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Setting conservation priorities within monophyletic groups: An integrative approach

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ABSTRACT

Species differ in their need for conservation action and in their relative importance for conserving current and historic ecological and evolutionary diversity. Given the present biodiversity crisis and the lack of resources, threatened species must be differentiated from each other so that those presenting higher conservation priority can be attended first. Here we propose a novel approach to calculate a priority index (PI) for species within monophyletic groups, by combining life history traits, extrinsic factors, ecological singularity, and phylogenetic distinctness. To test our approach we used a group of Neotropical snakes, the pseudoboines, as our model lineage. To create the PI we combined four different indices: intrinsic vulnerability to extinction (IVE, comprised by six factors), extrinsic vulnerability to extinction (EVE, comprised by three factors), ecological oddity (EO, four factors) and phylogenetic distinctness (PD). Intrinsic vulnerability to extinction was evenly distributed across the clade and EVE was higher in species present in the Brazilian hotspots of Biodiversity, Atlantic Forest and Cerrado. As expected due to the nature of the index, a few species that differ from the average phenotype presented high EO values, whereas PD values did not vary greatly among pseudoboines. Representatives from almost all clades within the pseudoboines appear among the ten highest PI values, maximizing the phylogenetic diversity of the prioritized taxa. Although it is not possible to compare values obtained in studies to different lineages (indices are clade-specific), extending this approach to more inclusive lineages (e.g., families) might enhance the quality of future prioritization processes. The method we propose would be especially useful for taxonomically driven conservation action plans.

Introduction

Given the biodiversity crisis and the relative scarcity of resources (Barnosky et al. 2011; Brooks et al. 2006) threatened species must be differentiated from each other so that those presenting higher conservation priority can be attended to first (Wilson et al. 2009). Thus, a major challenge for conservation focused on species is to set priorities for conservation efforts (Pimm et al. 2001; Wilson et al. 2006). Although the prioritization of conservation efforts may involve several factors such as socioeconomic and political issues (Eklund et al. 2011; Polasky 2008; Wilson et al. 2009; Wilson et al. 2011), having the knowledge of the vulnerability to extinction of a species can help to predict the outcomes of different future scenarios (Jones et al. 2003; Pimm et al. 1988; Webb et al. 2002; Wilson et al. 2006).

Vulnerability to extinction is related to extrinsic factors, such as habitat loss and disturbance (Brooks et al. 2006; IUCN 2009; Pimm et al. 1995), and there are several ways to infer the effects of these factors on species vulnerability. For example, the degree of habitat fragmentation or disturbed habitat within the species' range can be an important factor (Laurance 2008), given that species isolated in small habitat patches may present an increased probability of extinction due to genetic problems and environmental stochasticity (Lande 1993; Tanentzap et al. 2012). Furthermore, the amount of human infrastructure within the distributional range can also be considered a potential cause of species vulnerability to extinction (e.g., the human footprint; Sanderson et al. 2002). Likewise, a species' vulnerability to extinction can also be influenced by intrinsic traits (Foufopoulos & Ives 1999; Mckinney 1997) such as ecological specializations (e.g., in diet or in habitat requirements;

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Mckinney 1997; Segura et al. 2007), restricted geographic range (Cardillo et al. 2008; Purvis et al. 2000; Rabinowitz et al. 1986), and life histories attributes that might decrease the rate at which new individuals are incorporated in the populations (e.g., late maturation, small litter size, large body size; for reviews see Brown 1995; Mckinney 1997; Purvis et al. 2000).

Besides vulnerability to extinction other factors may be considered when prioritizing species for conservation purposes. For example, it has already been proposed that biodiversity measures should also consider the representation of evolutionary history (Cadotte & Davies 2010; Faith 1992, 2002; Isaac et al. 2007; May 1990; but see Winter et al. 2013). Phylogenetic distinctness (PD) is one of the metrics developed to measure the evolutionary uniqueness of a group (May 1990; Vane-Wright et al. 1991). Phylogenetic distinctness measures the uniqueness of the terminal taxa within the group: the more relictual a species is, the higher its PD, and therefore, the greater the amount of historical features being conserved (for a range of approaches see Collen et al. 2011; Heard & Mooers 2000; Mace et al. 2003; Steel et al. 2007).

