Prioritization of areas in China for the conservation of endangered birds using modelled geographical distributions

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Summary

We developed distributional models for 90 threatened bird species in China, and used heuristic complementarity algorithms to prioritize areas for conservation. The pixel-based area selection prioritized 20 areas for protection, which covered all species analysed. Area selecting for endangered species based on the existing biosphere reserve system included only 37–62 species in eleven reserves, leaving 28–53 species unprotected. We employed algorithms for area selection based on species richness and rarity and obtained two views of a most efficient reserve network. We used the distributional hypotheses to identify additions to the reserve system that would improve its effectiveness substantially. The pixel-based area selection approach includes species much more efficiently on a per-area basis, and thus offers exciting perspectives for improved protection of the country's endangered avifauna.

Introduction

Geographical information system applications in conservation biology have proceeded in two general directions. The first consists of developing algorithms to predict species' geographical distributions. Species' ecological niches are characterized in multivariate environmental space, and geographical areas fitting these conditions are then taken as the predicted distribution, filling gaps created by uneven sampling (Nix 1986, Walker and Cocks 1991, Carpenter *et al.* 1993, Sperduto and Congalton 1996). The second direction is prioritizing areas for conservation, as exemplified by Gap Analysis and other applications (e.g. Daniels *et al.* 1991, Russell-Smith and Bowman 1992, Bojórquez-Tapia *et al.* 1995, Harrison and Martinez 1995, Kiester *et al.* 1996), in which distributional information is integrated into strategies for reserve portfolio design. Integrated, these two efforts can provide a strong basis for decisions on geographical priorities for conservation (Peterson *et al.* 2000).

The *Red List of Threatened Species* (IUCN 2000) includes 128 bird species that occur in China, 85 of which are listed as Critically Endangered, Endangered, or Vulnerable, and 28 of which are endemic to China. Many efforts have focused on conservation of these species and their habitats, but natural habitats across vast areas of the country have already been disturbed. Indeed, it is difficult to find undisturbed habitats and landscapes in China because of a burgeoning human population and rapid economic development. The application of new,

quantitative methodologies in the region may be useful for addressing the challenge of preserving biological diversity and landscape in this region more effectively.

In this paper, we bring new tools from biodiversity informatics and quantitative geography to bear on the challenge of prioritizing areas in China for conservation action. Geographical distributions of endangered bird species are modelled, foci of species richness identified, and prioritizations assembled based on the maximum complementarity among areas or manual representation approaches of rare species. These approaches produce defendable, quantitative prioritizations, and offer a new perspective on conservation strategies in the region.

Methods

Distributional data

This study concentrates on 90 of the 128 species of threatened or endemic birds found in China (IUCN 2000), falling into the categories of Critically Endangered (four species), Endangered (seven species), Data Deficient (one species), Vulnerable (59 species), and lower risk but endemic (16 species), and protected birds for China (three additional, G. Chui pers. comm). We assembled sets of occurrence points from the scientific literature (Salvadori 1895, Peters 1940, Cheng 1979, 1987, Meyer de Schauensee 1984), and via the kind collaboration of BirdLife International (M. Crosby pers. comm.). We obtained 3–55 unique occurrence points per species. Textual geographical references were converted to latitude-longitude pairs by direct consultation of 1:200,000 maps. When species had more than one distributional area (e.g. breeding and wintering ground) within China (two cases), we treated them separately and weighted them equally in our analyses. For the remaining 38 threatened species, fewer than three occurrence records were available, and so these species were excluded from analysis.

Geographical data

We obtained base geographical data coverages from ESRI (1996). We used 23 variables: snow cover (low and high); annual, January and July precipitation (low and high); annual, January and July temperature (low and high); land use; geomorphology; solar radiation (low and high); human population; soils; vegetation; morphological structure; and frost-free period. Tests of the effects of inclusion and exclusion of particular variables (e.g. land use) were used to detect sensitivity in the result (Peterson and Cohoon 1999). We converted data coverages into ASCII raster grids using ArcView (version 3.1), and deposited them at the Biodiversity Species Workshop (BSW; http://biodi.sdsc.edu) facility as base coverages. Covering all of China, these base data sets are now publicly available for other applications (Chen and Peterson 2000).

