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Conservation assessment and prioritization of areas in Northeast India: Priorities for amphibians and reptiles

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ABSTRACT

This study combines niche modeling and systematic area prioritization using distribution data for 131 species of amphibians and reptiles from Northeast India and Burma, with two objectives: (i) to evaluate the performance of the current conservation area network in Northeast India with respect to the representation of amphibians and reptiles, and (ii) to identify potential areas for expanding the current conservation area network. In a two-step protocol, maximum entropy niche modeling was used to project species' potential geographic occurrences, and the resulting probabilistic distribution data were used to prioritize areas with algorithms that maximize the representation of all species in minimal total area. The results provided a critical assessment of conservation priorities in this data-deficient region, and indicate the utility of combining niche modeling with systematic area prioritization in such situations. Many areas that had been overlooked in previous assessments were identified. Although the existing protected areas were found to be inadequate for representation of amphibian and reptile diversity, the prioritization results show that by targeting a minimal representation of 5% of the current total area suitable for each species, the gaps can be filled with a relatively modest (0.41%) increase in the current total area covered by the network. Extended analyses were also performed to assess the effects of putatively rare species on reserve selection, which showed that the inclusion of these taxa can change the prioritization solutions significantly. The prioritization results also highlight areas of Northeast India that warrant attention from future surveys.

1. Introduction

The selection and management of conservation areas in biodiversity rich tropical regions poses many challenges. On one hand, the tropics have some of the fastest rates of degradation of natural land cover, while on the other, they are generally data-poor and cash-strapped (Myers et al., 2000; Mittermeier et al., 2004). Resource constraints generally preclude systematic data collection for multiple taxonomic groups, making it difficult to ensure maximal representation

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of overall biodiversity of the region in a set of conservation areas. This situation therefore requires the development of methods that make maximal use of the information content in available biological data. In the last few years, the integration of two different techniques has shown great promise towards achieving this goal: ecological niche modeling combined with systematic area prioritization (Sanchez-Cordero et al., 2005; Fuller et al., 2006).

Niche modeling (also called habitat modeling; Kearney, 2006) aims at predicting species' geographic distributions using data on observed presence records and associated environmental variables (which may be biotic or abiotic). It is based on an assumption of niche conservatism, that is, the tendency of species to retain ancestral ecological niches (Peterson et al., 1999; Wiens and Graham, 2005). Niche models identify areas that are ecologically suitable for the presence of a species based upon samples of its realized niche (typically by establishing environmental correlates of observed geographical occurrences). Systematic area prioritization aims at selecting conservation area networks using algorithms that seek to maximize biodiversity representation in as little land as possible, often also incorporating other spatial criteria such as size or compactness of each individual area (Margules et al., 2002; Sarkar et al., 2002).

Combining these two methods, this study performs a systematic area prioritization for the Northeast (NE) India region. For area prioritization, multiple biological groups should ideally be included to maximize overall biodiversity coverage. However, sufficient data to do this are rarely available, and such analyses frequently have to make do with available taxonomic groups. The taxonomic groups used in this study are amphibians and reptiles. Thus, what this study directly establishes is a network of priority areas for conservation of these groups. Amphibians and reptiles are important components of biodiversity which are often under-represented in conservation planning. NE India and Burma are known to harbor a diverse amphibian and reptile fauna with a high percentage of endemic, threatened species (see study area description below). Moreover, amphibians have emerged as a major conservation concern in many areas of the world because of the global declines in their numbers in recent decades (Alford and Richards, 1999). Area prioritization with these groups in NE India will therefore offer an important preliminary evaluation of the conservation status of the Himalaya and Indo-Burma global biodiversity hotspots (the region forms a significant major part of both these hotspots; see below), both of which have hitherto been subjected to negligible conservation evaluation or area prioritization (Conservation International, 2006).

Many studies make the explicit or implicit assumption that the taxa being used for area prioritization are adequate surrogates for overall biodiversity in the region. There is mounting evidence however, that this assumption is often not valid (Flather et al., 1997; Moritz et al., 2001; Lund and Rahbek, 2002; Kati et al., 2004; Sarkar et al., 2005). Recent work on cross-taxon biogeographical concordance in this region also indicates that amphibians and reptiles may be reasonable surrogates for certain subgroups of birds, but probably not for birds as a whole (Pawar et al., 2006). The results of this study, therefore, should not be taken to identify priority areas for other taxonomic groups. To conserve all of biodiversity adequately in NE India will require the incorporation of further analyses using other groups to augment the results reported here.

This study has two main objectives: (i) evaluation of the existing set of protected areas with respect to its performance in representing the chosen biotic groups (amphibian and reptile species) adequately, and (ii) identifying priority areas for expanding the existing protected areas. The prioritization is based upon projected distributions generated by niche modeling of amphibian and reptile occurrence data collected from extensive surveys in India and Burma.

2. Methods

2.1. Study area

NE India lies between 29.46°– 21.96°N and 97.39°–89.87°E, covering a total area of about 255,168 km^2 that includes eastern and western parts of the Himalaya and Indo-Burma global biodiversity hotspots, respectively (ca. 8.2% of the 3,114,763 sq. km occupied by both the hotspots; Mittermeier et al., 2004). The region covers seven Indian states: Arunachal Pradesh, Assam, Manipur, Meghalaya, Mizoram, Nagaland, and Tripura. Physiognomically and biogeographically, the region can be broadly differentiated into the Eastern Himalayas in the north, the Northeast Hills in the south, and the Brahmaputra River Basin in between (Mani, 1974) (Fig. 1). Of these, the Eastern Himalayas and Northeast Hills are primarily montane with differing geological origin and morphology, while the Brahmaputra River Basin consists of the flood plains and lower catchments of the Brahmaputra river (Mani, 1974). NE India harbors exceptional biological diversity and has a relatively complex biogeography due to a combination of factors, including its age, unique plate tectonic and palaeoclimatic history, location at the confluence of distinct realms (Afrotropic, Palearctic, and Indo-Malay; Olson et al., 2001), wide physiognomic range (e.g., altitude ranging from about 100 to >7000 m above sea level) and vegetation diversity (from tropical to alpine) (Mani, 1974).

Although both the Himalaya and the Indo-Burma hotspots are data-deficient, existing knowledge about plant and vertebrate diversity provide clear indications of their biodiversity values (Mittermeier et al., 2004). In case of the Himalaya hotspot, 32% of the 10,000 known vascular plant species, 40% of the 105 known amphibian species, and 27.3% of the 176 known reptile species are endemic (Conservation International, 2006). In the case of the Indo-Burma hotspot, 52% of the 13,500 known plant species, 53.8% of the 286 known amphibian species, and 39.1% of the 522 known reptile species are endemic (Conservation International, 2006). A significant proportion of these species are considered threatened (although the precise numbers are poorly known; Conservation International, 2006).

2.2. Species' distribution datasets

Species' distribution data were collected from NE India, Burma, and Yunnan Province, China. A majority of the data came from the Myanmar Herpetological Survey Project, a