Additionally, a recent approach to conservation incorporates the ecological distinctness of species, assuming that ecological features are associated to different ecological roles and ecosystem functions (Cadotte & Davies 2010; Petchey & Gaston 2006; Redding et al. 2010). In this sense, Redding et al. (2010) proposed the ecological oddity as measure of ecological distinctness, where odd is defined as the "absolute distance from the average phenotype" (Redding et al. 2010). Therefore, the more distinct a species is in relation to the other species within a clade, the higher its ecological oddity. Redding et al. (2010) used this metric to measure how the protection of evolutionarily distinct and globally endangered species (EDGE; Isaac et al. 2007; Redding & Mooers 2006) would capture the ecological diversity of a given clade.

Thus, species are expected to differ regarding the threats to which they are subjected, and thereby, differ in their need for conservation action and in their relative importance for conserving both their ecological and evolutionary diversity (Heard & Mooers 2000; Redding et al. 2010). The objective of this study is to propose an index of species prioritization considering all these aspects as a way to set conservation priorities within lineages. To demonstrate our index, we used a Neotropical clade of snakes (tribe Pseudoboini, subfamily Xenodontinae, family Dipsadidae) as our model. The most widely used method for creating red lists is the one proposed by IUCN (2001), but this method only distinguishes species by their threat status (e.g., vulnerable), not providing a ranking within each category. The purpose of our method is not to highlight threatened species, which is the aim of Red Lists, but to address the "agony of choice" (Vane-Wright et al. 1991) through an index of species prioritization that encompasses threats, vulnerabilities, ecological and evolutionary uniqueness, when closely related species are assessed. This method would be especially useful for taxonomically driven conservation action plans (e.g., Donaldson 2003; Gascon et al. 2007; Reeves et al. 2003).

Material and methods

The model lineage

The tribe Pseudoboini (family Dipsadidae, subfamily Xenodontinae, *sensu* Grazziotin et al. 2012; Zaher et al. 2009) is monophyletic group of snakes that includes 47 species and 11 genera (*Boiruna*, *Clelia*, *Drepanoides*, *Mussurana*, *Oxyrhopus*, *Paraphimophis*, *Phimophis*, *Pseudoboa*, *Rhachidelus*, *Rodriguesophis* and *Siphlophis*; Grazziotin et al. 2012). The tribe is distributed throughout the Neotropics (Ferrarezzi 1994; Jenner & Dowling 1985), from Mexico to Argentina (Gaiarsa et al. 2013). Most pseudoboines feed on lizards and small mammals, whereas some species are specialized in other prey types (e.g., *Rhachidelus brazili* feeds on bird eggs; Gaiarsa et al. 2013). Additionally, the tribe is composed predominantly of terrestrial species (e.g., *Clelia* spp. and *Boiruna* spp.), although some species are semi-arboreal (e.g., *Drepanoides anomalus* and *Siphlophis cervinus*) or semi-fossorial (*Phimophis* spp.; Gaiarsa et al. 2013). Hence, this tribe is an ideal model for this study because of its diversity of ecological features and the relative wealth of natural history data (Gaiarsa et al. 2013). Full details of the data set and sources are available elsewhere (Tables A1 and A2; Alencar et al. 2013; Gaiarsa et al. 2013). We followed the taxonomy of Grazziotin et al. (2012) and Zaher et al. (2009) and made no distinction among subspecies.

Vulnerability to extinction

We adapted the method of Millsap et al. (1990) using data on factors known to affect species survival to create two indices of vulnerability to extinction: intrinsic and extrinsic vulnerability to extinction (IVE and EVE, respectively; see below). We only included in the analysis species for which data was available for at least 50% of the factors used to create each index.

