in studies on badger ecology, from which badger population abundance was estimated at local scales (Tuyttens et al., 2001), and its distribution pattern modelled at broad spatial scales (Etherington et al., 2009; Reid et al., 2012).

In Spain the relevance of badgers for bTB was recently pointed out in some northern areas: 12.4% *M. bovis* positive badgers were detected by bacteriology and histopathology (Balseiro et al., 2011), and shared isolates between cattle and badgers were found at some localities (Balseiro et al., 2013). Currently, only weak evidence on the role of badgers in bTB epidemiology in Spain exists. However, given the increasing trend of badger populations in Spain (Sobrino et al., 2009) and the role of badgers in bTB epidemiology in UK and the Republic of Ireland (Griffin et al., 2005; Bourne et al., 2007), the last bTB task force in Spain advised that baseline values of species abundance should be established (www.ec.europa.eu/food/animal/diseases/docs/tb_subgroup_spain_oct2012_en.pdf). In the absence of a major field study on badger abundance in Atlantic Spain, and given the severe cuts in budget for research in this country, this paper aims to reuse the spatial models of badger sett suitability for England and Wales (Etherington et al., 2009) and for Northern Ireland (Reid et al., 2012) in order to predict badger abundance in Asturias province (Atlantic Spain). Two secondary objectives emerged: (i) to carry out field work in Asturias to determine badger sett abundance to conduct an independent validation of the model predictions; and (ii) to measure badger group size and the distance between different main setts for a more in depth characterization of badger population status in this territory. The resulting information, besides being of interest for badger management and conservation, could help in the understanding of potential transmission of *M. bovis* between badgers and livestock.

2. Methods

Two regions were considered in this study (Fig. 1): (i) parts of the UK where the new statistical models for predicting badger sett suitability were calibrated (training areas), and (ii) Asturias province, in Atlantic Spain, where the new models were transferred and assessed with data from field work (evaluation area).

2.1. Analytical design: generalizing and transferring the statistical models

The starting point of this study was the predictive spatial models of badger sett suitability for Northern Ireland (Reid et al., 2012), and for England and Wales (Etherington et al., 2009), referred to as the original models hereafter. Based on well designed field

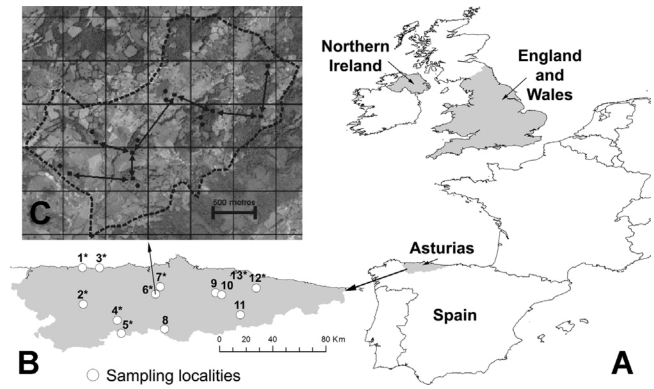

Fig. 1. (a) Location of the three study territories (in grey), the training areas (Northern Ireland and England & Wales) and the evaluation area (Asturias). (b) Detail of sampling localities in the evaluation area. (c) Schematic representation of one of the sampled localities (400 ha). Main setts (black squares), secondary setts (black circles) and distance between main setts (arrows) were determined within the sampling area (dashed line) that was delimited by roads. Sampling localities; 1: Otur, 2: Allande, 3: Busto, 4: Somiedo-Cores, 5: Somiedo-Puerto, 6: Grado, 7: Las Regueras, 8: Puerto Agueria, 9: Nava-Lieres, 10: Nava-Fuensanta, 11: Caso, 12: Pares. *Trapping areas, including Villaviciosa (13) that was not selecting for sampling setts.

surveys and a large amount of data, Reid et al. (2012) and Etherington et al. (2009) modelled the distribution and abundance of badger setts. The original models aimed to predict sett suitability and main sett density, in a broad sense, which has been used as a surrogate of badger relative abundance assuming one social group per main sett (Clements et al., 1988; MacDonald et al., 1996). But the original models used fine-resolution environmental variables as predictors that were only available for the UK (see Appendix A in the Supplementary Material for further descriptions). Thus, the first step required to transfer the original models to Asturias was the calibration of new models by using broad-scale environmental predictors that were also available for the evaluation area, i.e., the generalization of these models.

In the absence of the raw data from field work on badger abundance in the UK, we opted for a novel approach for generalizing the original models (Fig. 2). The outputs – i.e., suitability values – of the original models in UK were used as the response variables to calibrate new models (one for Northern Ireland [NI model hereafter], another for England and Wales [EW model hereafter] and one more pooling both datasets [NIEW model hereafter]) using broad-scale available databases as predictors. Thus, in contrast to the

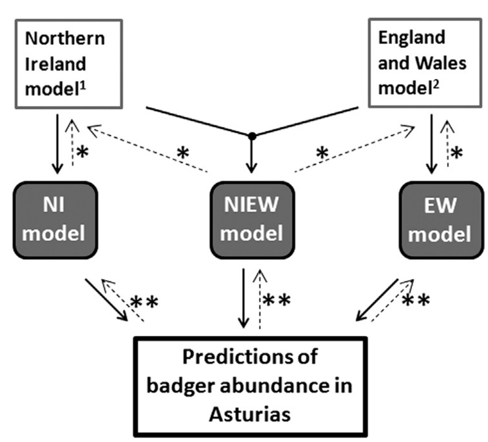

Fig. 2. Schematic representation of the analytical design for the generalization of models on badgers abundance in Northern Ireland ([1] Reid et al., 2012) in England and Wales ([2] Etherington et al., 2009). New models (NI, EW and NIEW; see text for details) predictive performance (dashed arrows) were assessed on independent datasets in the training areas (*) and on field data in the evaluation area Asturias (**).