



An assessment of the efficiency of protection status through determinations of biodiversity hotspots based on endemic bird species, Taiwan



Chia-Ying Ko^{a,b,c,d}, Shidan C. Murphy^e, Terry L. Root^f, Pei-Fen Lee^{g,*}

^a Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT 06520, USA

^b School of Forestry and Environmental Studies, Yale University, New Haven, CT 06511, USA

^c Delta Electronics Foundation, Taipei 114, Taiwan

^d Research Center for Environmental Changes, Academia Sinica, Taipei 115, Taiwan

^e Great Lakes Laboratory for Fisheries and Aquatic Sciences, Fisheries and Oceans Canada, Burlington, ON, Canada L7R 4A6

^f Woods Institute for the Environment, Stanford University, Stanford, CA 94305, USA

^g Institute of Ecology and Evolutionary Biology, National Taiwan University, Taipei 106, Taiwan

ARTICLE INFO

Article history:

Received 12 June 2014

Received in revised form 8 August 2014

Accepted 14 August 2014

Keywords:

Avian

Biodiversity conservation

Endemic species

Frequency histogram approach

Hotspots

Protected areas

ABSTRACT

Evaluations of species richness patterns have been performed at diverse scales, and biodiversity hotspots, especially endemism hotspots, have received much attention in conservation biology. We estimated the distributions of endemic bird species based on a 12-yr avian inventory project in Taiwan, identified biodiversity hotspots of endemism on a regional scale based on predictions from the ensemble forecasting framework and frequency histogram approach, and assessed the efficiency of protected areas. The results indicated that the predicted endemism hotspots were mostly located in mid- and high-elevation areas along the Central Mountain Range of Taiwan. An observed endemism hotspot was defined as one in which at least five of Taiwan's 17 endemic bird species were present. This criterion was used because the 5% of the sampled grid squares that were the richest in endemic bird species all had 5 endemic bird species or more. Seventy to seventy-one percent of the observed biodiversity hotspots matched the predicted biodiversity hotspots. This outcome was obtained whether the richness biodiversity in a grid square was based on summed predicted probability or summed predicted richness. The majority of the protected areas for these Taiwanese endemic bird species were national parks, protecting 24.1% of the predicted hotspot areas, whereas nature reserves and wildlife refuges protected less than 7%. Most of the predicted endemism hotspots were not adequately protected. We conclude that the ensemble forecasting framework and the frequency histogram approach are useful for selecting critical habitats and biodiversity hotspots for endemic species and for appraising the efficiency of the protection status provided by governments.

© 2014 Elsevier GmbH. All rights reserved.

Introduction

Worldwide biodiversity levels are in a state of decline (Butchart et al., 2010; Rands et al., 2010; Hoffmann et al., 2011), and the past 60 years have witnessed a steeper decline than that occurring at any previous time in human history (Edwards & Richardson, 2004; Domisch, Jaehnig, & Haase, 2011). Anthropogenic threats, such as pollution, habitat destruction, introduced species, and climate change, are leading to irreversible losses of biodiversity, and ecosystem services are also expected to be affected by these losses

of animal or plant species from the food chain (Worm & Emmett, 2003).

Protecting species' critical habitats and biodiversity hotspots (Myers, 1988; Myers, Mittermeier, Mittermeier, da Fonseca, & Kent, 2000) are effective methods of sustaining and increasing biodiversity (Dobson et al., 2006; Schmitz, Hawlena, & Trussell, 2010). Studies have found that in protected habitats, plants and animals are more than twice as likely to move toward recovery as species in unprotected habitats (Myers, 1988; Myers et al., 2000). However, identifying critical habitats and hotspots remains highly challenging because the comprehensive data on species distribution and abundance that are required for such identification are often lacking (Clemens, Weston, Haslem, Silcocks, & Ferris, 2010; Clemens, Herrod, & Weston, 2014). To overcome this limitation, species

* Corresponding author. Tel.: +886 233662469; fax: +886 223623501.
E-mail address: leepf@ntu.edu.tw (P.-F. Lee).

distributions are predicted by either (1) associating individual species occurrences with known habitat preferences, constructing relationships between environments and species distribution at the individual species level, and then combining distribution information from different species (Austin, 2002; Elith et al., 2006; Araújo & New, 2007; Elith & Leathwick, 2009) or (2) using a cross-covariance matrix to find linear combinations of environments and a group of species' distributions that have a maximum correlation with each other at the community level (Ferrier & Guisan, 2006; Johnson & Wichern, 2007). Both approaches provide critical but slightly different elements for use in identifying species' critical habitats. A major drawback is that cross-covariance matrices cannot furnish any information about the detailed composition of species community assemblages and/or the biotic interactions that may affect species' spatial co-occurrence patterns, whereas the individual species-level approach can (Baselga & Araújo, 2009; Chapman & Purse, 2011; Dubuis et al., 2011). For this reason, the individual species-level approach (i.e., species distribution models, SDMs) is currently used relatively more widely to estimate species richness and to identify further hotspot locations. Here, we used the individual species-level approach for Taiwanese endemic bird biodiversity.

Species distribution models predict the distributions of species by correlating habitat characteristics with species occurrences (presence only or presence/absence; Elith et al., 2006; Stockwell, 2007). Such SDMs were first applied in terrestrial systems, and the utilization and complexity of species distribution models have increased rapidly. A wide variety of methods associated with SDMs have been developed over the past 20 years and applied to various conservation cases (e.g., Manel, Dias, & Ormerod, 1999; Elith et al., 2006; Ferrier & Guisan, 2006; Araújo & New, 2007; Meynard & Quinn, 2007; Phillips & Dudik, 2008; Baselga & Araújo, 2009; Ko, Lin, Ding, Hsieh, & Lee, 2009; Araújo, Alagador, Cabeza, Nogués-Bravo, & Thuiller, 2011; Chapman & Purse, 2011; Barbet-Massin, Thuiller, & Jiguet, 2012; Wu, Walther, Chen, Lin, & Lee, 2014). The results of individual SDMs are accumulated to estimate modeled species richness. The sum of the continuous probability/suitability values furnished by the individual SDMs represents a direct estimate of total species richness. Alternatively, a threshold for converting continuous probability/suitability values to binary values (presence/absence) can be set for each species, and all individual SDMs are then overlapped to derive a possible value for species richness. On average, the latter (i.e., threshold) approach usually exhibits a statistical artifact that may cause the over-prediction of species richness (i.e., commission errors, Guisan & Rahbek, 2011; Calabrese, Certain, Kraan, & Dormann, 2014). In contrast, the former approach may shape a lower possible species richness due to a low contribution of the species' predicted probability/suitability (although the species may be present) to the sum. To fill the aforementioned gaps, we chose a percentage-based highest scoring prediction of grid locations rather than the traditional number calculated from species-based thresholds to determine predicted species biodiversity hotspots in this study.