Modelling

The fundamental ecological niche of a species, defined here as the conjunction of ecological conditions within which it is able to maintain populations without

immigration (Grinnell 1917), can be depicted as a polyhedron or polyhedrons in multidimensional ecological space (MacArthur 1972). Several approaches have been used to approximate fundamental ecological niches of species, including BIOCLIM (Nix 1986) and logistic multiple regression and generalized linear modelling (Austin *et al.* 1990). Here, we employ the Genetic Algorithm for Rule-set Prediction (GARP), which includes these methods, among others, in an iterative, machine-learning approach (Stockwell and Noble 1992, Stockwell and Peters 1999). Individual algorithms are used to produce component ''rules'' in a broader rule-set, and hence portions of the landscape may be identified as inside or outside of the niche based on different algorithms. GARP therefore represents a superset of other approaches, and should generally have greater predictive ability than any one of them. Extensive testing of GARP has indicated excellent predictive ability for species' geographical distributions (Peterson and Cohoon 1999, Peterson 2001, Peterson *et al.* 2001, 2002). Indeed, recent sensitivity analyses addressing the ability of GARP to provide statistically robust distributional predictions indicated that 10–20 occurrence points are sufficient to achieve 90% of maximum predictive accuracy in almost all species (Stockwell and Peterson 2001a).

GARP results were output in the form of ASCII raster grids and imported into ArcView GIS (version 3.2) for analysis. Grids were reclassed to binary coverages, with 0 representing absence and 1 representing presence. In 77 cases, disjunct areas of overprediction, usually owing to historical effects in limiting species' geographical distributions (Peterson *et al.* 1999), were eliminated by taking the intersection of the crude GARP prediction and a polygon indicating the known geographical limits of the species' distribution (Peterson *et al.* 1999). Ideally, model results would have been tested with field inventories; however, few or no studies presented single-site inventory data in a convincingly complete form for Chinese localities.

Analysis

For the richness-based complementarity analyses, we summed predicted distributions to create a surface of predicted species richness (Peterson *et al.* 2000). We identified areas as groups of adjacent pixels with uniform species composition. The first priority area was identified as the area with highest numbers of co-occurring species. We identified and eliminated species present in this first area, and summed the remaining species. The area of maximum species richness based on this reduced set of species was taken as the second priority area. We continued this procedure of summing distributional maps of remaining species until the highest species richness was of single species (Peterson *et al.* 2000). We also applied a rarity based algorithm (Csuti *et al.* 1997). Here species richness is weighted by the multiplicative inverse of range-size (rarity), and area selected so as to maximize the sum of the weighted richness values.

We also considered the 19 existing biosphere reserves across China (http://www.unesco.org/mab/wnbr.htm) to place our results in a more practical context. These biosphere reserves are Baishuijiang, Bogeda, Changbaishan, Dinghushan, Fanjingshan, Fenglin, Gaoligong Mountain, Huanglong, Jiuzhaigou Valley, Maolan, Nanji Islands, Shankou Mangrove, Shennongjia, Tianmushan, Wolong,

Wuyishan, Xilin Gol, Xishuangbanna, and Yancheng, ranging from 4,284 to 1,077,450 ha in size. We evaluated them against the above analysis to determine their effectiveness. After tallying species occurring in each area by eye in ArcView, we chose the protected area richest in bird species as the first one to enter into the heuristic system, eliminated those species from consideration, and identified further priority areas based on the remaining species and repeated the steps mentioned above.

We used two assumptions regarding species distributions to decide whether or not a species is found in a particular reserve. First, we tallied species' presences no matter how large their distributions were within a reserve (''any-occurrence''). In the second assumption, we considered a species as present in a reserve only if it was predicted as present in more than half of the reserve (''range-centre''). We prioritized the species left unprotected under each assumption to identify important area additions to the existing reserve system.

Results

Distributional predictions

The 90 species in this study showed a diversity of geographical patterns, ranging from broadly to narrowly distributed (Figure 1). For example, White-tailed Eagle *Haliaeetus leucogaster* and Baikal Teal *Anas formosa* were predicted to have ample distributions across the country: the former is predicted to be found in 13 of the 19 existing reserves, and the latter in six. In contrast, other species (e.g. Chinese Crested Tern *Sterna bernsteini*, Western Tragopan *Tragopan melanocephalus*) were predicted to have micro-scale distributions; these species are predicted to be present in a single reserve or no reserve.

Analysis

Based on the ''any-occurrence'' assumption, among existing biosphere reserves, Wolong was predicted to hold 23 species, and therefore entered first in the prioritization. Dinghushan was entered second in the system with 16 species, of which 11 were new to the system (i.e. not also in Wolong). Gaoligong entered third, with nine species new to the system. Next in order were Xilin Gol (adding six species), Tianmushan (four species), Jiuzhaigou (three species), Fenglin (two species), and Changbaishan, Bogeda, Shankou Mangrov, and Yancheng, each of which added single species (Table 1). Therefore, among existing protected areas and based on any occurrences, 62 of the 90 endangered species are protected (Figures 2a, 3). A similar area selection using the range-centre assumption became asymptotic at 37 species in 10 reserves, with areas in the following order: Jiuzhaigou (15 species), Dinghushan (adding eight species), Tianmushan (four species), Xilin Gol (three species), Wolong (two species), and Wuyishan, Shennongjia, Maolan , Fenglin and Changbaishan (each adding one species) (Figures 2b, 3).