Intrinsic vulnerability to extinction (IVE)

We selected six factors that are related to characteristics that could decrease a species' ability to cope with negative alterations in its habitat, and that are either related to narrow niches and/or to low abundance (Mckinney 1997): (i) body size, (ii) mean fecundity, (iii) dietary specialization, (iv) geographic distribution, (v) elevational range and (vi) ability to persist in altered habitats. We initially included habitat breadth (HB, measured as the number of Terrestrial Ecoregions of the World in which the species occurs, Olson et al. 2001, encompassed by a species geographic range) as a seventh factor. However, preliminary analyses indicated a high correlation between HB and the factor geographic distribution (GD; $r = 0.81$, Table A3; see below for information on how GD was quantified), so we excluded habitat breadth from IVE calculations. The remaining factors had a relatively low correlation ($r < 0.45$ in all cases, Table A3). Factors were as follows:

1. *Body size* (BS): larger species tend to be more vulnerable to extinction because they are in general less abundant, have later sexual maturity and are more long-living, thus being less able to recover from population declines (e.g., Foufopoulos & Ives 1999; Mckinney 1997; Purvis et al. 2000). We used the maximum known snout-vent length for each species, regardless of the sex.
2. *Mean fecundity* (MF): low fecundity populations tend to be more prone to extinction because they take longer to recover from declines than do high fecundity populations (e.g., Mckinney 1997; Pimm et al. 1988; Purvis et al. 2000). We used mean clutch size, regardless of the number of litters available.
3. *Dietary specialization* (DS): animals that are specialists in resource use (e.g., prey, habitat) tend to be less able to cope with changes in the resource base (either by anthropogenic or natural causes) and thus, are more vulnerable to extinction (e.g., Mckinney 1997; Purvis et al. 2000). To characterize the degree of diet specialization we used the percentage of the most important prey item in the diet. Thus, the greater the contribution of one type of prey to the diet, the more specialized in one prey the species is. Prey items considered were: amphibians, lizards, lizard eggs, snakes, birds, bird eggs, and mammals. We considered every record, regardless of the number of individual prey available for each species.

4. *Geographic distribution* (GD): the smaller the geographic distribution the more vulnerable to extinction a species tends to be (see, e.g., Cardillo et al. 2008; Fisher & Owens 2004; Purvis et al. 2000). We used occurrence points from museum records and literature data to estimate the geographic distribution of each species (for a discussion on different methods see Attorre et al. 2013). Because good distribution maps are not available for most snakes (see, e.g., Uetz 2013), and very few were available for our model lineage, GD was calculated according to the available data (for details on how GD was calculated for pseudoboine snakes, see supplementary material). Our geographic distribution factor is equivalent to the IUCN's extent of occurrence (EOO; IUCN 2001).
5. *Elevational range* (EL): animals occurring in a restricted vertical distribution may be more vulnerable to extinction because they tend to be stenothermics and stenobarics, and thus less able to cope with habitat change (either by anthropogenic or natural causes; e.g., Mckinney 1997). We assessed this factor by calculating the elevational range within the species' geographic distribution (with the same database used to calculate the factor "Geographic Distribution").
6. *Ability to persist in altered habitats* (AAH; adapted from Filippi & Luiselli 2000): vulnerability to extinction tends to be greater in animals that are less able to persist in altered habitats (e.g., Fisher & Owens 2004; Purvis et al. 2000). This factor was assessed based on the personal experience of researchers. Experienced researchers were asked to assign values for each species as follows: 0–5 for species which are able to persist in disturbed habitats (including urban areas); 6–11 for those which may occasionally persist in disturbed habitats (found in rural areas where small patches of natural vegetation are available); 12–17 for species which rarely persist in disturbed habitats (may be found in habitat patches); and 18–23 for species which do not persist in disturbed habitats (found only in large extensions of natural habitat). We employed the mean of the scores given by each expert for each species. Even though in some cases the opinion of researchers varied considerably (probably due to the subjectivity involved, see e.g., Keith et al. 2004; Regan et al. 2004, but also because of geographical variation in this feature), we believe this metric is still an informative measure of species sensibility to human disturbance.