The purpose of this study was to (1) use multiple individual-species distribution models and structure a frequency histogram approach to determine the locations of endemism hotspots for bird species in Taiwan and (2) evaluate whether the current protected areas are suitably located. We considered that endemic bird species would furnish an ideal metric and serve well as both conservation concern and critical links to the biotic community within the forest space (i.e., provision of ecosystem functions; Whelan, Wenny, & Marguis, 2008). We interpreted areas with high endemism at a regional scale as biodiversity hotspots (Myers, 1988; Pressey, Humphries, Margules, Vane-Wright, & Williams, 1993; Myers et al., 2000; Orme et al., 2005).

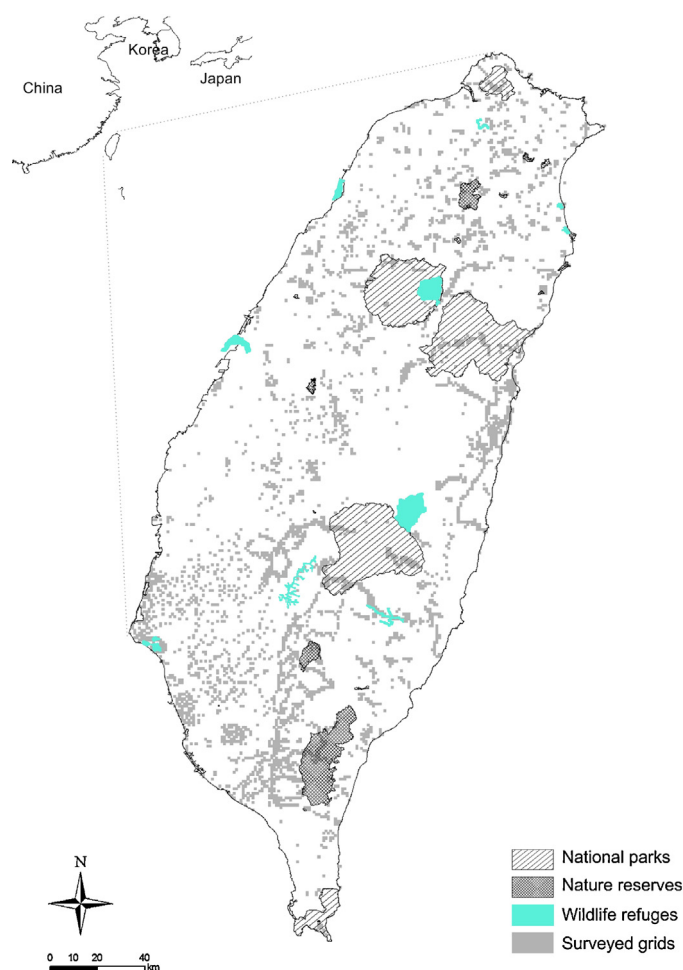


Fig. 1. The location of Taiwan, grid squares surveyed in this study, and protected areas in Taiwan.

Methods

Study area

Taiwan, an island with an area of more than 36,000 km², is located in the western Pacific Ocean and the importance of Taiwan's rich variety of endemic species has been noted frequently in Asian and global studies (Fig. 1; Myers et al., 2000; Ceballos & Ehrlich, 2006). Among the taxa belonging to Taiwan's biota, bird species are a well-defined and complex group, and standardized bird inventories in Taiwan have been implemented for more than 10 years (e.g., Koh, Lee, & Lin, 2006). Moreover, the Taiwanese endemic bird species are the subject of frequent studies (Nieh, 1999; Lee, Ding, Hsu, & Geng, 2004; Koh et al., 2006; Ko, Lin, & Lee, 2010; Wu et al., 2014) and are often used as indicators to represent potential patterns of changes that may affect other species (Ko et al., 2009).

Study species

Seventeen endemic bird species were selected in this study (Table 1). Among them, six species are listed as near threatened or vulnerable species on the International Union for Conservation of Nature (IUCN) Red List; (<http://www.iucnredlist.org/>). Fifteen of the bird species were recognized as endemic species before 1990, and the endemic status of the other two species was recently confirmed: the Taiwan Hwamei (*Garrulax taewanus*) in 2006 and the Taiwan Barbet (*Megalaima nuchalis*) in 2008. These species belong

Table 1
List of 17 endemic bird species in Taiwan. The family, common English name, and scientific name of each species are based on “The eBird/Clements checklist of birds of the world: Version 6.7” by Clements et al. (2012).

Family	English name	Scientific name	IUCN red list criteria ^a	No. of occurrences in grid squares	Elevation range (mean; m)
Corvidae	Formosan Magpie	<i>Urocissa caerulea</i>	LC	156	7–1487 (486)
Leiothrichidae	Taiwan Hwamei	<i>Garrulax taewanus</i>	NT	482	2–2735 (373)
	White-whiskered Laughingthrush	<i>Garrulax morrisonianus</i>	LC	207	100–3707 (2363)
	White-eared Sibia	<i>Heterophasia auricularis</i>	LC	779	7–3358 (1400)
	Steere's Liocichla	<i>Liocichla steerii</i>	LC	673	98–3155 (1624)
	Taiwan Barwing	<i>Actinodura morrisoniana</i>	LC	102	7–3015 (2043)
Locustellidae	Taiwan Bush Warbler	<i>Bradypterus alishanensis</i>	LC	135	147–3422 (2200)
Megalaimidae	Taiwan Barbet	<i>Megalaima nuchalis</i>	LC	1,657	2–2956 (564)
Muscicapidae	Collared Bush Robin	<i>Tarsiger johnstoniae</i>	LC	202	100–3707 (2283)
	Formosan Whistling Thrush	<i>Myophonus insularis</i>	LC	481	7–2764 (877)
Paridae	Yellow Tit	<i>Macholophus holsti</i>	NT	151	7–2815 (1569)
Phasianidae	Taiwan Partridge	<i>Arborophila crudigularis</i>	NT	408	18–2630 (1162)
	Mikado Pheasant	<i>Syrnaticus mikado</i>	NT	30	100–2979 (1918)
	Swinhoe's Pheasant	<i>Lophura swinhoii</i>	NT	95	100–2457 (1343)
Pycnonotidae	Styan's Bulbul	<i>Pycnonotus taivanus</i>	VU	414	3–2321 (282)
Regulidae	Flamecrest	<i>Regulus goodfellowi</i>	LC	112	378–3707 (2551)
Zosteropidae	Taiwan Yuhina	<i>Yuhina brunneiceps</i>	LC	772	7–3358 (1545)