Assessing the avifauna without considering existing protected areas (Figure 4), an area in southernmost Sichuan Province (centre 102.8°E, 27.0°N) was predicted to hold 20 of the 90 species (Table 1). A second area along the western Heilongji-
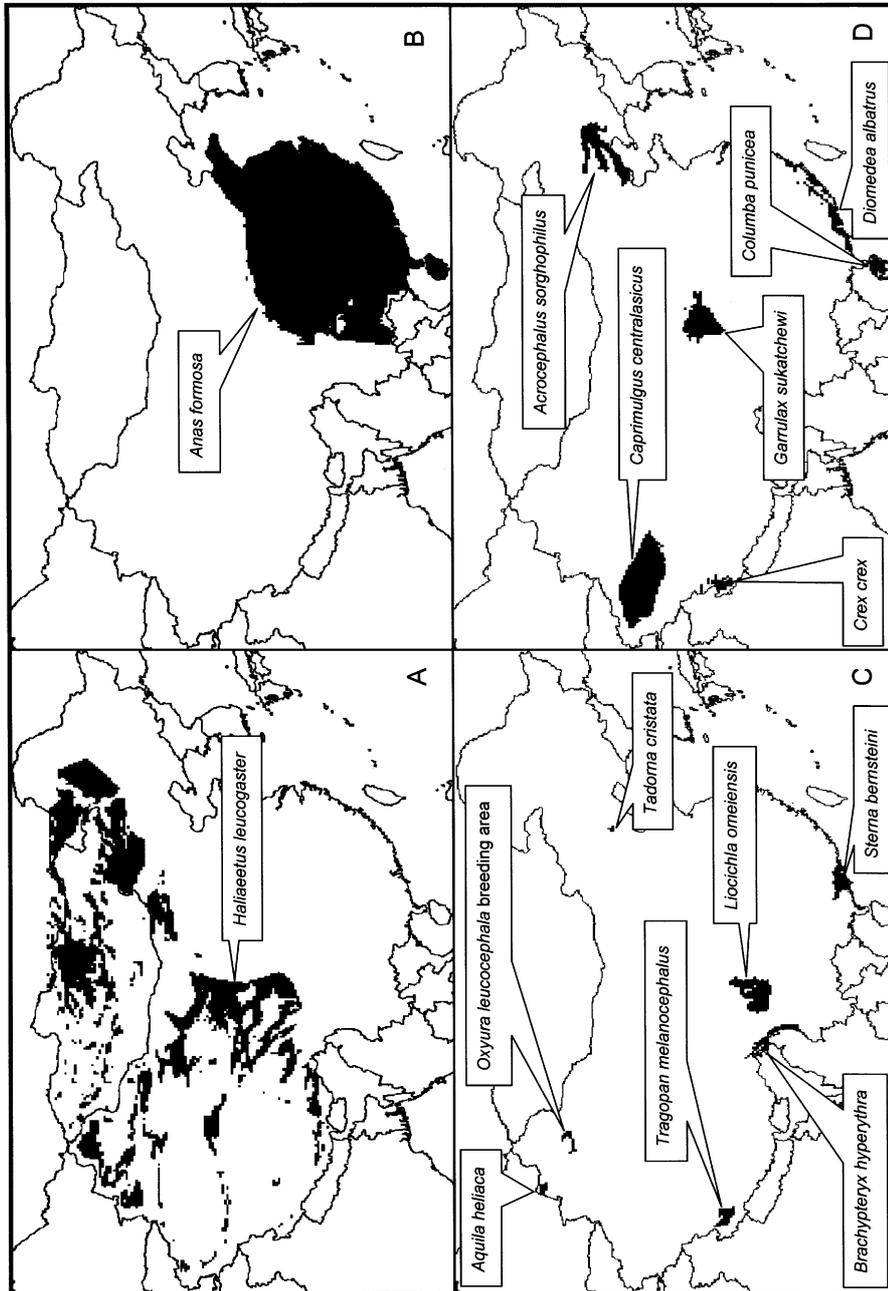
Figure 1. Example distributional models developed in this study for 15 species.