Extrinsic vulnerability to extinction (EVE)

Because the greatest threat to species diversity is habitat destruction (Barnosky et al. 2011; Brooks et al. 2006; IUCN 2009), we included EVE in our assessment to represent this process. This index was calculated from three factors: (i) percentage of remaining natural vegetation within species distribution; (ii) coverage of the protected areas within species distribution; and (iii) mean human influence index along species distribution. We initially included density of remaining fragments as a fourth factor (DF; measured as the area of the remaining fragments in the species geographic distribution) but preliminary analyses indicated a high correlation between this factor and the percentage of the remaining habitats (RH; $r = -0.94$, Table A3) and DF was excluded. Mean human influence index along the distribution (HII) was correlated to two other factors: the intrinsic factor geographic distribution (GD, $r = 0.65$) and the factor protected areas (PA, $r = 0.57$). However, we decided to keep them in the analysis because they are related to different processes (see explanations of each factor). The remaining factors had a correlation smaller than 0.43 (Table A3) and were thus kept in the analysis. All the following factors were assessed based on species' geographic range.

1. *Percentage of remaining habitats* (RH): we reclassified the 2009 GlobCover map v. 2.3 (ESA 2008) into habitat and non-habitat classes according to the habitat preferences and tolerance to disturbance of each species (Table A4). Then, we calculated the percentage of remaining habitat inside each species' geographic distribution.
2. *Percentage of the protected areas within the distribution* (PA): assuming that species whose range overlap with protected areas have a reduced extinction risk, we calculated the percentage of the species' geographic distribution within protected areas (cf. "covered species", Rodrigues et al. 2004). Since sustainable use reserves may allow some degree of habitat degradation, we used only strict protection categories (IUCN categories I–IV, cf. IUCN & UNEP 2009; Rodrigues et al. 2004).
3. *Mean human influence index along the distribution* (HI): human influence is one of the most important threats to biodiversity (Lande 1993). To assess this factor we employed the Human Influence Index proposed by Sanderson et al. (2002), which considers factors such as population density, land use, built-up areas or settlements, among others. Index maps were downloaded from the "Last of the Wild" website (Last of the Wild Data Version 2 2005) and overlapped with species' geographic distribution. Mean index score within the species range was employed as our HI factor.

For each index (IVE and EVE) we ranked the species for every factor and assigned their ranking number such that the higher the score the greater the contribution of that factor to the vulnerability to extinction. When ties occurred, we employed the mean ranking score, as usual in ranking statistical procedures (Zar 1999). Afterwards, we used the mean of factors' mean to create the indices of vulnerability to extinction (IVE and EVE), separately. We chose to use a linear ranking system to build the indices of vulnerability to extinction because in our case (in which many biological data is used and complete data sets are available for several species) this system provides a great resolution among taxa (Millsap et al. 1990; Todd & Burgman 1998; for a review of the methods for setting conservation priorities see Mace et al. 2007).

Ecological oddity

We used the ecological oddity index (EO) proposed by Redding et al. (2010), which considers the distance of a given trait of a given species in relation to the lineage mean for that trait. This factor is comparative and considers how each species is ecologically distinct in relation to the other species of the clade. We calculated EO for four traits: three continuous (body size, mean fecundity and habitat breadth, as described above) and one categorical (dietary breadth). We only included in the analysis species for which data was available for at least 50% of the factors. We are aware that the use of more variables like population density, home range, body mass and life span (cf. Redding et al. 2010) would result in a better representation of EO, but these sort of data are scarce for snakes.