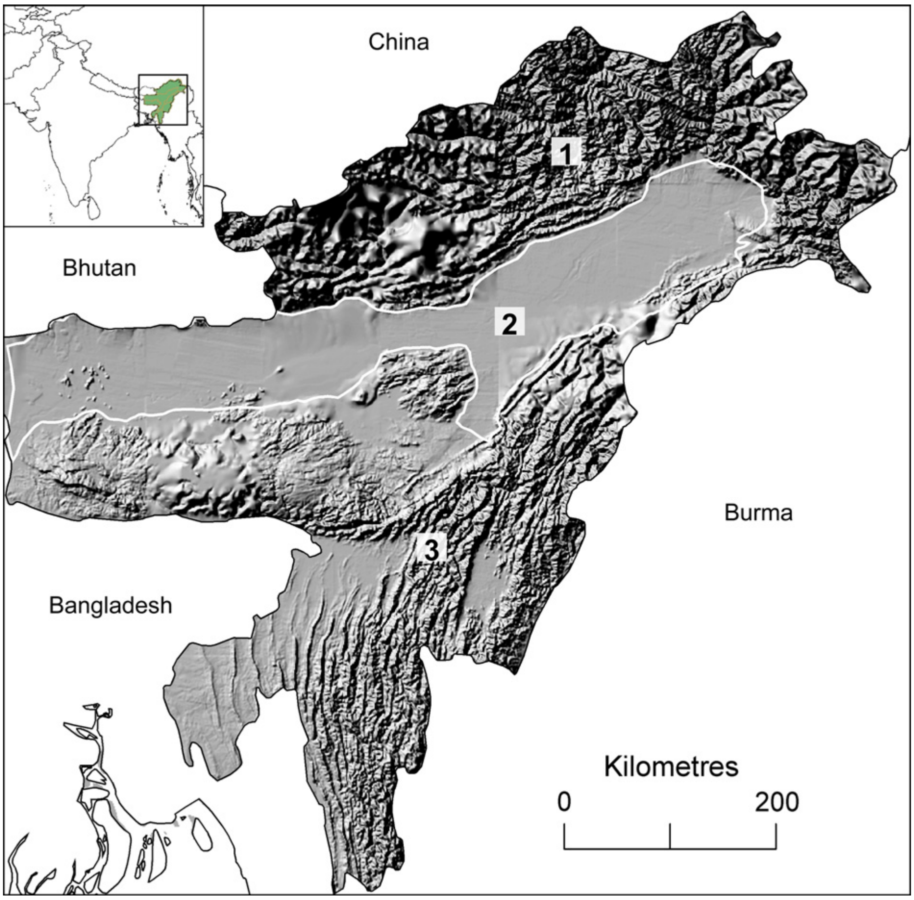

Fig. 1 – Map showing digital elevation model of Northeast India (shaded region in the inset map of South Asia) with major subregions (delineated by white lines) (modified from Olson and Dinerstein, 2002; GIS data from World Wildlife Fund, 2006). The subregions are: [1] Eastern Himalaya (East Himalayan forest zones of Olson and Dinerstein, 2002), [2] Brahmaputra River basin (the Brahmaputra valley forest zone of Olson and Dinerstein, 2002), and [3] Northeast Hills (Meghalaya and Mizoram–Manipur–Kachin forest zones of Olson and Dinerstein, 2002).

collaborative effort between the Nature and Wildlife Conservation Division (a division of the Forest Department of Burma), the Department of Herpetology at the California Academy of Sciences, and the Division of Amphibians and Reptiles at the National Museum of Natural History, Smithsonian Institution. The surveys were conducted from November 1999 through May 2004. All data from within NE India were collected by the Biodiversity and Biocultural Conservation Laboratory at the University of Texas at Austin and collaborators based in India.

Field techniques: Amphibians and reptiles were located by nocturnal and diurnal opportunistic searching in appropriate terrestrial and freshwater habitats. All animals retained as voucher specimens were humanely killed according to the guidelines established by the American Society of Ichthyologists and Herpetologists, The Herpetologists' League, and the Society for the Study of Amphibians and Reptiles (American Society of Ichthyologists and Herpetologists et al., 1987). Specimens were fixed with 10% neutral-buffered formalin. In the case of the Myanmar Herpetological Survey Project, all amphibian and reptile taxa encountered were collected, except those listed in CITES Appendix 1 or on the US Endangered Species List; instead, photographic vouchers of these species were taken and deposited at California Academy of Sciences. Detailed microhabitat data and GPS locations were recorded for all specimens encountered. As far as possible, each specimen was identified to species in the field and verified in the laboratory. The protocol for the data collection in NE India was similar, except that specimens were collected according to area-specific permits given by the Ministry of Environment and Forests, India (Pawar and Birand, 2001).

Secondary data: A small proportion (2.4%) of the data was retrospectively georeferenced from historical museum data. Procedures for retrospectively georeferencing written locality descriptions follow the protocol of HerpNET (www.herpnet.org; last accessed on August 14, 2006) and the methodology followed by Wieczorek et al. (2004). Place names were located with gazetteers from NIMA-GeoNET Names Server or with paper topographic maps. Offsets (unless specified) were assumed to take place along a road or trail, and likely paths were thus sought out. If none were available, air distances were assumed and measured out. In either case, these measurements were calculated in a GIS application (ESRI ArcView®3.3) or digitized from paper maps. In all cases, maximum distance error values were calculated using the online java Applet: http://elib.cs.berkeley.edu/manis/gc.html (last accessed on August 14, 2006). Commonly used base map sources included: Digital Chart of the World (for roads and hydrology, at 1:1,000,000 scale; available from http://www.maproom.psu.edu/dcw/dcw_about.shtml#DCW, last accessed on August 14, 2006); Australian Centre of the Asian Spatial Information and Analysis Network (for secondary and tertiary administrative boundaries; available from http://www.asian.gu.edu.au/; last accessed on August 14, 2006); GTOPO (30 minute Digital Elevation Models, available from http://edc.usgs.gov/products/elevation/gtopo30/gtopo30.html; last accessed on August 14, 2006). Georeferencing was verified by comparing the historical localities against basic administrative boundaries (primary, secondary, tertiary, etc.) or known ranges by experts to search for obvious outliers that may indicate transcription or georeferencing errors.

Data processing: The unprocessed data set consisted of 10,685 records (10,154 from Burma, 369 from Yunnan Province, China, and 223 from NE India). Of these, 98.2% of the data were collected between 1997 and 2005. The seasonal (monthly) distribution of sampling effort is summarized in Fig. 2. Much of the data included taxa that are either undergoing taxonomic revision, or can only be identified tentatively. To address this problem, expert opinion and identifications were solicited from researchers (see Acknowledgments). Taxa that could not be assigned species-level identification, but clearly belonged to a monophyletic clade, were placed under a pseudotaxon with the generic epithet (typically by adding "sp." to the genus name). Taxa known to be particularly problematic in terms of their taxonomic status or were unlikely to be monophyletic were then removed. Taxa with only single records were also removed.

The processed dataset consisted of 184 species (63 amphibian and 121 reptile species) represented by a total of 2908 records, with a range of 2–208, and a median of 8 (Fig. 2).

2.3. *Niche modeling*

Niche modeling was performed using the Maxent software package (version 2.2) (Phillips et al., 2004, 2006). Maxent uses the maximum entropy principle: in the estimation of an unknown probability distribution (over some space), the least biased solution is the one that maximizes its entropy, subject to some constraints that reflect available information. In the case of ecological niche modeling, the target is to calculate a probability distribution (the niche model) for a species over the given geographical space (the pixels), using information from the observed association of the species' localities with environmental variables (e.g., climatic layers). Maxent calculates this maximum entropy distribution, using the observed association between the species' and environmental layers to set the following constraint: the expected value (expectation) of each "feature" (which is either an independent variable itself, or one derived from it) under the estimated distribution must be similar to its observed average over sample locations. The resulting model is a probability distribution over all grid cells in the chosen geographical space (the values across all the cells add to 1), and expresses the suitability of each grid cell as a function of the environmental variables in it. A high value of the function at a particular grid cell indicates that it is predicted to have suitable conditions for that taxon. Maxent has been shown to be robust for modeling presence-only occurrence data, outperforming many other traditional techniques such as GARP (Elith et al., 2006).

Ninteen environmental variables, each at a resolution of 30″ (0.008333° × 0.008333°, or ≈1 sq. km), were obtained from the WorldClim database (interpolated from global climate datasets; Hijmans et al., 2005). An additional spatial layer of elevation from 30″ SRTM data was also used. Table 1 provides a list of the environmental variables. All layers were clipped to an area bounded by 29°34′ 25.56″N by 87°49′ 20.77″E and 8°43′ 39.94″N by 101°19′36.44″E, a rectangular box containing all of NE India and Burma, and covering all the sample data points (many of which lay in adjoining regions). Additional environmental layers were not included in the niche modeling primarily because GIS data at 1 km resolution were not available for the region. A coarsening of spatial resolution would have allowed the use of soil and vegetation type data, but given the relatively small spatial extent of the NE India region, preference was given to a fine-scale analysis, albeit with fewer environmental variables. In addition, a coarsening of resolution would have excluded many taxa from the analysis because Maxent was run without duplicates; at most one

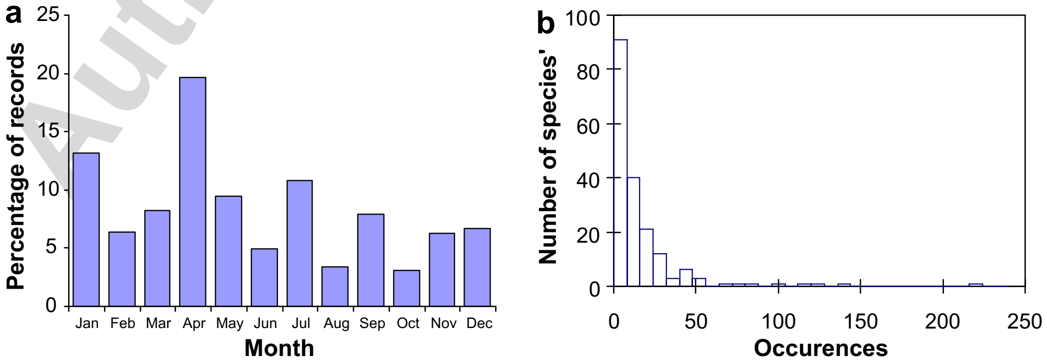

Fig. 2 – (a) Temporal distribution and (b) frequency distribution of occurrence data for amphibians and reptiles from NE India and Burma.