Table 1. Summary of predicted presences and absences of bird species in 19 biosphere reserves in China, as well as in 14 'optimal' areas selected based on our complementarity analyses. Species are numbered, and names are provided in the footnote.[a] 1, any occurrence; 2, range–center occurrence

Area	Area (ha)	1	11	21	31	41	51	61	71	81	91
Existing Areas											
Baishuijiang	213,750	0012221220	1111021021	0100000000	0000000000	0000200000	0001110000	0000000000	0000000000	0000000000	00
Bogeda	217,000	0000000000	0000001000	0000000000	0000000000	0000000100	0000000000	0000000000	0000000000	0010000000	00
Changbaishan	196,465	0000000010	0000000000	0001000000	0000000000	0001011000	0000002100	0000000000	0000000000	0000000000	00
Dinghushan	1,133.4	0000100002	2010000000	0200120022	0210000000	0000000021	1110000000	0000000000	0000000000	0000000000	00
Fanjingshan	38,300	0000200000	2020000000	0220000000	0000000000	0000000000	1000000000	0000000000	0000000000	0000000000	00
Fenglin	28,353	0000000000	0000000000	0000000000	0000000000	0000110000	0000002000	0000000000	0000000001	0000000000	00
Gaoligong Mountain	293,564	1201000100	0000100000	0000000000	0001111000	1100000000	0000000000	0000000000	0000000000	0000000000	00
Huanglong	138,000	1122222220	1112121021	0000000000	0000000000	0000100000	0002110000	0000000000	0000000000	0000000000	00
Jiuzhaigou Valley	106,090	1022222220	1221121022	0000000000	0000000000	0000200000	0002210000	0000000000	0000000000	0000000000	00
Maolan	21,330	0000200002	2020000000	0210000010	0110000000	0000000000	1200000000	0000000000	0000000000	0000000000	00
Nanji Islands	20,629	0000000000	1000000000	0000110011	1110000000	0000110011	0000000000	0000000000	0000000000	0000000000	00
Shankou Mangrove	8,000	0000000001	0000000000	0100110021	0200000000	0000000010	0000000000	0000000000	0000000000	0000000000	01
Shennongjia	147,467	0000200010	2020010010	0220000000	0000000000	0000200000	0000000000	0000000000	0000000000	0000000000	00
Tianmushan	4,284	0000100000	2000000000	0002222211	1110000000	0000000000	0000000000	0000000000	0000000000	0000000000	00
Wolong	200,000	2222222221	1111111111	1110000000	0000000000	0000000000	0000000000	1000000000	0000000000	0000000000	00
Wuyishan	56,527	0000200000	2000200000	0000011222	1120000000	0000000010	0000000000	0000000000	0000000000	0000000000	00
Xilin Gol	1,077,450	0000000000	0000002000	0000000000	0000000000	0022211100	0000000000	0000000000	0000000000	0000000000	00
Xishuangbanna	241,700	0000000100	0000000000	0000000000	0001000000	1000000000	1000000000	0000000000	0000000000	0000000000	00
Yancheng	280,000	0000000000	2000000000	0001210000	0100000000	0000000000	0000000000	1000000000	0000000000	0000000000	00
Potential Areas											
Area 1	485,862	1111111111	1010110000	1000000000	0000011001	1000000000	0000000000	0000000000	0000000000	0000000000	01
Area 2	74,748	0000000000	0000001000	0001010000	0000010000	0010111000	0000011000	0000001100	0000000001	1100000111	00
Area 3	1,345,464	0000000000	1000000000	0000110000	0100000000	0000000000	1100000000	0010000000	0100001000	0000001000	01
Area 4	560,610	0011111110	0101011011	0000000000	0000000000	0000100000	0001110000	0000000000	0000000000	0000000000	00
Area 5	560,610	0000100000	1000000000	0000110111	1110000000	0000000011	0000000000	0000000000	0000000000	0000000000	00
Area 6	560,610	1111000000	0000000000	0000000000	0000000100	0100000000	0000000000	0001010000	0001010000	0001000000	00
Area 7	1,233,342	1111010000	0100001000	0000000000	0000000000	0000000000	0000000000	0000100010	0000100010	0000010000	00

Table 1. Continued

Area	Area (ha)	1	11	21	31	41	51	61	71	81	91
Area 8	6,316,206	0000100000	1000000000	0010001110	0010000000	0000000000	1000000000	0000000000	0000000000	0001000000	00
Area 9	597,884	0000000000	0000001000	0000000000	0000000000	0000000000	0000000000	0000001100	1000000000	0000000000	00
Area 10	298,992	0000000100	0010000000	0000000000	0001000011	1000000000	0000000000	0000000000	0000000000	0000001000	00
Area 11	74,748	0000000000	0000000000	0000000000	0000000000	0011101100	0000000010	0000000000	0000000000	0100000000	00
Area 12	224,244	0000000000	0000000000	0000000000	0000000000	0010101000	0000000000	1000000000	0000100000	0100000000	10
Area 13	672,732	0000000001	1000000000	0100110011	0100000000	0000000011	0110000000	0000000000	0000000000	0000000000	00
Area 14	373,740	0000000000	0000001000	0000000000	0000000000	0000000000	0000000000	0000000000	0011000000	0000000001	00