^a Abbreviation: LC, least concern; NT, near threatened; VU, vulnerable.

to 11 families that vary in abundance, and they occur at various elevations throughout Taiwan.

Bird distribution data

Presence and absence records of the 17 Taiwanese endemic bird species were compiled from a 12-year avian survey (from 1993 to 2004; Hsu, Yao, Lin, Yang, & Lai, 2004; Koh et al., 2006). The avian survey was based on distance sampling methods, including point-count and transect-count methods (Buckland, Anderson, Burnham, & Laake, 1993; Buckland, Goudie, & Borchers, 2000), in which the entire island of Taiwan was surveyed using 1 × 1-km grid squares (a total of 37,552 grid squares). The point-count method involved following a sampling route, 1500 m long, with 10 counting points 150 m apart. Each counting point along the sampling route was surveyed for 6–10 min in a 50-m fixed radius. Differences in sampling duration at each counting point were caused by the local landscape and experience of the surveyors (Shiu & Lee, 2003). The transect-count method involved following a fixed transect line that covered a distance of 2 km at a walking speed of 1.5 km/h without stopping at any specific site. Both the counting points and the transect lines were sampled once per year during the breeding season or once per season during one year. To avoid biases resulting from the time of day, the surveys were conducted between 0600 and 1000 h. Both visual and auditory records of species were included. The coordinates of each sampled point were recorded and transformed to the grid-square system. Given the limitations of personnel, time, and funds, 4082 grid squares representing 11% of the area of Taiwan were surveyed (Fig. 1). Each species was present in a different number of grid squares (Table 1).

Species distribution models

Four categories of environmental variables (a total of 14 variables), including topography, climate, vegetation, and human disturbance, with high correlations between species distributions and environments were chosen by Ko et al. (2009) and Ko, Ko, Lin, and Lee (2013) and used in the following five different individual-species distribution models: logistic regression (LR), discriminant analysis (DA), genetic algorithm for rule-based prediction (GARP), artificial neural network (ANN), and maximum entropy (MAXENT). These models are widely used and have been shown to provide effective conservation management strategies based on estimates

of the spatial distributions of those species requiring attention (Elith et al., 2006; Meynard & Quinn, 2007; Phillips & Dudik, 2008).

Values of the mean/total, standard deviation, and range of elevation, precipitation, and temperature, warmth index, percentage of forest cover, normalized difference vegetation index (NDVI), percentage of building areas, and road density were generated as variables in the four categories of environmental variables. Elevation variables in the topographical category were derived from a map of a digital elevation model with 40-m resolution. Climatic variables, including precipitation, temperature, and warmth index, were calculated from monthly meteorological monitoring records obtained for the past 30 years by the Central Weather Bureau of Taiwan, which has operated 25 long-term climate-monitoring stations since the 1950s and an additional 102 auto-rain gauges since 1990 around the entire island of Taiwan. We used a data assimilation method, a technique employing statistical analysis and interpolation to integrate irregularly distributed observations into regular model grids (Wang, Zou, & Zhu, 2000), to generate high-resolution grid temperature and precipitation data. The warmth index was defined as the accumulated mean monthly temperature above 5 °C in response to plant growth conditions (Liu & Su, 1992). Variables related to vegetation and human disturbance (i.e., percentage of forest cover, NDVI, percentage of building areas, and road density) were calculated from a land-cover map generated by a supervised classification of SPOT mosaic images taken in 2002. The forest cover was calculated as forest density in percent (%), as the ratio of forest area to a grid square's area. The percentage of building areas was calculated as the ratio of total building areas to a grid square's area. The road density was calculated as the ratio of the total length (m) of all levels of paved roads to a grid square's area. Both topographic and land-cover maps were provided by the Aerial Survey Office, Forestry Bureau, Taiwan. To be consistent with the bird distribution data, we averaged and transformed data at a 1 × 1-km resolution for all categories of environmental variables. Additional details about each environmental variable were presented in Lee et al. (2004) and Koh et al. (2006).

The five individual-species distribution models in this study are based on different theoretical concepts and mathematical statistics. Three of the models (i.e., LR, DA, and ANN) are presence/absence models, and the others (i.e., GARP and MAXENT) are presence-only models. Surveyed grid squares with multiple sampling times but without occurrence records for a specific species were regarded as absences of that species. We applied an ANOVA to compare the records of the presences and absences of species and kept the

variables that could differentiate species occurrences; we then used backward elimination to select significant variables (down to 5–7 variables for each species in the final models; Tables S1 and S2) in both the LR and DA models. The significant variables at each step had to significantly reduce the scaled deviance, and the range of the scaled deviance was approximately distributed as χ^2 (McCullagh & Nelder, 1989). GARP searches iteratively for non-random correlations between species presence and absence and environmental parameter values using several types of rules, including atomic, logistic regression, bioclimatic envelope, and negated bioclimatic envelope rules (Scachetti-Pereira, 2001; Meynard & Quinn, 2007). In our study, four rules (i.e., atomic rules, range rules, negated range rules, and logit rules) were combined to perform 100 runs per species, with a maximum of 1000 iterations and a convergence limit of 0.01. We derived a probability map for each species according to 100 runs. ANN is a computational model that was inspired by the structure and/or functional aspects of biological neural networks (Manel et al., 1999). The algorithm of ANN consists of an interconnected group of artificial neurons, and it processes information using a connectionist approach to computation. To construct a network for a given species, one hidden layer with five neurons was used in this study (also see other detailed implementation instructions in Manel et al., 1999). MAXENT serves to estimate a target species' distribution by finding the distribution of maximum entropy (closest to uniform) subject to the constraint that the expected value of each feature under this estimated distribution matches its empirical average (Phillips & Dudik, 2008). This distribution is equivalent to the maximum likelihood Gibbs distribution. We used the default setting in MAXENT, except for the maximum number of iterations. A maximum of 1000 background points and iterations was used for all of our species.