Table 1 – Environmental data used in distribution modeling

Environmental datum
Annual mean temperature
Mean diurnal range
Isothermality
Temperature seasonality
Maximum temperature of warmest month
Minimum temperature of coldest month
Temperature annual range
Mean temperature of wettest quarter
Mean temperature of driest quarter
Mean temperature of warmest quarter
Mean temperature of coldest quarter
Annual precipitation
Precipitation of wettest month
Precipitation of driest month
Precipitation seasonality
Precipitation of wettest quarter
Precipitation of driest quarter
Precipitation of warmest quarter
Precipitation of coldest quarter
Altitude

sample (presence record of each taxon) was allowed per pixel. This was necessary because given the opportunistic nature of the survey effort, presence of multiple records within a pixel could not be interpreted as abundance.

Maxent was run using the linear, quadratic and product features (Phillips et al., 2006). The product feature captures the effect of interactions (covariances) between pairs of features (Phillips et al., 2006). Threshold and hinge features (both of which involve imposing cut-offs on continuous-valued environmental data) were not used because the theoretical basis for their use is unclear (Phillips et al., 2004, 2006), and exploratory models with the Indo-Burma data using these features were seen to result in spatially clustered predictions. Maxent is a relatively new method, and there have been few evaluations of how the results vary with changes in the algorithm convergence threshold across different taxonomic groups. Hence a convergence threshold of 10^{-5} was chosen, as it has been used in previous studies with Maxent (Phillips et al., 2004, 2006).

In Maxent, the stringency of the constraint that the features' observed averages and expectations must be similar, is controlled by a 'regularization' parameter beta β (Phillips et al., 2006). Due to biases associated with museum and survey data, empirical means of features will at best be crude approximations of the true mean of the environmental data that comprise a taxon's realized niche. For example, if surveys are biased towards certain areas, the sample data will be spatially clustered, and the sample mean will be a poor estimator. For small sample sizes, this predisposes the procedure towards overfitting, resulting in the modeled distributions tending to be clustered around sample localities. Maxent 2.2 attempts to minimize this problem by adjusting β according to each taxon's sample size (achieved by setting β to "auto" in the graphic user interface) and the types of features used (Phillips et al., 2006). Fig. 3 shows a plot of β values versus sample sizes for the full set of 184 species. If this approach towards regularization is sufficient to reduce overfitting, a linear increase in the number of iterations to convergence is expected across all taxa. To test this, a test run of Maxent was conducted with 1000 iterations with a subset of the data that had relatively small sample sizes (<50) for the NE India–Burma dataset. However, no significant increase was noted and for a number of taxa with <20 samples, convergence is not achieved even after a large number of iterations (Fig. 4). An examination of the geographical distribution of the data also suggested that spatial clustering of sample occurrences might be an additional factor resulting in overfitting. Thus, despite adjustment of the regularization parameter β, overfitting would remain a problem for a large part of the dataset. Hence, an additional technique was used to reduce overfitting by lowering the number of iterations (350). This number was chosen on the basis of convergence pattern in the sample run; a number of small sample-sized taxa (samples <30) had iteration values above this threshold (Fig. 4).

To gauge the accuracy of the niche models, Maxent performs threshold-dependent as well as threshold-independent tests ("threshold" here refers to the Maxent output, and not to the derived environmental features mentioned above). Both methods require random subsets of the data to be set aside for testing. For threshold dependent testing, the continuous numerical value of each pixel is converted to binary presence/absence using some threshold. A one-tailed binomial test is then used to determine whether a the model predicts the test localities significantly better than random (Phillips et al., 2006). Maxent 2.2 implements 10 different thresholding methods and reports one-tailed p-values for the binomial test of each. The threshold-independent test consists of the receiver operating characteristic analysis procedure modified for presence-only data (Phillips et al., 2006). In this method, a receiver operating characteristic curve is obtained by plotting sensitivity (fraction of correctly predicted presences) on the y-axis and 1 – specificity (specificity is fraction of all absences correctly predicted as such) on the x-axis for all possible thresholds (all possible cutoffs for probability of presence). The area under the curve then provides a measure of model performance that is independent of any particular choice of threshold. Values for area under the curve >0.5 indicate a

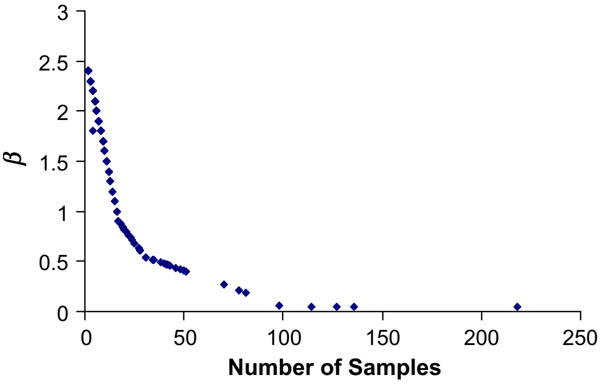

Fig. 3 – The relationship between sample size and the regularization parameter β of MaxEnt for the initial set of 184 taxa used in the niche modeling. See the text for discussion.

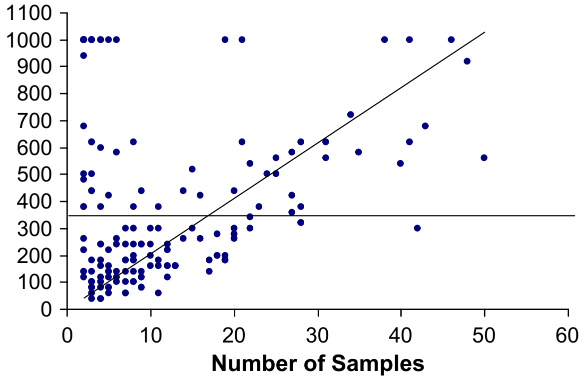

Fig. 4 – Number of iterations to convergence as a function of sample size (number of occurrences) in a sample MaxEnt run with the iteration limit set to 1000. The straight line, obtained by forcing a least squares regression through zero is meant to depict the kind of relationship that might be expected, given the kind of adjustment for β (Fig. 3) that is implemented in MaxEnt. The horizontal line (at 350) is the uniform cutoff that was chosen for curtailing iterations, based upon the fact that a large number of species with small sample sizes (<30) either do not converge at all, or do so at well beyond this cutoff, potentially resulting in overfitting. See text for further discussion.

better-than-random model prediction. 25% of the records for each taxon were set aside for performing these tests, which eliminated all species that had <4 records, reducing the total number of taxa from 184 to 131 (46 amphibians, 35 lizards, and 50 snakes). Results of both the statistical tests for niche models of each of these 131 species were then screened, and the subset whose models met the criteria of area under the curve >0.75 (receiver operating characteristic test) and p-value <0.05 for at least one of the 10 binomial tests (corresponding to the 10 different thresholds applied) were kept aside. Niche models for 80 species met these criteria (25 amphibians, 26 lizards, and 29 snakes), and these were the only models used to perform the main ResNet analyses. All these had $\geqslant 9$ occurrences, indicating that undersampled (and potentially rare) species tended to have relatively inaccurate niche models.

2.4. *Evaluation of existing protected area network and area prioritization*

Data on existing protected areas: The data were obtained from IUCN's World Database on Protected Areas dataset (WDPA Consortium, 2006), and verified using Landsat imagery and other independent sources. Only designated sanctuaries and national parks were included in the prioritization analysis, excluding all other areas such as protected and reserved forests as well as those proposed for formal designation but not yet gazetted. These areas were excluded because the level of protection they enjoy and the amount of conservation resources invested in them is typically poor due to their legal status.

Area selection algorithms: The ResNet software package (Garson et al., 2002) was used for the existing protected area evaluation and area prioritization. ResNet incorporates a computationally efficient algorithm for large data sets and has a framework that allows both presence–absence as well as probabilistic distribution data to be used with a flexible set of algorithms (Kelley et al., 2002; Garson et al., 2002; Sarkar et al., 2004). The algorithms implemented in the software are heuristic (belonging to a family of algorithms originally proposed by Margules et al., 1988), designed to select places on the basis of rarity (presence of rare taxa) and complementarity (maximizing representation of those taxa that have not yet achieved their targets in the selected set). The procedure seeks to achieve a given target of representation (fraction of the total cells in which a taxon is present) for all biodiversity taxa in as little area as possible. Constraints on the maximum area of the selected cells and the cumulative cost of selection can also be imposed optionally. The prioritization procedure is initialized either by the selection of a first cell on the basis of rarity, richness, or from a user-defined set of areas (the last option being relevant if the existing set of protected areas is to be augmented). Areas are then iteratively added to the network on the basis of rarity, breaking subsequent ties using complementarity. Should ties still remain, adjacency can be used optionally (an area adjacent to already selected ones being preferred to one that is not). Final ties are broken by selection of a random area. The iterations are repeated until the chosen targets of representation for all taxa are achieved, a cost or area constraint is exceeded, or no cells with data are left. Finally, because this procedure does not guarantee that cells do not become redundant by the time the solution is found, cells that can be removed while still achieving the representation target for all taxa, are eliminated.