[a] (1) *Crossoptilon crossoptilon*, (2) *Gallinago nemoricola*, (3) *Grus nigricollis*, (4) *Ithaginis cruentus*, (5) *Latoucheornis siemsseni*, (6) *Leptopoecile elegans*, (7) *Lophophorus lhuysii*, (8) *Luscinia obscura*, (9) *Turdus mupinensis*, (10) *Alcippe variegaticeps*, (11) *Anas formosa*, (12) *Tetrastes sewerzowi*, (13) *Chrysolophus pictus*, (14) *Crossoptilon auritum*, (15) *Garrulax bieti*, (16) *G. lunulatus*, (17) *Haliaeetus leucogaster*, (18) *Liocichla omeiensis*, (19) *Paradoxornis conspicillatus*, (20) *P. przewalskii*, (21) *P. zappeyi*, (22) *Pericrocotus cantonensis*, (23) *Syrmaticus reevesii*, (24) *Coturnicops exquisitus*, (25) *Egretta eulophotes*, (26) *Larus saundersi*, (27) *Megalurus pryeri* wintering area, (28) *Syrmaticus ellioti*, (29) *Arborophila gingica*, (30) *Emberiza sulphurata*, (31) *Pelecanus crispus*, (32) *P. philippensis*, (33) *Tragopan caboti*, (34) *Aceros nipalensis*, (35) *Brachypteryx hyperythra*, (36) *Chrysomma poecilotis*, (37) *Harpactes wardi*, (38) *Lophophorus sclateri*, (39) *Pavo muticus*, (40) *Sitta magna*, (41) *S. yunnanensis*, (42) *Tragopan blythii*, (43) *Anser cygnoides*, (44) *Aythya baeri*, (45) *Sitta villosa*, (46) *Aquila clanga*, (47) *Emberiza jankowskii*, (48) *Falco naumanni*, (49) *Eurynorhynchus pygmeus*, (50) *Diomedea albatrus*, (51) *Leptoptilos javanicus*, (52) *Oriolus mellianus*, (53) *Sterna bernsteini*, (54) *Garrulax sukatschewi*, (55) *Luscinia ruficeps*, (56) *Nipponia nippon*, (57) *Buteo buteo*, (58) *Mergus