To evaluate the predictive performance of the SDMs for each species, we used a random subset (two-thirds) of species distribution data to determine the models (i.e., as a training set) and then used the remaining data for evaluation (i.e., as a testing set) with two prevalence-independent values: the area under the receiver operating characteristic curve (AUC) and the true skill statistic (TSS; Pearce & Ferrier, 2000; Allouche, Tsoar, & Kadmon, 2006). Both have been widely used for accuracy measures in various disciplines over many years (Youden, 1950; Pearce & Ferrier, 2000; Allouche et al., 2006). The AUC value, also a threshold-independent value, was calculated from the probability that a model will rank a randomly chosen species presence higher than a randomly chosen species absence, and it indicates a better predictive performance as the value nears 1 (Pearce & Ferrier, 2000). TSS was derived from elements of a confusion matrix and defines an average of the net prediction success rate for species presences and absences (Youden, 1950; Allouche et al., 2006). TSS ranges from –1 to 1, where 1 indicates perfect predictive performance and values of zero or less indicate a performance no better than random.

Predicted distribution maps covering the entire island of Taiwan for each species were obtained from each model. In addition to using the predicted species distributional probability maps, we also transformed the predicted species distributional probability maps into predicted species distributional presence/absence maps based on a threshold that selected a high value between a species' AUC and its prevalence, i.e., if the AUC value was greater than the species prevalence, we used the AUC value as the threshold for the species; otherwise we used the prevalence (Ko et al., 2009).

Hotspot definition and estimation

We used an ensemble forecasting framework based on the individual-species predicted probability and presence/absence distributions and assigned a value of 1 to each species without considering prevalence differences. For both the predicted

probability and presence/absence species distributions, we overlapped the 17 species' predicted maps analyzed by each model (i.e., LR, DA, ANN, GARP, and MAXENT) with values from 0 to 17, representing the probable biodiversity (0 to high biodiversity) or the number of species (0 to 17) predicted to be present in a grid square. The highest-scoring 5% of the grid squares (definition according to the observed biodiversity, see below), including all the grid squares that tied at the lowest score in this range, were identified as summed predicted probability (for the probability score) and summed predicted richness (for the species number) hotspots. Each model exhibited specific hotspots in this step. We then summarized the results from the five models in a frequency histogram with six classes of hotspots (0–5: 0, no hotspot predicted; 1, predicted by only 1 model; 2, predicted by 2 models; 3, predicted by 3 models; 4, predicted by 4 models; and 5, predicted by all models). The ensemble forecasting framework and the frequency histogram approach used in this study can enable more robust decision making in the face of uncertainty and have much to offer to conservation planning, as advocated in 2007 (Araújo & New, 2007).

Grid squares with at least five (Fig. S1, showing the highest-scoring 5% biodiversity of sampled grid squares) out of 17 different endemic bird species occurrences were defined as observed

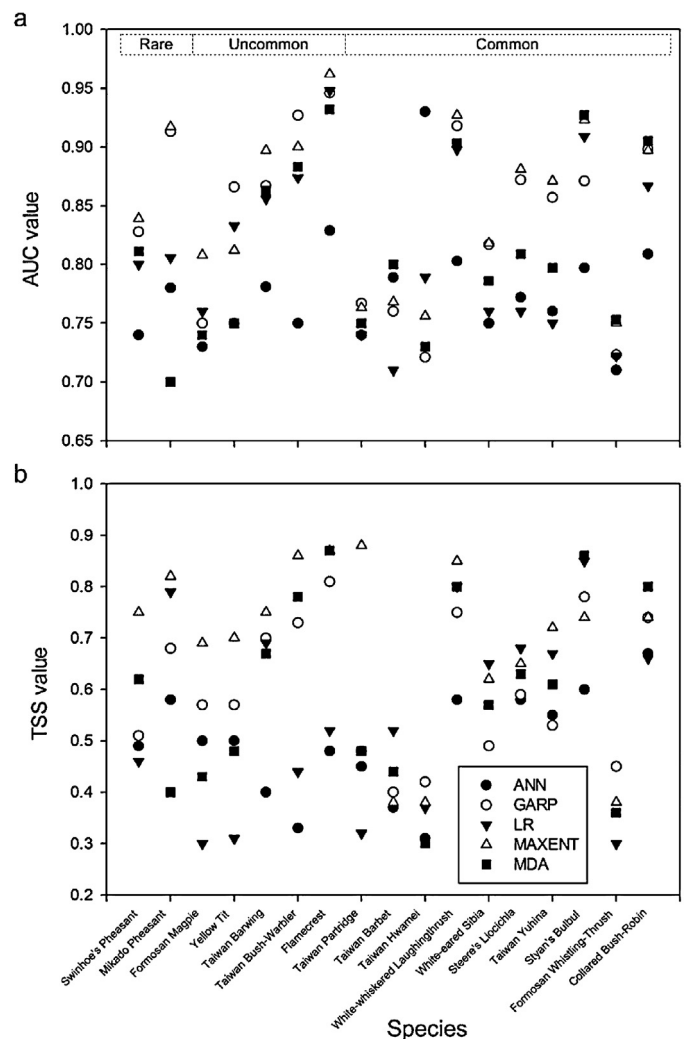


Fig. 2. Model performance measured by (a) the area under the receiver operating characteristic curve (AUC) and (b) the true skill statistic (TSS) of each model for each species. Abbreviations for the models: LR, logistic regression; DA, discriminant analysis; GARP, genetic algorithm for rule-based prediction; ANN, artificial neural network; MAXENT, maximum entropy.

hotspots. To evaluate differences between observation and prediction, we calculated the area of overlap of the observed and predicted hotspot grids. To estimate the protection status of the endemic bird species in Taiwan, protected areas designated as national parks, nature reserves, and wildlife refuges were used to analyze the efficiency of protection. The number of grid squares belonging to the above-predicted hotspots that were included in the protected areas was used to measure protection status.