For the continuous factors we log transformed the values and then calculated the absolute distance of each species score to the mean score of that variable (cf. Redding et al. 2010). For the categorical variable dietary breadth, the value assigned to a species was the sum of the frequency of the prey category divided by the number of species in the entire data set that also consume that prey (cf. Redding et al. 2010). Therefore, the more a species feeds upon a food type that a great number of other species also feed, the smaller the EO value for that species. For example, since the majority of the species consumes lizards, all species that consume lizards will present a small value for this variable. On the other hand, species that consume unique items in relation to the other species of the Tribe (e.g., snakes and lizards' eggs) will present the highest values of the variable dietary breadth. We only considered prey items representing over 20% of the diet. The mean of these four factors was then ranked, such that the higher the score, the greater the species rank and when ties occurred we employed the mean ranking score.

Phylogenetic distinctness

We used the most recent published phylogenetic hypothesis for the tribe Pseudoboini (Grazziotin et al. 2012; Fig. A1). We also included species that were not in the original phylogeny considering their affinities with the species that were already included (see, e.g., Martins et al. 2001) using literature information (e.g., Vidal et al. 2010; Zaher et al. 2009; Fig. A1) and expert knowledge (H. Zaher, pers. comm.). We considered May's distinctness measure (May 1990) as our phylogenetic distinctness (PD) scores, which "measures the sum of the number of descendants of nodes on path from root to a species, scaled inversely by the maximum value" (Maddison & Mooers 2007). Phylogenetic distinctness was calculated on Tuatara module (Maddison & Mooers 2007) of the Mesquite software (Maddison & Maddison 2007). As performed for the other indices, we then ranked the species so that the higher the PD value, the higher the species rank, and when ties occurred we employed the mean ranking score.

Priority index

Although the indices (IVE, EVE, EO, and PD) used to calculate the priority index (PI) have different magnitude, when we used the rankings of each species they became standardized, rendering them comparable. We then tested for correlation among indices using a Pearson rank correlation test (after testing indices for normality; Table A5). We only included in the analysis species for which at least three of the indices were available.

Table 1

Ranking of factors' scores used to build the index of intrinsic (IVE) and extrinsic (EVE) vulnerability to extinction and the values for ecological oddity (EO) and Phylogenetic Distinctness (PD) for the species of the tribe Pseudoboini (refer to text for further details). Species appear in alphabetical order. BS: body size; MF: mean fecundity; DS: dietary specialization; GD: geographic distribution; EL: elevational range; AAH: ability to persist in altered habitats; RH: percentage of remaining habitats; PA: percentage of protected areas along the distribution; HI: mean human influence index along the distribution; HB: habitat breadth; DB: dietary breadth. Variables for which data was not available are indicated with "–". Habitat breadth and DF were excluded from the calculation of IVE and EVE, respectively (refer to text for further details).