squamatus*, (59) *Acrocephalus sorghophilus*, (60) *Alcedo hercules*, (61) *Anser erythropus*, (62) *Aquila heliaca*, (63) *Arborophila ardens*, (64) *A. mandellii*, (65) *Babax koslowi*, (66) *B. waddelli*, (67) *Bradypterus major*, (68) *Caprimulgus centralasicus*, (69) *Carpodacus roborowskii*, (70) *Ciconia boyciana*, (71) *Columba eversmanni*, (72) *C. punicea*, (73) *Crex crex*, (74) *Crossoptilon harmani*, (75) *C. mantchuricum*, (76) *Emberiza koslowi*, (77) *Gorsachius magnificus*, (78) *Grus japonensis*, (79) *G. leucogeranus*, (80) *G. vipio*, (81) *Ketupa blakistoni*, (82) *Megalurus pryeri* breeding area, (83) *Oxyura leucocephala* breeding area, (84) *O. leucocephala* wintering area, (85) *Phoenicurus alaschanicus*, (86) *Saxicola insignis*, (87) *Sitta formosa*, (88) *S. solangiae*, (89) *Tadorna cristata*, (90) *Tragopan melanocephalus*, (91) *Turdus feae*, (92) *Urocissa whiteheadi*.
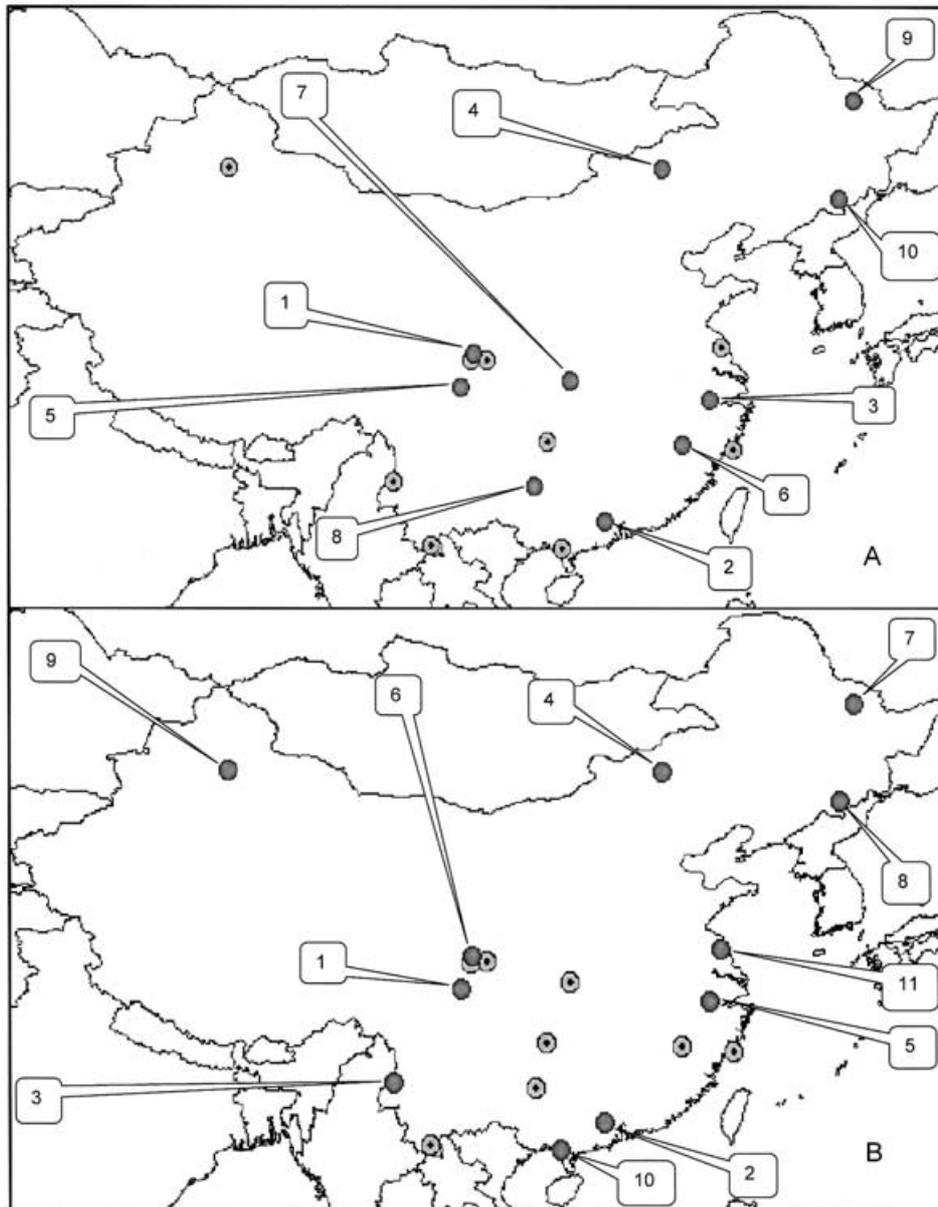
Figure 2. Prioritizations of existing reserves, with numbers corresponding to order of conservation priority: (A) for existing reserves, based on range-centre assumption; and (B) for existing reserves, based on any-occurrence assumption. Dotted circles indicate reserves not included in the priorization based on inability to add species to the system.
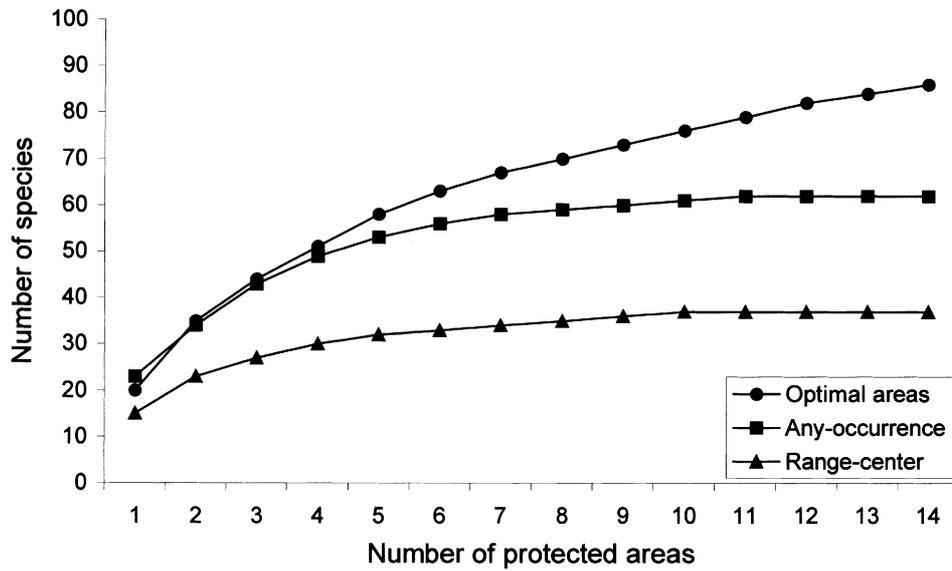
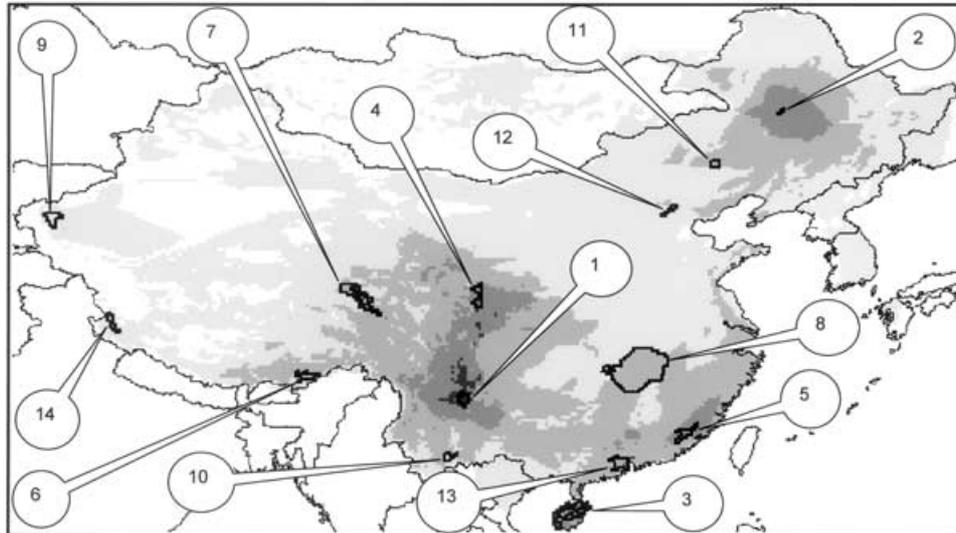Figure 3. Accumulation of species in area selection analyses of existing reserves and of pixels (i.e. without regard to existing reserves) across China.