All modeling, evaluation, and statistical analyses were performed using R version 2.12 (except for GARP, which was performed with the “DesktopGarp” interface; R Development Core Team, 2010), and the maps were produced using ESRI ArcMap version 9.3.

Results

The five models for each species all showed AUC values >0.7 and TSS values >0.3 and demonstrated relatively good model performance for application to our hotspot analyses (Fig. 2). Among the models, GARP and MAXENT showed the highest values of model performance for most species.

The biodiversity hotspot areas for Taiwanese endemic bird species were primarily located along the Central Mountain Range, showing a continuous distribution both on the summed predicted probability and richness hotspot maps (Fig. 3). With the exception of the MAXENT predictions, which identified almost none of the endemism hotspots in the middle of the island, all maps derived from the ensemble forecasting framework showed similar patterns. The area of summed predicted probability hotspots found by GARP (2,759 km²) was the highest, followed by MAXENT (2179 km²), ANN (2003 km²), LR (1918 km²), and DA (1683 km²). Although slightly different results were obtained, the summed richness hotspots ranked by largest to smallest predicted area were GARP (2702 km²), ANN (2691 km²), MAXENT (2636 km²), LR (1796 km²), and DA (1683 km²). Based on the combined hotspot maps (i.e., frequency histogram approach), the hotspots in class 5 were predicted to cover approximately 1% of the area of Taiwan (summed predicted probability hotspots: 0.91–1.18%, summed predicted richness hotspots: 1.18–1.90%). The four models, except for DA, contributed similar predictions in class 4 (approximately 95%). However, for classes 1–3, there were no consistent contribution patterns among the models between the summed predicted probability and richness hotspots.

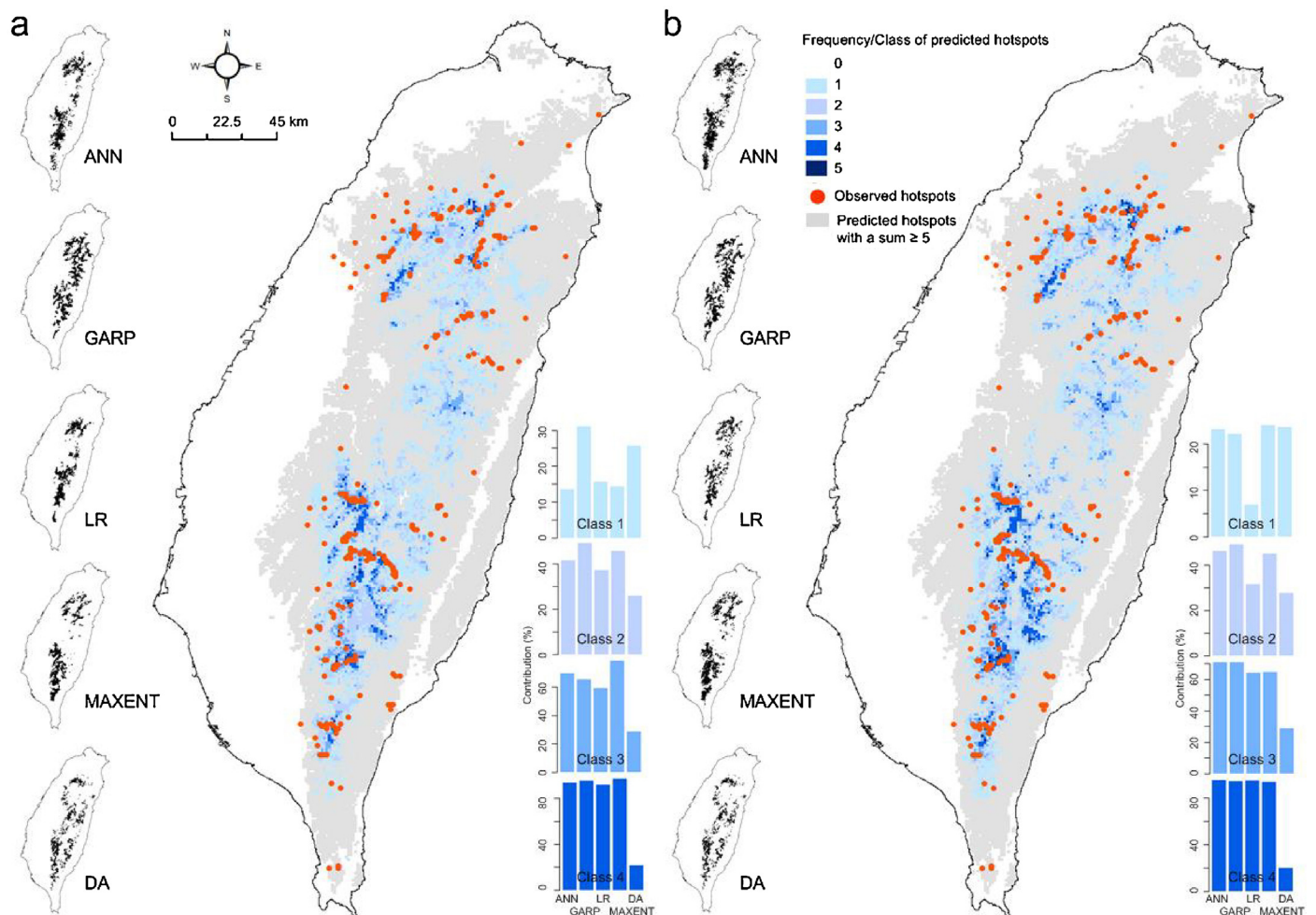


Fig. 3. Spatial distributions of observed and summed predicted (a) probability and (b) richness biodiversity hotspots. The observed biodiversity hotspots were grid squares with at least five endemic bird species. The predicted biodiversity hotspots were obtained through predictions using five individual-species distribution models, including logistic regression (LR), discriminant analysis (DA), genetic algorithm for rule-based prediction (GARP), artificial neural network (ANN), and maximum entropy (MAXENT). For each model, the predicted distributions of the 17 endemic species were combined to yield summed values whose values ranged from 0 to 17, the grid squares were ranked according to their summed probability/richness, and the highest-ranked grid squares were then selected (see the text). The final predicted biodiversity hotspots were then obtained through a frequency histogram approach by establishing six classes of hotspots, numbered 0 through 5, based on the number of models that identified that particular hotspot.