As noted earlier, the raw Maxent output is a relative probability distribution over all pixels in the area chosen for niche modeling. The value of each pixel is hence typically very small and cannot be interpreted as a probability of occurrence. For use in ResNet, the Maxent output for each species was therefore rescaled by dividing all pixel values by the highest relative probability over the entire area (maximum cell value across the landscape). This yielded values ranging from 0 to 1, which could be interpreted as probabilistic expectations of occurrence (Sarkar et al., 2004). This rescaling incorporates the assumption that a species is present at the pixel at which the niche model attributes the highest relative probability for it in the entire geographic space. Appendix 1 gives the species' list and their total expected occurrence in NE India.

The parameter settings chosen for the ResNet runs in this analysis mostly follow Sarkar et al. (2002). Two types of cells were masked (excluded) from all ResNet runs: those that did not lie within the political boundaries of Northeast India, and those that were identified as being unsuitable for use in conservation planning because of land use status. The latter were eliminated using categories 11–13 (classified as cropland, bare ground, and urban land, respectively) of the Global Land Cover Characterization data at a 1 sq. km resolution (Hansen et al., 1998). The resulting ResNet input data consisted of 285,461 cells covering a total area of 218,663 km^2. Of these cells, 13,662 (10,465 km^2) were located in the existing protected areas (5.2% of the total area). This is slightly less than the actual area covered by the existing protected areas in the region (11,309 km^2) because some of the areas excluded from the analysis due to lack of suitable land cover lay within protected areas.

For evaluation of the existing protected areas, ResNet runs were initialized with rarity to assess what proportion of the selected area (cells) lay outside the existing protected areas. Initialization with richness was not chosen because it is known to result in inefficient area selection (Garson et al., 2002). In contrast, for area prioritization, initialization with the existing protected areas was used. This procedure identifies areas by which the existing protected area network can be augmented rather than proposing a new conservation area network that reconfigures the existing one, which is not feasible logistically or politically. Redundant areas were always removed from the final solution.

For both evaluation and prioritization, targets of representation of 5%, 10%, 15%, and 20% of the total expected occurrence (across all cells) of all taxa were used, resulting in a total of 8 runs. For each species, Appendix 1 shows the difference in taxon representation between the existing protected areas (the expectation sum within protected areas projected by the niche models) and that needed across the chosen range of representation targets (the expectation sum that ensures a given percentage of representation of each taxon in the landscape). This is the deficit in representation that ResNet seeks to eliminate as economically as possible. This particular range of targets was chosen because those typically used in conservation planning fall within this range (e.g., 10% (IUCN, 1983); and 12% (Hummell, 1995) of the total area). Adjacency was not used in any of the runs in order to carry out the assessments in the simplest scenario, i.e., only using the criteria of taxon representation and minimization of the conservation area network's geographical extent. Neither maximum cost nor maximum area constraints were set for any of the runs because this is an initial evaluation and it is difficult to parameterize these criteria at this relatively early stage of systematic conservation planning for this region.

In addition, ResNet analyses were conducted using all 131 species, irrespective of the accuracy of their niche models. The purpose of including all species was to gauge the effect of eliminating potentially rare species. That species excluded based on poor modeling performance are potentially rare is strongly indicated by the fact that all but 5 of the 51 had $\leqslant 9$ sample occurrences. To compare results using the two different sets of taxa (one a subset of the other), percentage overlap was calculated for the solutions of the ResNet runs with both types of algorithm initializations (rarity and existing protected areas).

3. Results

A summary of the ResNet results using the subset of 80 species is given in Table 2. Fig. 5 maps the selected conservation area network and existing protected areas for different values of species representation targets.

3.1. *Evaluation of existing protected areas*

By initializing ResNet with rarity alone, the place prioritization procedure seeks areas of potential importance without any constraint about whether from the existing protected areas must be included. With this initialization, the efficiency (spatial economy) of the solution measured as the total selected area relative to the total available area (for other measures of efficiency, see Pressey and Nicholls, 1981), increases rapidly with taxon representation target from 4.02% to 17.03% of total area (Table 2). This is a difference in area from the existing set of protected areas ranging from −1.14% (greater efficiency) to +11.86% (lower efficiency). The corresponding overlap between the existing protected areas and the selected cells ranges from 3.82% to 19.96% across representation targets. Fig. 5a clarifies the sources of spatial disparity between selected sites and existing protected areas across representation targets. Relative to currently protected areas, prioritized areas are noticeably more represented in the eastern parts of the Eastern Himalayas, southern and western parts of the Northeast Hills and western and northeastern parts of the Brahmaputra River Basin across solutions of all representation targets (Fig. 1). Even at 20% representation, no cells are selected at the western end of the Eastern Himalayas or the northeastern parts of the Northeast Hills.

Table 2 – Summary of results of the NE India conservation area network evaluation and prioritization using ResNet with 80 species

Algorithm initialization	Taxon representation target (%)	Area selected (percent of total area)	Change from current set of protected areas (%)	Intersection between current set of protected areas and selected conservation area network (%)
By rarity (conservation area network evaluation)	5	8812 (4.02%)	−1.14	3.82
	10	18,033 (8.25%)	+3.08	7.85
	15	27,465 (12.56%)	+7.39	12.35
	20	37,237 (17.03%)	+11.86	19.96
By conservation area network (area prioritization)	5	12,208 (5.58%)	+0.41	100.00
	10	19,753 (9.03%)	+3.86	100.00
	15	28,898 (13.22%)	+8.04	100.00
	20	38,351 (17.54%)	+12.37	100.00

All areas are in km^2. The last column shows percentage of selected area that was previously protected (existing protected areas: 9831 km^2), corresponding to the areas of intersection shown in the maps in Fig. 5.

3.2. *Area prioritization*

Initializing the selection algorithm by currently protected areas puts constraints on the selection of areas that do not already exist in the conservation area network. Compared to initialization by rarity, this results in a greater increase of area projected to be required by the conservation area network (Table 2). This increase over the existing protected area network ranges from 0.41% (for 5% representation) to 12.37% (for 20% representation) of the total area of NE India. Fig. 5b (upper map) shows that to achieve the 5% representation target for all species, a few additional areas would need particular consideration in the eastern Eastern Himalayas, southern and western Northeast Hills and western and northeastern Brahmaputra River Basin (compare with Fig. 1). For the high-end value of 20% as the representation target, the overall solution appears to converge on the one for the same target with initialization by rarity (lower map in Fig. 5b), but key differences remain. For example, no selected areas appear in the western Eastern Himalayas even at this level of representation. However in terms of efficiency alone, the solutions based on either initialization type converge with increasing targets