Figure 4. Richness map for the 90 species and selected pixel-based areas. White indicates species richness of 1–5, light grey 6–10, medium grey 11–15, and dark grey > 16. Dark lines indicate pixel-based potential protected areas, and numbers correspond to order of conservation priority.

ang–northwestern Jilin border (centre 123.3°E, 46.6°N) held 15 species new to the prioritization. A third site in northern Hainan Province (centre 109.9°E, 19.0°N) added nine species to the system. Succeeding areas were southernmost Ganshu Province (seven species), southern Fujian Province (seven species), south-eastern Tibet (five species), southern Qinghai Province (four species), southern Hubei, north-eastern Hunan, and north-western Jiangxi (three species), westernmost Xinjiang Province (three species), southern Yunnan Province (three species), eastern Nei Mongol Province (three species), western Beijing and eastern Hebei Province (three species), southern Guangdong Province (two species) and westernmost Tibet (two species). The area selection ended at iteration 15, in which the six remaining species (*Liocichla omeiensis, Brachypteryx hyperythra, Aquila heliaca, Oxyura leucocephala* breeding area, *Phoenicurus alaschanicus* and *Tadorna cristata*) did not co-occur. Therefore, this area-selected system held 86 species in 14 areas, and 20 areas were identified that included all 90 species (Figure 3). Interestingly, accumulation of species in existing reserves under the ''any-occurrence'' in biosphere reserves assumption equalled the no-reserve approach through the fourth iteration; thereafter, however, accumulation of species in the no-reserve system outstripped that in the existing reserve system.

While assessing the avifauna using a rarity-based approach, without considering existing protected areas, an area in Hebei Province was predicted to hold five of the 90 species. A second area in southern Yunnan Province held eight species new to the prioritization. A third site in northern Hainan Province added 11 species to the system. Succeeding areas were north-western Xinjiang Province (two species), northern Xinjiang Province (one species), western Tibet (two species), eastern Tibet (10 species), southern Guangdong Province (seven species), southern Ganshu and northern Sichuan Provinces (12 species), Sichuan Province (four species), south-western Heilongjinag and northern Jilin Provinces (nine species), western Xinjiang Province (three species), eastern Nei Mongol and northern Liaoning Provinces (three species), eastern Hunan and western Jianxi Provinces (five species), western Beijing and eastern Hebei Province (three species), Qinghai Province (three species), southern Tibet (two species), and south-western Guizhou Province (two species).