Approximately 98% of the observed biodiversity hotspots were located within a region for which at least one model predicted occupation by at least five endemic species, whereas 70–71% of the observed biodiversity hotspots were found in the summed predicted probability and richness hotspots (Fig. 3). With the frequency histogram approach for the summed predicted probability hotspots, 8.6% of the observed hotspots were located in class 5 and class 4, 18.7% in class 3, 24.9% in class 2, and 17.9% in class 1. For the summed predicted richness hotspots, 12.1% of the observed hotspots were located in class 5 and class 4, 14.8% in class 3, 23.7% in class 2, and 20.2% in class 1. For both the summed predicted probability and the summed predicted richness hotspots, the nonlinear models (i.e., ANN, LR, GARP, and MAXENT) generally predicted 76.6% of the observed hotspots as possible hotspots, whereas the linear model (i.e., DA) predicted 59.1%. Individually, the hotspots predicted by the MAXENT model covered the most observed hotspots, at 63.8%, followed by ANN at 48.9%, DA at 46.8%, GARP at 37.2%, and LR at 33%.

Protection status

The broad patterns of the high values of hotspot classes were concentrated in relatively few regions, those above 2000 m a.s.l. Based on the frequency histogram approach, we identified the classes with values of 3 or higher (i.e., classes 3–5), including the summed predicted probability and richness hotspots, with a total area of 1538 km² (4.1% of Taiwan Island), as hotspots that were ultimately critical for estimating protection status. Most of the protected areas for the 17 endemic bird species were national parks. Unfortunately, most of the predicted hotspots were not protected (Table 2). Only 24.1% of the predicted hotspots were under protection as national parks. Shei-Pa and Yushan National Parks contributed more than the others, and no predicted hotspots occurred in Yangmingshan or Kenting National Parks. Nature reserves and wildlife refuges protected 6% and 0.4%, respectively, of the predicted hotspot areas.

Discussion

The biodiversity hotspots for Taiwanese endemic bird species appeared to be rather consistent among the predictions of the five individual-species distribution models considered in this study. In general, the mid- and high-elevation areas have higher species richness. These areas are remote and less disturbed, providing more suitable habitats than other areas for the 17 endemic bird species. Nevertheless, low elevations remain important, especially for Taiwan Hwamei (*Garrulax taewanus*), Styan's Bulbul (*Pycnonotus taivanus*), and Formosan Magpie (*Urocissa caerulea*; Ko et al., 2010). Because the low elevations received a relatively low ranking using the frequency histogram approach, special consideration should be given to the protection of these low-elevation species.

Using the frequency histogram approach, the spatial distributions of predicted biodiversity hotspots showed that the high-value

areas for the 17 Taiwanese endemic bird species were geographically cohesive and a good match with those regions that have traditionally been defined as 'principal ecological habitats' in Taiwan (Lue & Chang, 1999). Unfortunately, not all the observed hotspots were projected to be in the predicted hotspots. These results cannot yet be explained. Errors in the modeling processes occurring in each model for each species might produce this outcome. However, the performance of the models was estimated in the initial phase of the model-building processes, and the results obtained indicated that the effects of model errors were relatively small.

Using empirical estimates of species richness or rarity to represent critical habitats and hotspots of biological diversity is more common than the use of predicted species distributions (Myers, 1988; Myers et al., 2000; Orme et al., 2005; Ceballos & Ehrlich, 2006). However, given the limited information available on real and complete species distributions, our determination of biodiversity hotspots can provide a basis for the decision to classify habitats as critically important for biodiversity. This tool can also be applied to understand how species distributions will shift under climate change. Giving equal weight to species with differing prevalence may not be a perfectly adequate method of identifying biodiversity hotspots if the foremost task in the conservation process is to rate different hotspots for their holdings of rare, threatened, or endemic species. Nevertheless, we believe that this approach can provide basic knowledge about species' distributions and help locate areas and habitats with a high concentration and/or biodiversity of species such that critical habitats and biodiversity hotspots would attain priority for conservation.

The protection of Taiwanese endemic bird species is inadequate because only approximately 30% of the biodiversity hotspots we identified are located within established protected areas (i.e., national parks, nature reserves, and wildlife refuges). More than 70% of the areas that are important have not received notice. Although the government of Taiwan has recently designated a conservation corridor along the Central Mountain Range that would encompass some of the biologically important areas we identified, the designation is not legally binding, and the boundaries of the corridor are not well defined. The lack of such legal designation and the lack of clear boundaries will most likely prevent the corridor from achieving the intended conservation goals.

Considering endemic birds as an indicator of all breeding birds in Taiwan may reduce the time and energy needed for conservation assessments due to the difficulty of obtaining distribution data for all breeding bird species but has been debated by different authors (Nieh, 1999; Lee et al., 2004; Koh et al., 2006; Wu et al., 2014). The lack of congruence may be caused by the use of different spatial scales, especially evident at a smaller spatial scale such as a fine scale of 1 × 1-km grid squares in our and Wu et al.'s (2014) study (Lund & Rahbek, 2002; Moore et al., 2003; Franco et al., 2009). Moreover, whether endemic bird species can be used as an indicator of overall taxonomic species is unknown and requires further investigation. Ceballos and Ehrlich (2006) indicated that the broad hotspot patterns in bird distributions are remarkably similar to those in mammalian distributions throughout the world, but the rough scale in that study may not be representative of the finer-scale situation in this study. We must, therefore, maintain a conservative position about the overall representativeness of Taiwan's endemic bird species.

Acknowledgments

We thank two anonymous reviewers for comments that improved the manuscript. We thank the Endemic Species Research Institute in Taiwan for support in the use of bird species data and

Table 2
Percentage of predicted biodiversity hotspots of the Taiwanese endemic bird species protected by national parks, nature reserves, and wildlife refuges.