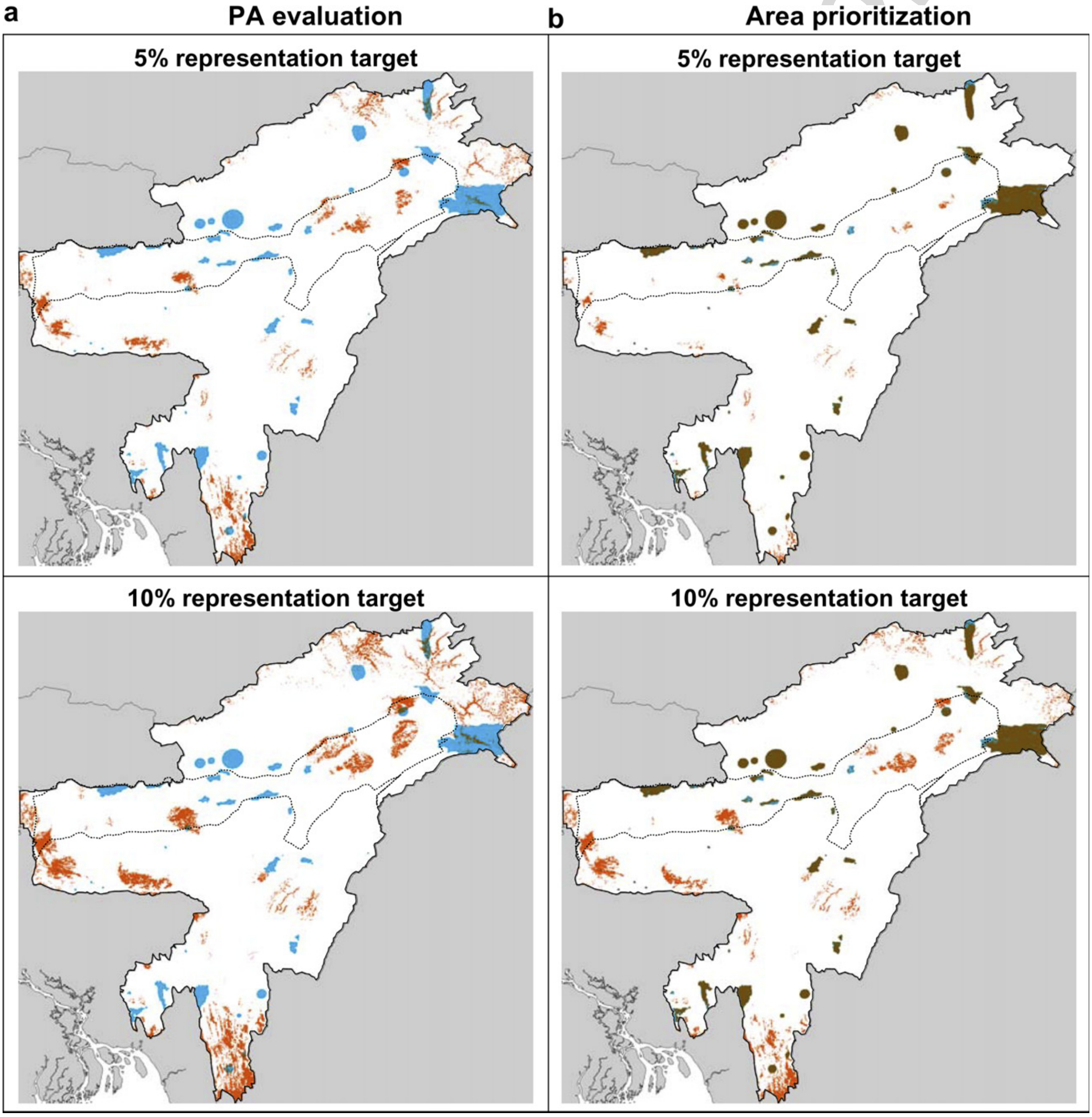

Fig. 5 – Conservation area network evaluation (initialization by rarity) and area prioritization (initialization by conservation area network) for NE India obtained by ResNet analyses. The boundaries of the three subregions are shown with dotted lines (compare with Fig. 1). Note that the maps in the panel B have 100% intersection between selected and conservation area network area because the initialization was by existing protected areas. Across both types of initialization, the area covered by selected cells (dark grey) increases with targeted representation of taxa. See Table 2 for a numerical summary of these results.

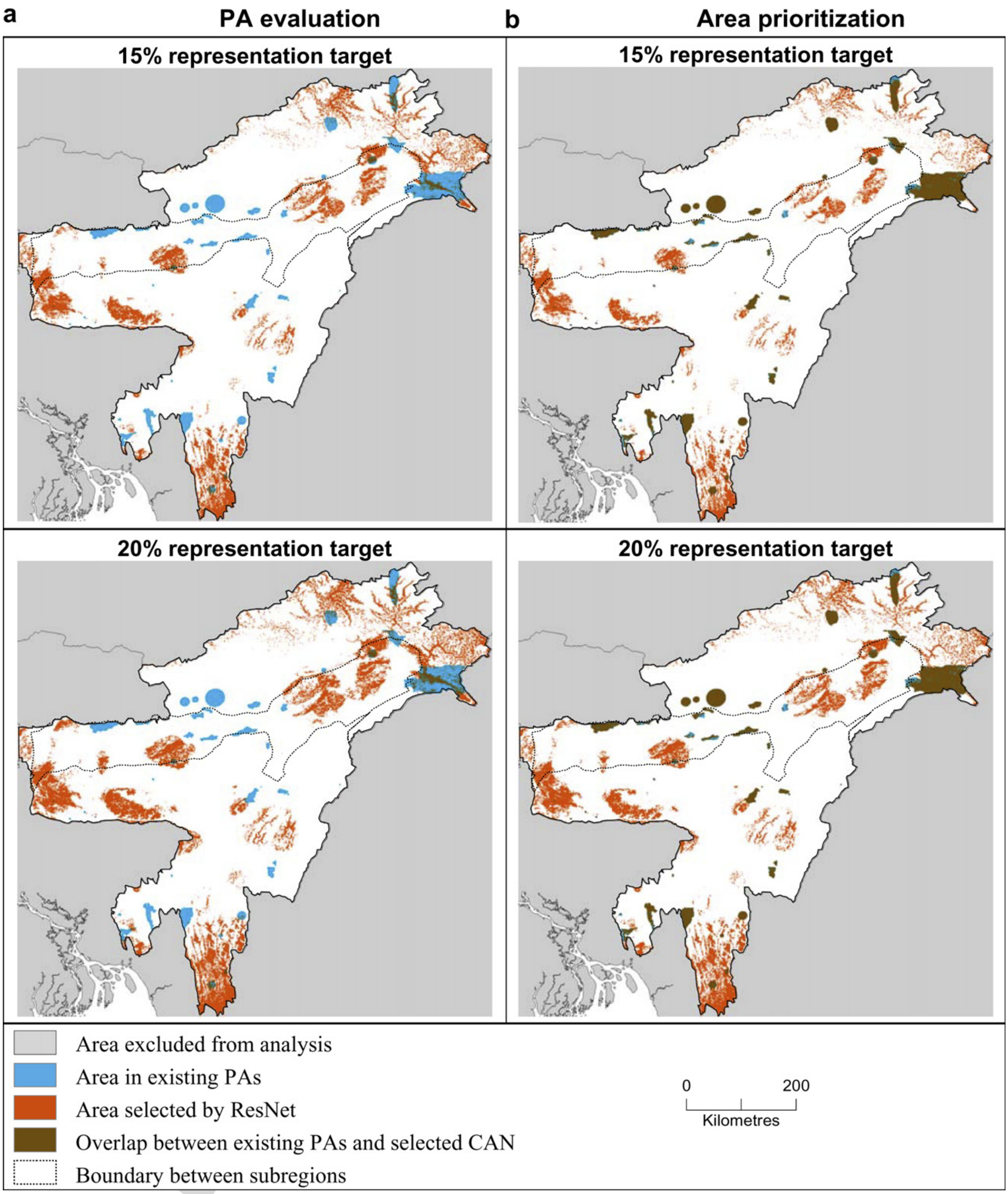

Fig. 5 – *continued*

on very similar values (at 20% representation target, the efficiency is 17.03% for rarity initialization, and 17.54 for the conservation area network initialization; Table 2).

3.3. *Evaluation and prioritization with all species*

Changes in the salient features of the ResNet solutions due to inclusion of all 131 species for which niche modeling was performed, are shown in Table 3. Fig. 6 overlays the areas selected using the two taxon sets. For initialization by rarity, across the range of representation targets, the selected area using all 131 species increases relative to that using the 80 species subset, from 8812 km^2 (4.02% of total area) to 10,951 km^2 (5.0% of total area) for 5% representation, and from 37,237 km^2 (17.03% of total area) to 43,970 km^2 (20.15% of total area) for 20% representation. The overlap between the two solutions is only 56.8% and 65.4%, respectively for the two representation target values, indicating that the differences

Table 3 – Comparison of ResNet solutions based upon the niche models of two different sets of species; all 131 species and a subset of 80 species with robust niche models

Algorithm initialization	Taxon representation target (%)	Area selected (percent of total area)		Intersection between the two solutions (%)
		Using 80 species' subset	Using 131 species	
By rarity (conservation area network evaluation)	5	8812 (4.02%)	10,951 (5.0%)	56.8
	20	37,237 (17.03%)	44,051 (20.1%)	65.4
By conservation area network (area prioritization)	5	12,208 (5.58%)	12,388 (5.7%)	96.1
	20	38,351 (17.54%)	43,970 (20.1%)	72.6

Upper and lower-end values of taxon representation targets are shown. All areas are in km^2. Intersection between the two solutions is expressed as the percentage of cells in the all-species solution that are also present in the solution based upon the subset of species (corresponding to the areas of intersection shown in Fig. 6).

in the solutions lies in the extent of the selected cells as well as in their geographical locations. Solutions based upon initialization by the existing protected areas also show an increase but of a smaller magnitude. The percentage overlap between the two solutions is naturally higher here because both were initialized by the same set of cells. The change in representation of areas is broadly similar to that for initialization by rarity. In terms of representation of selected areas within the three subregions, a few noticeable differences appear by inclusion of the additional 51 species in both initializations; relatively more areas appear in the southern Brahmaputra River Basin, northern Northeast Hills, and to a lesser extent, the western end of the Eastern Himalayas (the light grey areas in Fig. 6).