Finally, to assess the 55 species not included in existing reserves under the range-centre assumption, we selected areas for just those species to identify the most critical additions to the existing reserve network (Figure 5). An area in north-eastern China (centre 123.5°E, 46.2°N) was predicted to hold 8 of these 55 species; a second area in western Yunnan Province added eight species to the prioritization; and a third site in Hainan Province added seven species to the system. Succeeding areas were in southern Qinghai Province (five species), Sichuan Province (four species), south-eastern Guangdong Province (three species), western Beijing and eastern Hebei Province (three species), western Xinjiang Province (three species), Nei Mongol, Ganshu, Qinghai and Ningxia provinces (two species), south-eastern Tibet (two species) and western Tibet (two species). The area selection ended at iteration 13, in which the six remaining species (*Aquila heliaca, Brachypteryx hyperythra, Oxyura leucocephala* breeding and wintering areas, *Sitta formosa*, and *Tadorna cristata*) did not co-occur. While assessing the 55 species not included in existing reserves under the range-centre assumption with species-richness method, we obtained almost the same results.
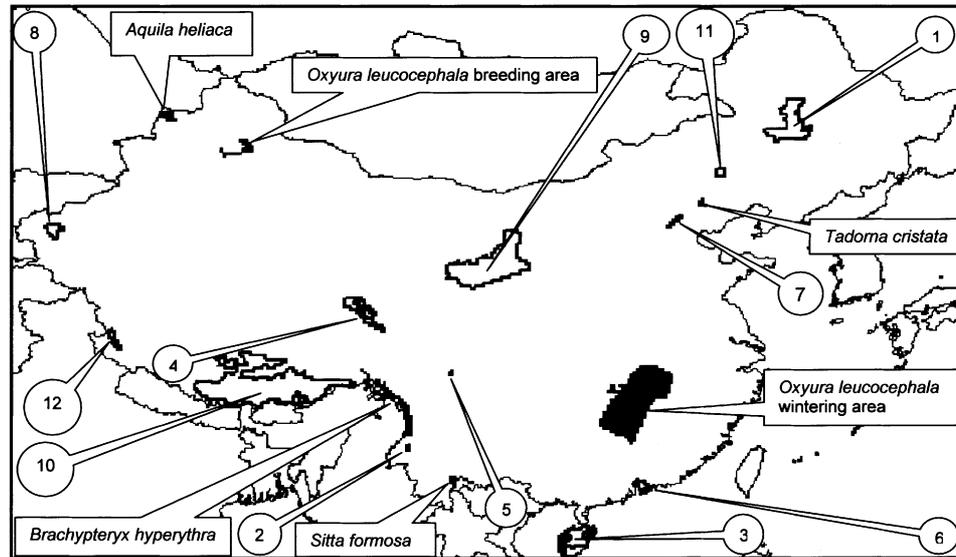
Figure 5. Potential additions to the existing reserve network, based on analysis of 55 species not included in existing reserves, based on the range-centre assumption. Priority areas are indicated in order by numbers, and the six species that do not co-occur with other species are also shown.

Discussion

Several considerations need to be taken into account concerning the area selection procedure employed. Obviously, the conclusions of this study are only as good as the distributional predictions on which they are based. However, several studies indicate that GARP is a valid approach to predicting the distribution of species (Stockwell and Peterson 2002a, b, Peterson 2001, Godown and Peterson 2000, Peterson *et al.* 2001, 2002). In general, although statistical tests were not feasible owing to the relatively small amount of occurrence data available, we expect that about 90% of the models developed and used predict geographical distributions much better than would be expected at random.

The application of complementarity methods to predictive models is also in the early stages of development. Complementarity can produce odd combinations of areas because of its clear emphasis on the most different faunal compositions, and for that reason further area selection procedures have been developed, such as the rarity approach used herein. Application of more complex methodologies (e.g. Williams *et al.* 1996) in the present example, however, is complicated by the enormous number of pixels under consideration in our analyses, in contrast to the usual applications of such methods (Peterson *et al.* 2000). Nevertheless, previous applications of our approach (Peterson *et al.* 2000) have shown clear utility in identifying important areas for conservation action.

The pixel-based area selection (i.e. no attention paid to existing reserves) includes 86 of the 90 species in the first 14 areas (Figure 3), whereas the selection among existing reserves can only protect 62 (any-occurrence assumption) and 37 (range-centre assumption) species, respectively. Curves based on existing reserves

were asymptotic after 10–11 reserves. Our analysis of unprotected species identified additional areas for exploration as potential next priorities for protection.

Our comparison of pixel-based area selection with those of existing protected areas suffers somewhat from differences of scale. Existing protected areas range as large as 10^6 ha, whereas individual pixels are 37,300 ha each, nearly two orders of magnitude smaller. Hence, this contrast further emphasizes that the pixel-based area-selection approach not only achieves better coverage of species, but also does it much more efficiently per unit area.

Acknowledgements

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