Protected areas	% Of hotspots protected
National parks	24.1
Yangmingshan	0
Shei-Pa	8.3
Taroko	2.3
Yushan	13.5
Kenting	0
Nature reserves	6.0
Wildlife refuges	0.4

many researchers and volunteers for field work. We also thank Tzung-Su Ding, Anne Lee, Chung-Ming Liu, Shu-Hua Lin, and five anonymous reviewers for comments and suggestion on an earlier version of the paper. C.-Y. Ko thanks the National Science Council Taiwan Grant in Taiwan (097IPFA0100038) for partial support of this study. This work was partially supported by the National Park Division of the Construction and Planning Agency, Ministry of the Interior, Taiwan, and the National Science Council Taiwan.

Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.jnc.2014.08.012>.

References

- Allouche, O., Tsoar, A., & Kadmon, R. (2006). Assessing the accuracy of species distribution models: Prevalence, kappa and the true skill statistic (TSS). *Journal of Applied Crystallography*, *43*, 1223–1232.
- Araújo, M. B., & New, M. (2007). Ensemble forecasting of species distributions. *Trends in Ecology & Evolution*, *22*, 42–47.
- Araújo, M. B., Alagador, D., Cabeza, M., Nogués-Bravo, D., & Thuiller, W. (2011). Climate change threatens European conservation areas. *Ecology Letters*, *14*, 484–492.
- Austin, M. P. (2002). Spatial prediction of species distribution: An interface between ecological theory and statistical modeling. *Ecological Modelling*, *157*, 101–118.
- Barbet-Massin, M., Thuiller, W., & Jiguet, F. (2012). The fate of European breeding birds under climate, land-use and dispersal scenarios. *Global Change Biology*, *18*, 881–890.
- Baselga, A., & Araújo, M. B. (2009). Individualistic vs community modelling of species distributions under climate change. *Ecography*, *32*, 55–65.
- Buckland, S. T., Anderson, D. R., Burnham, K. P., & Laake, J. L. (1993). *Distance sampling: Estimating abundance of biological populations*. London: Chapman and Hall.
- Buckland, S. T., Goudie, I. B. J., & Borchers, D. L. (2000). Wildlife population assessment: Past developments and future directions. *Biometrics*, *56*, 1–12.
- Butchart, S. H. M., Walpole, M., Collen, B., van Strien, A., Scharlemann, J. P. W., Almond, R. E. A., et al. (2010). Global biodiversity: Indicators of recent declines. *Science*, *328*, 1164–1168.
- Calabrese, J. M., Certain, G., Kraan, C., & Dormann, C. F. (2014). Stacking species distribution models and adjusting bias by linking them to macroecological models. *Global Ecology and Biogeography*, *23*, 99–112.
- Ceballos, G., & Ehrlich, P. R. (2006). Global mammal distributions, biodiversity hotspots, and conservation. *Proceedings of the National Academy of Sciences of the United States of America*, *103*, 19374–19379.
- Chapman, D. S., & Purse, B. V. (2011). Community versus single-species distribution models for British plants. *Journal of Biogeography*, *38*, 1524–1535.
- Clemens, R. S., Weston, M. A., Haslem, A., Silcocks, A., & Ferris, J. (2010). Identification of significant shorebird areas: Thresholds and criteria. *Diversity and Distribution*, *16*, 229–242.
- Clements, J. F., Schulenberg, T. S., Iliff, M. J., Sullivan, B. L., Wood, C. L., & Roberson, D. (2012). *The eBird/Clements checklist of birds of the world: Version 6.7*. Downloaded from (<http://www.birds.cornell.edu/clementschecklist/downloadable-clements-checklist>)
- Clemens, R. S., Herrod, A., & Weston, M. A. (2014). Lines in the mud; revisiting the boundaries of important shorebird areas. *Journal of Nature Conservation*, *22*, 59–67.
- Dobson, A., Lodge, D., Alder, J., Cumming, G. S., Keymer, J., McGlade, J., et al. (2006). Habitat loss, trophic collapse, and the decline of ecosystem services. *Ecology*, *87*, 1915–1924.
- Domisch, S., Jaehnic, S. C., & Haase, P. (2011). Climate-change winners and losers: Stream macroinvertebrates of a submontane region in Central Europe. *Freshwater Biology*, *56*, 2009–2020.
- Dubuis, A., Pottier, J., Rion, V., Pellissier, L., Theurillat, J.-P., & Guisan, A. (2011). Predicting spatial patterns of plant species richness: A comparison of direct macroecological and species stacking modelling approaches. *Diversity and Distribution*, *17*, 1122–1131.
- Edwards, M., & Richardson, A. J. (2004). Impact of climate change on marine pelagic phenology and trophic mismatch. *Nature*, *430*, 881–884.
- Elith, J., & Leathwick, J. R. (2009). Species distribution models: Ecological explanation and prediction across space and time. *Annual Review Ecology Evolution System*, *40*, 677–697.
- Elith, J., Graham, C. H., Anderson, R. P., Dudík, M., Ferrier, S., Guisan, A., et al. (2006). Novel methods improve prediction of species distributions from occurrence data. *Ecography*, *29*, 129–151.
- Ferrier, S., & Guisan, A. (2006). Spatial modeling of biodiversity at the community level. *Journal of Applied Crystallography*, *43*, 340–393.
- Franco, A. M. A., Anderson, B. J., Roy, D. B., Gillings, S., Fox, R., Moilanen, A., et al. (2009). Surrogacy and persistence in reserve selection: Landscape prioritization for multiple taxa in Britain. *Journal of Applied Crystallography*, *46*, 82–91.
- Guisan, A., & Rahbek, C. (2011). SESAM—A new framework integrating macroecological and species distribution models for predicting spatio-temporal patterns of species assemblages. *Journal of Biogeography*, *38*, 1433–1444.
- Hoffmann, M., Belant, J. L., Chanson, J. S., Cox, N. A., Lamoreux, J., Rodrigues, A. S. L., et al. (2011). The changing fates of the world's mammals. *Philosophical Transactions of the Royal Society of London, Series B*, *27*, 2598–2610.