4. Discussion

4.1. *Protected area evaluation and area prioritization in Northeast India*

This appears to be the first conservation assessment for the entire NE India region. Previously, the most comprehensive study for the region was by Sarkar et al. (2006), who included only mountainous zones above 400 m. They also used ResNet, but with environmental surrogate data and algorithm runs initialized only by rarity. The environmental surrogates were expected to capture all biological taxa, but this was not explicitly tested. In terms of the efficiency of the conservation area network solution, their results are similar to the current study (4.91% of total area for 5% representation versus 4.02% in this study, and 9.26% of total area for 10% representation versus 8.25% in this study) even though they did not use biological surrogates. The analyses based upon all 131 species also yield similar results. That the results are so similar in terms of total selected area warrants further comparisons of ResNet results based on other surrogates. In terms of representation in biogeographical zones however, the results of this study show notable differences from those of Sarkar et al. (2006). The western part of the Eastern Himalayas does not appear important in the results here, but Sarkar et al's analysis highlighted many areas in that part of the subregion. Also, the Mizoram–Manipur–Kachin forest areas along the north-south oriented mountains in the Northeast Hills (Fig. 1) have greater representation in the current analysis compared to the results of Sarkar et al. (2006). In part, these geographical differences in the conservation area network solution of the current study and that of Sarkar et al. (2006) is probably accounted for by fact that their study excludes elevations <400 m, and that they use environmental surrogates.

Because the ResNet solutions initialized by rarity shows a rather poor overlap with the existing set of protected areas (a maximum overlap of 19.96% at 20% representation target), the current reserve network appears inadequate for the conservation of reptiles and amphibians, whether or not it performs well for other taxa. A look at the species-specific representation deficit in the existing protected areas across the range of targets (Appendix 1) shows that only 32 of the 131 species have at least 5% representation in the existing protected areas. The maximum representation in the existing protected areas for any species is 17.3% (for *Ovophis monticola*, a snake).

At the same time, in terms of efficiency, the solutions based upon initialization by conservation area network are not very different from those based upon rarity. Thus relatively efficient solutions that retain the existing set of protected areas and yet achieve better representation of amphibian and reptile diversity are tenable, with only a modest increase in area. For example, to achieve 5% representation of all 80 species, the area covered by the existing protected areas would need to increase to 12,208 km^2 from the current total of 11,309 km^2 (Table 2). At higher representation targets, the amount of area increase projected by the ResNet solutions based upon conservation area network initialization appear unfeasibly large (for 20% representation, the projected conservation area network covers 38,351 km^2 covering 17.54% of the total available area of the region's area). Nevertheless, these values lie at the lower end of the range (i.e., at the upper end of the range of efficiency) reported for solutions based upon different taxa (and spatial resolutions) across the globe (Kelley et al., 2002; Wilson et al., 2005). The relatively high level of efficiency reported in this study may be due to the fine spatial scale (grain) of analysis (Pressey and Logan, 1998), which indicates that finer scales are more appropriate for practical conservation planning.

The results of this study can also be compared with a few subregional studies within NE India. For the Eastern Himalayas, land-cover and land-use based analyses by Menon et al. (2001) and Roy and Behera (2005) indicate that parts of the eastern limits of the zone are particularly important, especially in low to mid-elevation montane zones. A comparison

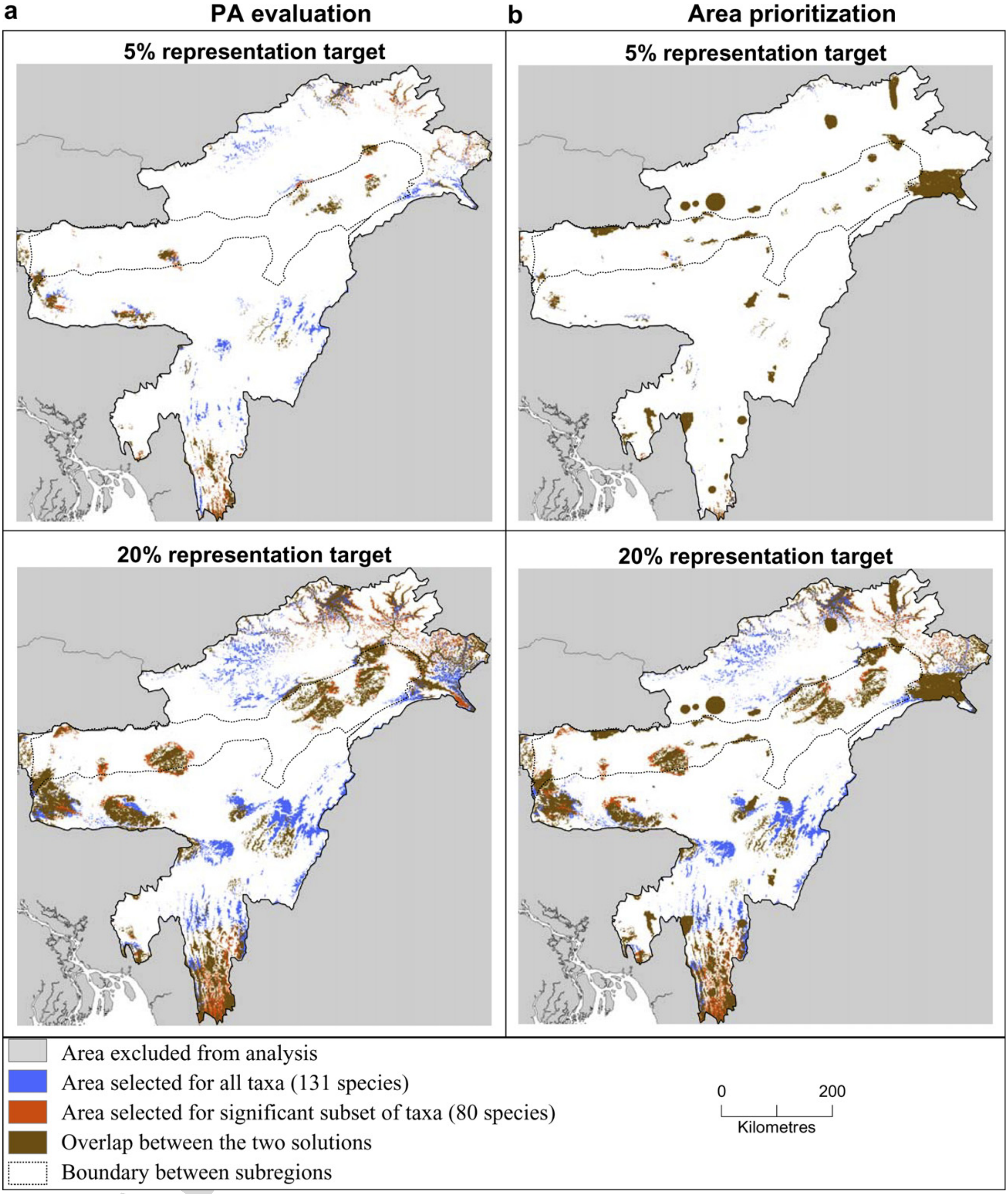

Fig. 6 – Comparison of the ResNet solutions for all 131 species vs. the subset of 80 with robust niche models, for upper and lower-end values of representation targets. See Table 3 for a numerical comparison of the two sets of solutions.

of Figs. 1 and 5 show that the results of this study also select large contiguous tracts of cells in these areas. These zones clearly need attention in terms of data collection and additional systematic assessments for other biological groups as well. Even for amphibians and reptiles, the eastern part of the Eastern Himalayas have yielded many new species and records (Pawar and Birand, 2001), and species lists continue to grow as more field and taxonomic work are being carried out.

For the other two subregions of NE India (Brahmaputra River Basin and Northeast Hills), only the study by Khan et al. (1997) for Meghalaya state is available for comparison. This area corresponds to the northwestern part of the Northeast Hills (subregion 3 in Fig. 1). Using data on plant species, Khan et al. (1997) concluded that, although species richness and endemism were highest in the low to medium elevation range (0–1500 m), high elevation areas were particularly under-represented in the existing protected areas (there are no national parks or sanctuaries at elevations >1500 m in the state). The results of this study indicate that even for the mid- and low-elevation areas, this part of the Northeast Hills subregion shows very poor concordance between priority areas and the existing protected areas. The ResNet results based upon initialization by rarity as well as existing protected areas (Fig. 5a and b) show that a number of potentially important areas lying in the low to mid-elevation zone (Fig. 1) are not yet adequately represented in the existing set of protected areas.

