Biological Conservation 152 (2012) 102–109

Contents lists available at SciVerse ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

# Species-specific habitat fragmentation assessment, considering the ecological niche requirements and dispersal capability

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ARTICLE INFO

*Article history:*
Received 10 September 2011
Received in revised form 16 March 2012
Accepted 5 April 2012
Available online 23 June 2012

*Keywords:*
BIOMOD
MaxEnt
Species distribution models
Habitat fragmentation
Dispersal
Galliformes
China

ABSTRACT

Habitat fragmentation assessment is quite important for the endangered risk assessing and conservation management for threatened animals. Note that even sympatric species may differ in habitat fragmentation, due to the various ecological niche requirements and dispersal capabilities. We therefore develop an integrated method for assessing the habitat fragmentation that combines habitat suitability with dispersal distance data to assess the patch isolation, within-patch fragmentation and identify the functional habitat fragmentation categories. Specifically, the ecological niche modeling enables us to identify the species-specific suitable areas through connecting the niche requirements and distribution, which indirectly includes the effects of habitat loss and degradation. The integrated fragmentation assessments enable the conservation planners to consider not only the population isolation level in large scale, but also the spatial connectivity within-patch and different fragmentation categories for landscape conservation that would otherwise appear cryptic under more typical habitat suitability or fragmentation assessing approaches. Furthermore, these assessments cal also be applied in the quantitatively endangered status ranking.

We applied this method in two sympatric montane Galliform birds in China, Chinese Grouse (*Bonasa sewerzowi*) and Blood Pheasant (*Ithaginis cruentus*) for comparison and illustration purpose. Generally, the suitable areas of Chinese Grouse were predicted to be significantly smaller than that of Blood Pheasant. The habitat of Chinese Grouse was also more severely fragmented than the Blood Pheasant through both scales of patch isolation and within-patch fragmentation. We therefore suggest that the Chinese Grouse should be even more threatened than previously considered.

## 1. Introduction

Effective conservation of wildlife populations requires an appropriate assessment of how habitat fragmentation influences the spatial patterns of habitat occupancy across landscapes (Hernandez et al., 2006). Fragmentation assessments often employ simple spatial landscape indices such as fractal dimensions (Milne, 1991) and shape index (Forman and Godron, 1986) of habitat patches, to identify suitable habitat species conservation. More recent studies have developed landscape-wide habitat suitability models to identify priority conservation areas for species threatened by fragmentation (Fouquet et al., 2010; Hu et al., 2010; Torres et al., 2010). However, such models often fail to recognize that different landscape components, such as forest Interior habitat, the forest-matrix edge, presence of small habitat patches, and the spatial configuration of habitat patches, often vary in their functional role for different wildlife populations.

Fewer studies have utilized key ecological traits such as dispersal capacity (Bélisle, 2005) to develop a more integrated method to assess species-specific responses to habitat fragmentation. Dispersal capacity is a major source of uncertainty for predicting future range shifts for species (Barbet-Massin et al., 2012) but plays a significant role in determining species distributions in relation to the distribution of suitable habitat (Pulliam, 2000) and population persistence within fragmented landscapes (Lens et al., 2002). Movements by animals between habitat patches are often limited by the distance between patches and the 'permeability' of the surrounding matrix (Fischer and Lindenmayer, 2002; Fischer et al., 2005). Consequently, species are often absent from the suitable habitat irrespective of their availability. The ability to assess habitat fragmentation effectively therefore requires developing appropriate species distribution models that specifically couple the dispersal capabilities of species to the surrounding landscape.

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0006-3207/$ - see front matter © 2012 Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biocon.2012.04.004

MaxEnt software (Phillips et al., 2006) has increasingly been used in recent years to model species distributions across fragmented landscapes and assess the impacts of habitat fragmentation. Numerous studies have suggested that this maximum entropy modeling framework MaxEnt consistently outperform other methods (e.g. Elith et al., 2006; Tsoar et al., 2007; Williams et al., 2009), exhibiting a good trade-off between model performance and data characteristics (Phillips and Dudik, 2008; Torres et al., 2010). Despite this general consensus, many of these comparative studies fail to evaluate important attributes such as model transferability, climate equilibrium of the species being modeled, or sources of uncertainty such as dispersal capacity. Instead, there appears to be a tendency of using combined predictions under the ‘ensemble forecasting approach’ proposed by Araújo and New (2007). A more robust approach to assess the impacts of habitat fragmentation would be to model species distributions using different modeling algorithms whilst also integrating dispersal data of the target species. This would enable conservation biologists to evaluate differences among the different models and combining projections to obtain a consensus projection.

Here we develop an integrated method to assess species-specific responses to habitat fragmentation. We model the potential distribution of two endangered bird species inhabiting highly fragmented montane forest landscapes using different modeling algorithms and apply a restriction to these models provided by field data on species dispersal capabilities. We first determine the most appropriate modeling algorithms and utilize these to identify the largest portions of suitable habitat for both target species. Second, we evaluate within-patch fragmentation distribution under both species predicted ranges. We infer that this assessment method is one that could be potentially applied to many different species, given that species-specific dispersal distances would be readily available.