- Hsu, F.-H., Yao, C.-T., Lin, R.-S., Yang, C.-C., & Lai, S.-J. (2004). Avian species composition and distribution along elevation gradient in the south Taiwan. *Endemic Species Research*, *6*, 41–66.
- Johnson, R. A., & Wichern, D. W. (2007). *Applied multivariate statistical analysis* (6th ed., pp. 767). Upper Saddle River, NJ, USA: Prentice Hall.
- Ko, C.-Y., Lin, R.-S., Ding, T.-S., Hsieh, C.-H., & Lee, P.-F. (2009). Identifying biodiversity hotspots by predictive models: A case study using Taiwan's endemic bird species. *Zoological Studies*, *48*, 418–431.
- Ko, C.-Y., Lin, R.-S., & Lee, P.-F. (2010). Distribution patterns and macrohabitat characteristics of endemic bird species in Taiwan. *Taiwania*, *55*, 216–227.
- Ko, C.-Y., Ko, C.-J., Lin, R.-S., & Lee, P.-F. (2013). Influences of temporal independence of data on modeling species distributions. *Basic and Applied Ecology*, *14*, 309–319.
- Koh, C.-N., Lee, P.-F., & Lin, R.-S. (2006). Bird species richness patterns of northern Taiwan: Primary productivity, human population density, and habitat heterogeneity. *Diversity and Distribution*, *12*, 546–554.
- Lee, P.-F., Ding, T.-S., Hsu, F.-H., & Geng, S. (2004). Breeding bird species richness in Taiwan: Distribution on gradients of elevation, primary productivity and urbanization. *Journal of Biogeography*, *31*, 307–314.
- Liu, T.-R., & Su, H.-J. (1992). *Forest plant ecology*. Taipei, Taiwan (R.O.C.): The Commercial Press, Ltd.
- Lue, K.-Y., & Chang, Y.-T. (1999). Hotspots investigation in Taiwan region. In *Proceedings of the third conference on the protected areas of East Asia (IUCN/WCPA-EA3)* (pp. 158–165).
- Lund, M. P., & Rahbek, C. (2002). Cross-taxon congruence in complementarity and conservation of temperate biodiversity. *Animal Conservation*, *5*, 163–171.
- Manel, S., Dias, J. M., & Ormerod, S. J. (1999). Comparing discriminant analysis, neural networks and logistic regression for predicting species distributions: A case study with a Himalayan river bird. *Ecological Modelling*, *120*, 337–347.
- McCullagh, P., & Nelder, J. A. (1989). *Generalized linear models*. London: Chapman and Hall.
- Meynard, C. N., & Quinn, J. F. (2007). Predicting species distributions: A critical comparison of the most common statistical models using artificial species. *Journal of Biogeography*, *34*, 1455–1469.
- Moore, J. L., Balmford, A., Brooks, T., Burgess, N. D., Hansen, L. A., Rahbek, C., et al. (2003). Performance of sub-Saharan vertebrates as indicator groups for conservation priority areas for conservation. *Conservation Biology*, *17*, 207–218.
- Myers, N. (1988). The threatened biota: 'Hot-spots' in tropical forests. *The Environmentalist*, *10*, 187–208.
- Myers, N., Mittermeier, R. A., Mittermeier, C. G., da Fonseca, G. A. B., & Kent, J. (2000). Biodiversity hotspots for conservation priorities. *Nature*, *403*, 853–858.
- Nieh, C. H. (1999). *Species richness pattern of breeding birds in Taiwan*. Taipei, Taiwan (R.O.C.): National Taiwan University (MS thesis).
- Orme, C. D. L., Davies, R. G., Burgess, M., Eigenbrod, F., Pickup, N., Olson, V. A., et al. (2005). Global hotspots of species richness are not congruent with endemism or threat. *Nature*, *436*, 1016–1019.
- Pearce, J., & Ferrier, S. (2000). Evaluating the predictive performance of habitat models developed using logistic regression. *Ecological Modelling*, *133*, 225–245.
- Phillips, S. J., & Dudík, M. (2008). Modeling of species distributions with Maxent: New extensions and a comprehensive evaluation. *Ecography*, *31*, 161–175.
- R Development Core Team. (2010). *R: A language and environment for statistical computing*. Vienna, Austria: R Foundation for Statistical Computing.
- Pressey, R. L., Humphries, C. J., Margules, C. R., Vane-Wright, R. I., & Williams, P. H. (1993). Beyond opportunism: Key principles for systematic reserve selection. *Trends in Ecology & Evolution*, *8*, 124–128.
- Rands, M. R. W., Adams, W. M., Bennun, L., Butchart, S. H. M., Clements, A., Coomes, D., et al. (2010). Biodiversity conservation: Challenges beyond. *Science*, *329*, 1298–1303.
- Scachetti-Pereira, R. (2001). *Desktop GARP*. Available at (<http://www.lifemapper.org/desktopgarp>).
- Schmitz, O. J., Hawlena, D., & Trussell, G. C. (2010). Predator control of ecosystem nutrient dynamics. *Ecology Letters*, *13*, 1199–1209.
- Shiu, H.-J., & Lee, P.-F. (2003). Assessing avian point-count duration and sample size using species accumulation functions. *Zoological Studies*, *42*, 357–367.
- Stockwell, D. (2007). *Niche modeling*. Boca Raton, FL, USA: Chapman and Hall/CRC Press.
- Youden, W. J. (1950). Index for rating diagnostic tests. *Cancer*, *3*, 32–35.
- Wang, B., Zou, X., & Zhu, J. (2000). Data assimilation and its applications. *Proceedings of the National Academy of Sciences of the United States of America*, *97*, 11143–11144.
- Whelan, C. J., Wenny, D. G., & Marguis, R. J. (2008). Ecosystem services provided by birds. *Annals of the New York Academy of Sciences*, *1134*, 25–60.
- Worm, B., & Emmett, J. (2003). Biodiversity, productivity and stability in real food webs. *Trends in Ecology & Evolution*, *18*, 628–632.
- Wu, T.-Y., Walther, B. A., Chen, Y.-H., Lin, R.-S., & Lee, P.-F. (2014). Reassessment of the conservation status and protected area coverage of Taiwanese birds: How distribution modelling can help species conservation. *Bird Conservation International*, *24*, 223–238.