Species	IVE						EVE			EO				PD
	BS	MF	DS	GD	EL	AAH	RH	PA	HI	BS	MF	HB	DB	
Boiruna maculata	39	13	12	13	21	10	27	35	26	0.290	0.068	0.271	0.231	1.333
Boiruna sertaneja	40	8	15	17	31.5	30	37	34	23	0.294	0.135	0.127	0.092	1.333
Clelia clelia	41	2	4.5	2	10	27	38	18	11	0.386	0.269	0.734	0.066	1.143
Clelia equatoriana	37	–	–	34	7	–	26	15	31	0.153	–	0.185	–	1.143
Clelia errabunda	36	–	–	–	–	–	–	–	–	0.146	–	–	–	–
Clelia hussami	23.5	–	–	41	41	–	40	40	27	0.040	–	1.030	–	1.143
Clelia langeri	34	–	30.5	39	8	–	–	2	14	0.119	–	0.252	0.077	–
Clelia plumbea	42	1	18	4	23	21	19	20	20	0.452	0.269	0.201	0.085	1.143
Clelia scytalina	29	–	–	30	9	–	24	38	37	0.082	–	0.116	–	1.143
Drepanoides anomalus	7	29	20	8	38	23	10	9	3	0.173	0.463	0.201	0.787	1.600
Mussurana bicolor	11	9.5	8	27	39	13	23	39	15	0.077	0.123	0.075	0.500	1.143
Mussurana montana	17	9.5	8	35	17.5	30	14	23	41	0.020	0.123	0.252	0.077	1.143
Mussurana quimi	22	5	16.5	15	15	–	25	30	34	0.029	0.220	0.185	0.058	1.143
Oxyrhopus clathratus	28	15	23	31	29	9	5	22	32	0.060	0.060	0.127	0.063	1.600
Oxyrhopus doliatus	3	–	–	–	–	–	–	–	–	0.431	–	–	–	–
Oxyrhopus erdisii	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Oxyrhopus fitzingeri	–	–	–	38	28	–	29	41	25	–	–	0.729	–	–
Oxyrhopus formosus	–	–	–	–	–	24.5	–	–	–	–	–	–	–	1.143
Oxyrhopus guibei	23.5	4	19	16	20	1	1	29	36	0.040	0.260	0.174	0.068	1.333
Oxyrhopus leucomelas	–	–	–	29	2	–	28	16	24	–	–	0.127	–	–
Oxyrhopus marcapatae	–	–	–	36	3	–	21	1	10	–	–	0.127	–	–
Oxyrhopus melanogenys	14	6	3	11	40	4	7	12	6	0.039	0.229	0.116	0.056	1.143
Oxyrhopus occipitalis	13	27.5	30.5	21	12	–	13	14	9	0.041	0.345	0.146	0.043	1.143
Oxyrhopus petola	27	16	1	10	5	3	6	21	19	0.050	0.022	0.678	0.288	1.333
Oxyrhopus rhombifer	18	12	4.5	3	14	17	34	32	22	0.012	0.086	0.249	0.059	1.333
Oxyrhopus trigeminus	12	14	11	6	30	7.5	33	24	18	0.059	0.068	0.293	0.050	1.333
Oxyrhopus vanidicus	15	3	8	18	11	–	12	5	2	0.036	0.248	0.049	0.060	1.143
Paraphimophis rusticus	38	11	8	20	6	19	11	36	30	0.274	0.117	0.174	0.083	1.600
Phimophis guerini	21	24	26	9	17.5	14	39	26	21	0.023	0.155	0.049	0.040	1.231
Phimophis guianensis	5	–	–	24	37	–	36	17	13	0.181	–	0.116	–	1.231
Phimophis vittatus	6	22	–	23	4	–	30	37	17	0.180	0.132	0.075	–	1.231
Pseudoboa coronata	26	25	2	1	35	7.5	9	7	4	0.045	0.170	0.332	0.212	1.143
Pseudoboa haasi	33	21	13	32	33	12	4	31	33	0.118	0.102	0.252	0.046	1.000
Pseudoboa martinsi	25	18.5	30.5	14	22	24.5	8	4	1	0.044	0.053	0.226	0.111	1.067
Pseudoboa neuwiedii	19	20	8	22	24	2	17	11	12	0.006	0.081	0.226	0.069	1.067
Pseudoboa nigra	32	7	14	12	25	5	2	28	29	0.107	0.146	0.313	0.029	1.000
Pseudoboa serrana	31	–	–	40	17.5	16	22	3	38	0.101	–	0.553	–	1.067
Rhachidelus brazili	35	26	21	28	26	11	16	33	39	0.144	0.178	0.428	0.800	1.600
Rodriguesophis chui	2	–	–	–	–	27	–	–	–	0.516	–	–	–	1.778
Rodriguesophis iglesiasi	4	30	30.5	19	34	22	35	19	16	0.346	0.530	0.185	0.043	1.778
Rodriguesophis scriptorcibatus	1	–	30.5	–	–	30	–	–	–	0.602	–	–	0.043	1.778
Siphlophis cervinus	20	23	22	7	1	18	15	10	5	0.002	0.143	0.417	0.035	2.286
Siphlophis compressus	30	17	27	5	36	20	18	13	7	0.096	0.039	0.332	0.042	2.286
Siphlophis leucocephalus	8	–	30.5	33	31.5	–	31	25	28	0.143	–	0.127	0.043	2.286
Siphlophis longicaudatus	16	18.5	16.5	25	17.5	6	32	27	35	0.024	0.053	0.127	0.060	2.286
Siphlophis pulcher	10	27.5	24.5	37	27	15	20	6	40	0.089	0.229	0.428	0.036	2.286
Siphlophis worontzowi	9	–	24.5	26	13	27	3	8	8	0.121	–	0.030	0.036	2.286