For other areas in the Brahmaputra River Basin and Northeast Hills, no comparable analyses are available, but some comments can be made on the basis of the current results and previous observations (Pawar and Birand, 2001). This study indicates that many areas projected to be of value for amphibian and reptile diversity lie in the Northeast Hills and Brahmaputra River Basin. In particular, the eastern and western parts of the Brahmaputra River Basin, and the eastern, southern and extreme western parts of the Northeast Hills hills deserve attention. Compared to the Eastern Himalayas, these zones appear particularly under-represented, with large patches of selected cells disjunct from the existing protected areas (Fig. 5b).

The results also highlight geographic gaps in the current biodiversity inventorying effort in NE India. A prominent conservation prioritization initiative in this region has been the 'Important Bird Areas' program, which assumes that birds are effective surrogates for other biota (International Council for Bird Preservation, 1992; Islam and Rahmani, 2004). The Important Bird Areas program has identified a number of sites in the region, a disproportionate number of which are in the Brahmaputra River Basin (41%) and adjoining areas of the Eastern Himalayas and Northeast Hills (Islam and Rahmani, 2004). However, the results of the current analysis show a relatively high representation of potentially important areas in the Northeast Hills and Eastern Himalayas subregions. In part, this discrepancy might arise if birds are not an adequate surrogate for amphibians and reptiles (very little is known about the surrogacy value of birds; Pain et al., 2005; O'Dea et al., 2006; Tushabe et al., 2006). However, an additional factor for this potential gap undoubtedly is that the relatively accessible Brahmaputra River Basin has been surveyed more frequently than the Northeast Hills and Eastern Himalayas, causing the Important Bird Areas prioritization effort to be geographically biased (Pawar and Birand, 2001). The results of the ResNet analysis based on initialization by rarity therefore indicate more efforts need to be invested in surveying the relatively inaccessible parts of NE India. Extending the analysis performed in this paper to birds using available data will also provide insights about such areas.

4.2. *The effects of rare species*

As mentioned before, the 51 species that were excluded from the main evaluation and prioritization analyses because of their relatively poor performance in the niche modeling consist of species that have small sample sizes. Given that all distribution data were collected during a relatively narrow time-period by the same set of people, it is unlikely that observer bias plays a large part in the under-representation of these taxa. It is likely that these taxa share certain biological attributes that either render them rare, and/or make them difficult to detect. To understand the effect of excluding such species, additional ResNet analysis were performed using the niche models of these species, the results of which indicated that these taxa would make a significant difference, especially when the distribution of selected cells are examined at a fine geographic scale. Few previous studies have compared the effects of rare species on systematic conservation prioritization. Using presence-only distribution data without niche modeling, Tognelli (2005) used ResNet to examine conservation priorities for terrestrial mammals at two spatial scales (Brazil and the South American continent), and found that a subset of rare species alone was an effective surrogate for the group as a whole. In contrast the results of this study show a considerable change in spatial configuration of the ResNet solution when ostensibly rare species are included. However, given that these species of amphibians and reptiles also have relatively unreliable niche models, additional data and further analyses are needed before any firm conclusion can be drawn. In future work, more data on rare species needs to be collected so that they can be used in final planning without problems of statistical significance. To this end, areas identified by the niche models may aid in the discovery of additional populations of these 51 species, and should be considered in future surveys (Guisan et al., 2006).

4.3. *General comments and caveats*

This study provides an initial assessment of conservation priorities for NE India based on amphibian and reptile distribution data, and also identifies areas with high potential for future biodiversity inventorying. Future analyses should seek to expand such analyses with respect to both taxonomic and geographic coverage. Including more biotic groups will clarify the levels of cross-taxon congruence in the region and refine conservation priorities (Pawar et al., 2006). Expanding geographical coverage will provide a more comprehensive analysis about the Himalaya and Indo-Burma biodiversity hotspots. To this end, a combined analysis for the entire NE India–Burma region and one for Burma will be reported in the future.

In the past, studies using species' distribution models for area prioritization have often converted probabilities of occurrence into presence absence data by using thresholds (defining what probability is high enough to be interpreted as a presence), due to lack of suitable methods for handling probabilistic data. However, new theoretical advances allow the use of probabilistic data directly (ReVelle et al., 2002; Cabeza, 2003; Sarkar et al., 2004; Moilanen, 2005; Tole, 2006), and thresholding can result in unnecessary loss of information and flexibility in choosing reserve networks (Wilson et al., 2005). This is the first study to perform systematic conservation planning using probabilistic distribution data for both amphibians and reptiles in Asia, and to the best of our knowledge, is only the second anywhere in the world (Tole, 2006). Tole (2006) used a different approach, developing niche models at the level of families (12 in all) by pooling species-level occurrence data and then using these 12 surrogates for conservation area network selection. This approach could result in a loss of information; other studies with different biotic groups have suggested that pooling to the level of families is less accurate than the level of genera or species (Balmford et al., 2000; Larsen and Rahbek, 2005). In a future analysis, this conclusion will be evaluated by pooling the taxa used in this study under genera and families before performing niche modeling and area prioritization.

Because the main assumption underlying the use of probabilistic data for area prioritization is that more suitable habitats identified by niche modeling reflect probability of occurrence (Araujo et al., 2002; Araujo, 2004; Cabeza et al., 2004), a prominent concern should be about reliability of the models. There is increasing evidence that groups with different life histories often show biogeographical discordance, stemming from a combination of factors (Moritz et al., 2001; Pawar et al., 2006; Graham et al., 2006). Thus, it is likely that the accuracy of niche models varies systematically across biological groups. From the results of a handful of studies that have performed an assessment of this issue, it does appear that taxon-specific characteristics make a difference (Pearce et al., 2001; Seoane et al., 2005; Carrascal et al., 2006). For example, plants, invertebrates, amphibians and reptiles are relatively poor dispersers, and using niche modeling techniques that have been calibrated with more vagile taxa such as birds and mammals (which also generally happen to be more data rich) may not be appropriate (Stockman et al., 2006). In addition, data on certain biological groups can also be biased because of taxonomic uncertainty and poor detectability in the field.

Apart from the problems raised by differences between biological groups, the possible inaccuracy of niche models, which is a general limitation, also needs to be considered while using modeled distributions for area prioritization. Recent work has indicated that the set of areas selected by methods such as ResNet is highly sensitive to changes in the distribution of species (Wilson et al., 2005; Moilanen, 2005; Moilanen et al., 2006). Consequently, any inaccuracy in a niche model has the potential to be amplified during the area selection process. This uncertainty is mitigated, but only partly, by the conservative use of niche modeling in this analysis.

Despite all these caveats, on the whole, the results of this study are a good demonstration of the advantages conferred by combining distributional modeling with algorithmic area prioritization, particularly in data-poor regions where few, if any other options are available for systematic conservation planning.

Acknowledgements

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Appendix 1

List of amphibian and reptile species used in the Northeast Indian conservation area network evaluation and area prioritization. "*N*" refers to the number of unique occurrence records available for each species. Species' with significant niche models are marked with an asterisk. For each species, the expected occurrence (E.O.) calculated from the Maxent niche models is shown for the total area and for within the existing protected areas. The percentage of total E.O. that the E.O. in the existing protected areas accounts for is shown in parentheses.

Species	N	Total E.O.	E.O. in existing protected areas (% representation)
Amphibians			
_Amolops afghanus_*	9	5358.8	190.99 (3.6%)
_Bufo andrewsi_*	10	21684.7	1286.44 (5.9%)
Bufo asper	4	12965.4	479.23 (3.7%)
_Bufo macrotis_*	9	54211.4	2332.57 (4.3%)
_Bufo melanostictus_*	98	17663.6	1196.08 (6.8%)
Bufo parvus	8	889.0	22.52 (2.5%)
Bufo stuarti	6	5302.8	432.24 (8.2%)
Bufoides meghalayana	4	8651.4	389.25 (4.5%)
Chirixalus doriae	11	6346.0	59.98 (0.9%)
Chirixalus nongkhorensis	7	360.5	27.44 (7.6%)
_Chirixalus vittatus_*	11	34351.8	1862.71 (5.4%)
Glyphoglossus molossus	7	4237.2	103.99 (2.5%)
Hyla annectans	4	15431.2	658.18 (4.3%)
_Kaloula pulchra_*	27	1448.6	26.89 (1.9%)
Megophrys parva	6	64673.5	2651.71 (4.1%)
_Microhyla berdmorei_*	31	5873.4	96.32 (1.6%)
_Microhyla heymonsi_*	13	41058.5	1501.48 (3.7%)