## 2. Materials and methods

We created habitat suitability models for two sympatric montane Galliforme species occurring within the recognized political boundaries of China: Chinese Grouse (*B. sewerzowi*) and Blood Pheasant (*I. cruentus*). Chinese Grouse is endemic to the forested mountain slopes on the southeast edge of Qinghai-Tibet plateau and currently listed as Near-threatened (IUCN, 2011). Blood Pheasant has a much wider range, occurring in both montane forest and scrub habitats from western Nepal to central China (Madge and McGowan, 2002). Both species exhibit considerable differences in foraging ecology (Jia et al., 2010; Wang et al., 2011) and have declined in numbers due to extensive habitat fragmentation and degradation within their respective ranges (Sun et al., 2003).

### *2.1. Bird occurrence and environmental data*

Occurrence data for both species were obtained from 30 peer-reviewed papers published during 1978–2004, specimen collections housed at the Chinese Academy of Sciences in Beijing, and unpublished fieldwork conducted by J.C.X in 2007. These resulted in 43 and 79 occurrence records for Chinese Grouse and Blood Pheasant respectively. These records reveal that both species occur in six provinces (Tibet, Yunnan, Gansu, Qinghai, Sichuan and Shaanxi) across a region that encompasses six endemic bird areas (Stattersfield et al., 1998).

We selected 24 environmental variables corresponding to three different data categories (bio-climatic, topographic and habitat) to construct the niche models for both species (Table S1). We obtained 19 bio-climatic variables and one topographic variable (elevation) from the WorldClim 1.4 database (Hijmans et al., 2005) commonly utilized in species modeling studies (e.g. Peterson et al., 2006; Cordellier and Pfenninger, 2009; Hu et al., 2010). Two topographic variables (slope and aspect) and two habitat variables (forest cover and forest density) were obtained from the USGS database (http://eros.usgs.gov). These variables are generally considered to be related to species’ life history traits such as foraging behavior, nest site preference and predator avoidance (Sun, 2000; Sun et al., 2003; Jia et al., 2010; Wang et al., 2011).

### *2.2. Habitat suitability modeling*

We employed a suite of commonly utilized species distribution modeling techniques to project and compare potential future species distributions. All techniques, except one machine learning framework, were implemented using the BIOMOD framework (Thuiller, 2003) for the R programming environment (R Development Core Team). The BIOMOD computational framework aims to maximize the predictive accuracy of current species distributions and the reliability of potential future distributions using several different statistical modeling techniques (Thuiller, 2003; Thuiller et al., 2009). For both target species the following techniques were used: artificial neural networks (ANN, Ripley, 1996); classification tree analysis (CTA, Breiman, 1984); random forest (RF, Breiman, 2001); generalized linear models (GLM, McCullagh and Nelder, 1989); generalized boosting models (GBM, Ridgeway, 1999); generalized additive models (GAM, Hastie and Tibshirani, 1990): and mixture discriminate analysis (MDA, Hastie et al., 1994). Further details regarding the differences between each modeling technique is provided in (Roberts and Hamann, 2011). We randomly split the dataset using 70% of the data to calibrate the models and the remaining 30% for evaluation (Barbet-Massin et al., 2012). Since only occurrence records were available for both target species, we generated random pseudo-absences (Elith et al., 2006) using the *RandomPoints* function of the R package *dismo* (Hijmans et al., 2010).

We also modeled potential future distributions of both target species using MaxEnt version 3.3.1 (Phillips et al., 2006). We used the recommended default settings for convergence threshold ($10^{-5}$) and the maximum number of iterations (500; Phillips and Dudik, 2008). Regularization values were selected automatically by the MaxEnt software to reduce model over-fitting (Pearson et al., 2007). The robustness of each model was examined using cross-validation with five replicates i.e. 20% of presence localities as test data during each replicate (Fouquet et al., 2010). Habitat suitability maps were created by applying each species distribution model to all cells within China using a logistic link function to yield a habitat suitability index ranging between 0 and 1 (Phillips and Dudik, 2008). We used the *optimal.thresholds* function in the *PresenceAbsence* R package to calculate the suitable thresholds for both species (Freeman and Moisen, 2008a). We selected *PredPrev* = *Obs* as the optimization criteria following (Freeman and Moisen, 2008b).

Model validation and predictive performance was evaluated using three measures (e.g. Leclere et al., 2011): Cohen’s kappa statistic (Cohen, 1960); the area under the curve (AUC) of receiver operating characteristics (ROC, Fielding and Bell, 1997) and true skills statistics (TSS, Allouche et al., 2006). Cohen’s kappa statistic corrects the overall accuracy of model predictions by the accuracy expected to occur by chance. Kappa values range from −1 to +1 where +1 indicates perfect agreement, and values $\leqslant 0$ indicate a performance no different to random (Cohen, 1960). AUC values are threshold-independent measures of model accuracy that illustrate the model’s discrimination ability (Fielding and Bell, 1997), where an AUC value of 0 indicates a model with no better discrimination than chance, an AUC value of 1 indicates perfect discrimination, and an AUC value >0.8 indicates excellent discrimination