Results

There was great variation in the biological features for the group studied (Table A1; Gaiarsa et al. 2013). In general, all the species with the highest IVE presented high values for the factors GD and BS (Table 1). The index of extrinsic vulnerability to extinction (EVE) was calculated for 41 species and ranged from 4.3 to 35.7, with a mean of 20.7 ± 8.8 (Table 2). The index of intrinsic vulnerability to extinction (IVE) was calculated for 39 species and ranged from 10.3 to 35.2, with a mean of 19.4 ± 5.3 (Table 2).

Ecological oddity (EO) was calculated for 39 species and ranged from 0.06 to 0.53 (Table 2), with a mean of 0.18 ± 0.11, and phylogenetic distinctness (PD) was obtained for 40 species. Due to polytomies in our phylogeny, all the species from the genus *Siphlophis* presented the highest PD (2.29), followed by the genus *Rodriguesophis* (Table 1 and Fig. A1). Finally, priority index (PI) was calculated for 39 species and ranged from 5.38 to 30.46 (Table 2).

Discussion

The approach we propose provides a systematic, transparent, and repeatable method for prioritizing species conservation within monophyletic groups (Joseph et al. 2009) explicitly using available information about life history and threats. Our method is both proactive and reactive, identifying species that may be currently threatened (IVE) and that are facing an imminent risk of decline due to extrinsic factors (EVE). In addition, we considered ecological and phylogenetic aspects (May 1990; Redding et al. 2010), since we do not know yet which traits (ecological, biogeographical, evolutionary) will be important in face of habitat loss and climate change (Myers & Knoll 2001).

When we consider the ten species with the highest EVE, with the exception of *Clelia scytalina* and *Oxyrhopus fitzingeri*, all of them are distributed in the Brazilian Cerrado and in the Atlantic Forest. Together, these biomes cover approximately one third of Brazil's surface and are considered Biodiversity Hotspots due to

Table 2

Mean ranking scores for all the indices: intrinsic vulnerability to extinction (IVE), extrinsic vulnerability to extinction (EVE), ecological oddity (EO), phylogenetic distinctiveness (PD) and priority index (PI) for the species of the tribe Pseudoboini. See text for further detail. Species are ranked in descending order according to their priority index. We only included in the analysis species for which at least three of the indices were available (*Clelia errabunda*, *Oxyrhopus doliatus*, *O. erdisii*, *O. fitzingeri*, *O. formosus*, *O. leucomelas*, *O. marcapatae* and *Rodriguesophis chui* were not evaluated). Missing values are indicated with "–".