Appendix 1 – *continued*

Species	N	Total E.O.	E.O. in existing protected areas (% representation)
*Microhyla ornata**	81	8015.7	181.17 (2.3%)
Microhyla pulchra	8	1281.3	3.17 (0.2%)
*Occidozyga lima**	28	5449.4	98.51 (1.8%)
Paa arnoldi	4	13249.6	558.23 (4.2%)
Philautus parvulus	5	89892.7	4222.74 (4.7%)
*Phrynoglossus borealis**	27	9188.5	273.50 (3.0%)
*Phrynoglossus tenasserimensis**	14	1717.6	21.45 (1.2%)
*Polypedates leucomystax**	48	8741.7	774.69 (8.9%)
Rana cubitalis	7	21545.0	1289.55 (6.0%)
Rana cyanophlyctis	4	129.3	6.27 (4.8%)
Rana doriae	8	10034.4	320.68 (3.2%)
*Rana erythraea**	9	26590.2	873.77 (3.3%)
Rana glandulosus	5	3140.6	423.91 (13.5%)
Rana hascheanus	8	53579.5	2522.78 (4.7%)
*Rana kuhlii**	28	7532.6	900.86 (12.0%)
Rana laticeps	7	18193.6	784.31 (4.3%)
*Rana leptoglossa**	14	33297.1	1242.32 (3.7%)
*Rana livida**	20	9383.3	529.40 (5.6%)
*Rana macrodactyla**	18	13403.3	722.83 (5.4%)
*Rana macrognatha**	11	674.3	15.30 (2.3%)
*Rana nigrovittata**	19	38187.4	1302.41 (3.4%)
*Rana taipehensis**	27	3633.5	60.96 (1.7%)
Rana yunnanensis	4	7654.3	879.77 (11.5%)
*Rhacophorus bipunctatus**	20	26726.2	2016.12 (7.5%)
*Rhacophorus maximus**	9	7715.1	556.75 (7.2%)
Rhacophorus naso	5	17542.3	832.56 (4.7%)
*Theloderma asper**	15	5364.7	532.79 (9.9%)
*Tomopterna breviceps**	28	4321.7	119.36 (2.8%)
Tylototriton verrucosus	8	75067.1	3696.73 (4.9%)
Reptiles: Lizards			
*Acanthosaura lepidogaster**	9	2193.1	13.44 (0.6%)
*Calotes chincollium**	31	3579.6	170.08 (4.8%)
*Calotes emma**	16	58665.6	3013.46 (5.1%)
*Calotes jerdoni**	10	16001.0	1484.17 (9.3%)
*Calotes mystaceus**	127	3765.6	92.06 (2.4%)
*Calotes versicolor**	218	16041.3	704.33 (4.4%)
*Cosymbotus platyurus**	12	64599.3	2116.91 (3.3%)
Cyrtodactylus slowinskii	6	452.1	18.46 (4.1%)
*Cyrtodactylus ayeyarwadyensis**	10	2307.2	11.11 (0.5%)
Cyrtodactylus khasiensis	5	8170.7	359.33 (4.4%)
Cyrtodactylus peguensis	9	362.7	1.64 (0.5%)
Draco blanfordi	7	105291.1	4409.13 (4.2%)
*Draco maculatus**	19	36062.0	1038.33 (2.9%)
*Draco taeniopterus**	9	21816.0	698.26 (3.2%)
*Gekko gecko**	50	5244.1	78.88 (1.5%)
*Hemidactylus bowringii**	78	34590.4	1915.96 (5.5%)
*Hemidactylus brookii**	24	9046.9	250.48 (2.8%)
*Hemidactylus frenatus**	114	12457.2	308.87 (2.5%)
*Hemidactylus garnotii**	13	62430.0	2104.59 (3.4%)
*Hemidactylus karenorum**	21	5096.8	50.50 (1.0%)
Japalura planidorsata	7	11572.7	400.64 (3.5%)
Japalura splendida	5	20279.7	1181.81 (5.8%)
*Leiolepis belliana**	25	544.0	17.62 (3.2%)
*Lygosoma bowringii**	11	939.9	16.28 (1.7%)
*Lygosoma lineolata**	38	2705.9	22.50 (0.8%)
*Mabuya macularia**	51	655.0	8.58 (1.3%)
*Mabuya multifascata**	42	11822.9	199.46 (1.7%)
*Mabuya novemcarinata**	35	158.6	2.76 (1.7%)

Appendix 1 – *continued*

Species	N	Total E.O.	E.O. in existing protected areas (% representation)
*Ptyctolaemus gularis**	17	22635.1	2104.56 (9.3%)
*Scincella reevesi**	18	7500.3	99.99 (1.3%)
*Sphenomorphus indicus**	41	7056.8	870.94 (12.3%)
*Sphenomorphus maculatus**	136	1801.5	220.10 (12.2%)
Takydromus sp1	4	29636.9	932.46 (3.1%)
Takydromus sexlineatus	8	8099.5	229.15 (2.8%)
Tropidophrous berdmorei	6	17133.4	405.23 (2.4%)
Reptiles: Snakes			
Acrochordus granulatus	4	321.1	0.41 (0.1%)
*Ahaetulla fronticinctus**	19	183.5	7.12 (3.9%)
*Ahaetulla nasuta**	46	529.4	8.04 (1.5%)
*Ahaetulla prasina**	22	43974.2	1727.60 (3.9%)
*Amphiesma stolata**	34	1957.8	47.08 (2.4%)
Amphiesma xenura	4	6446.9	190.58 (3.0%)
Bitia hydroides	6	50.1	1.26 (2.5%)
*Boiga multomaculata**	12	3430.7	29.67 (0.9%)
*Boiga ochracea**	19	12015.0	219.26 (1.8%)
Bungarus fasciatus	6	7852.4	158.10 (2.0%)
Bungarus magnimaculata	8	2870.4	71.90 (2.5%)
Calamaria pavimentata	5	6571.2	832.12 (12.7%)
Cantoria violacea	8	14.0	0.17 (1.2%)
*Cereberus rynchops**	25	562.3	9.99 (1.8%)
Chrysopelea ornata	22	7554.2	86.88 (1.2%)
*Cylindrophis ruffus**	10	2084.2	18.27 (0.9%)
*Daboia russelii**	18	2019.2	44.00 (2.2%)
*Dendrelapis pictus**	16	3060.6	14.56 (0.5%)
*Dendrelapis subocularis**	12	10911.0	146.94 (1.3%)
Denrelaphis cyanochloris	4	45061.3	2394.89 (5.3%)
Dinodon septentrionalis	7	15962.0	1310.53 (8.2%)
Elaphe porphyracea	4	31425.0	2247.83 (7.2%)
*Elaphe radiata**	13	10864.2	337.50 (3.1%)
Elaphe taeniura	8	9126.2	728.35 (8.0%)
*Lycodon aulicus**	41	8293.0	113.05 (1.4%)
Lycodon zawi	5	3619.3	6.09 (0.2%)
*Naja kaouthia**	12	62005.9	2487.34 (4.0%)
*Naja mandalayensis**	20	529.6	11.11 (2.1%)
*Oligodon cinereus**	9	72550.3	2990.83 (4.1%)
*Oligodon cyclurus**	15	8912.1	194.89 (2.2%)
Oligodon splendidus	7	5981.5	194.67 (3.3%)
*Oligodon theobaldi**	17	1559.4	39.44 (2.5%)
Ovophis monticola	4	3998.2	692.00 (17.3%)
Protobothrops jerdoni	5	28943.7	2136.01 (7.4%)
*Psammodynastes condanarus**	40	1393.3	15.74 (1.1%)
*Psammodynastes pulverulentus**	12	22881.7	908.58 (4.0%)
*Ptyas korros**	20	48451.9	2755.44 (5.7%)
*Ptyas mucosus**	23	4145.7	98.38 (2.4%)
*Ramphotyphlops braminus**	22	13111.1	427.93 (3.3%)
*Rhabdophis himalayanus**	9	5554.3	237.83 (4.3%)
*Rhabdophis subminiata**	28	35116.8	1220.33 (3.5%)
Sinononatrix yunnanensis	5	410.1	5.56 (1.4%)
Trimeresurus popeiorum	5	40442.0	2343.67 (5.8%)
*Trimeresurus albolabris**	43	979.0	29.43 (3.0%)
Trimeresurus erythrurus	6	11497.9	369.14 (3.2%)
*Trimeresurus purpureomaculatus**	21	243.8	4.16 (1.7%)
Typhlops diardi	8	11460.0	893.47 (7.8%)
*Xenochrophis piscator**	70	13211.5	315.59 (2.4%)
Xenochrophis punctatus	4	9.1	0.01 (0.1%)
*Xenopeltis unicolor**	11	5856.8	71.29 (1.2%)

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