Species	IVE	EVE	PD	EO	PI
Clelia hussami	35.17	35.67	12	39	30.46
Rhachidelus brazili	24.5	29.33	29.5	37	30.08
Rodriguesophis scriptorcibatus	20.5	–	33	34	29.17
Rodriguesophis iglesiasi	23.25	23.33	33	33	28.15
Siphlophis pulcher	23.5	22	37.5	29	28.00
Boiruna sertaneja	23.58	31.33	24.5	24	25.85
Boiruna maculata	18	29.33	24.5	30	25.46
Siphlophis leucocephalus	25.75	28	37.5	9	25.06
Paraphimophis rusticus	17	25.67	29.5	25	24.29
Drepanoides anomalus	20.83	7.33	29.5	38	23.92
Clelia equatoriana	26	24	12	26	22.00
Siphlophis compressus	22.5	12.67	37.5	15	21.92
Siphlophis longicaudatus	16.58	31.33	37.5	2	21.85
Pseudoboa serrana	26.13	21	4	35	21.53
Siphlophis cervinus	15.17	10	37.5	23	21.42
Clelia clelia	14.42	22.33	12	36	21.19
Phimophis guianensis	22	22	20	20	21.00
Mussurana bicolor	17.92	25.67	12	28	20.90
Oxyrhopus petola	10.33	15.33	24.5	32	20.54
Clelia plumbea	18.17	19.67	12	31	20.21
Oxyrhopus guibei	13.92	22	24.5	18	19.61
Phimophis vittatus	13.75	28	20	16	19.44
Clelia langeri	27.88	8	–	22	19.29
Oxyrhopus clathratus	22.5	19.67	29.5	4	18.92
Oxyrhopus trigeminus	13.42	25	24.5	12	18.73
Clelia scytalina	22.67	33	12	7	18.67
Oxyrhopus rhombifer	11.42	29.33	24.5	8	18.31
Mussurana montana	19.5	26	12	13	17.63
Mussurana quimi	14.7	29.67	12	14	17.59
Phimophis guerini	18.58	28.67	20	3	17.56
Pseudoboa haasi	24	22.67	1.5	17	16.29
Siphlophis worontzowi	19.9	6.33	37.5	1	16.18
Oxyrhopus occipitalis	20.8	12	12	19	15.95
Pseudoboa coronata	16.08	6.67	12	27	15.44
Pseudoboa nigra	15.83	19.67	1.5	21	14.50
Oxyrhopus melanogenys	13	8.33	12	11	11.08
Pseudoboa martinsi	22.42	4.33	4	10	10.19
Pseudoboa neuwiedii	15.83	13.33	4	5	9.54
Oxyrhopus vanidicus	11	6.33	12	6	8.83
Clelia errabunda	–	–	–	–	–
Oxyrhopus doliatus	–	–	–	–	–
Oxyrhopus erdisii	–	–	–	–	–
Oxyrhopus fitzingeri	–	31.67	–	–	–
Oxyrhopus formosus	–	–	12	–	–
Oxyrhopus leucomelas	–	22.67	–	–	–
Oxyrhopus marcapatae	–	10.67	–	–	–
Rodriguesophis chui	–	–	33	–	–

their remarkably high level of endemism and accelerated habitat loss (Myers et al. 2000). Likewise, all ten species with the highest PI scores also occur in these regions. Hence, our results corroborate the suggestion that Hotspots are not only important in terms of species diversity, but also are centers of unique and threatened evolutionary history (Sechrest et al. 2002).

The two genera that had no species among the ten highest PI were *Oxyrhopus* and *Pseudoboa*. The genus *Oxyrhopus* comprises mostly widespread, generalist and disturbance-tolerant species. However, it is important to point out that we were unable to evaluate almost half of the *Oxyrhopus* species (Table 2, Tables A1 and A2), all of which have narrow ranges (Gaiarsa et al. 2013). Since range size and tolerance to habitat alteration appear to be related, due to a synergistic combination of extinction-promoting traits (Mckinney 1997; Swihart et al. 2003), we recommend that future studies seek to better understand the biology and ecology of these poorly known species. On the other hand, we were able to evaluate all the *Pseudoboa* species, which had relatively high values of IVE and EO, but some of the lowest values of PD, which explain their low PIs.

A critical step and one of the main issues in assessing conservation priorities is how data deficient species are treated (O'Grady et al. 2004), since some key information about less studied species under assessment are usually missing (Sattler et al. 2007). In this study, we were unable to calculate PI for eight species mainly due to the lack of life history and ecological data (IVE and EO; Table 2). We chose not to evaluate these data deficient species in order to avoid wrong estimates because discrepancies in risk assessments can erode confidence in conservation decision (Mrosovsky 1997; Tanentzap et al. 2012). Furthermore, species misclassifications can lead to resource misdirection, especially when the error accumulates over criteria (Todd & Burgman 1998). However, it is important to note that our data deficient species can be at any point in the continuum from highly threatened to non-threatened. Since our method considers all species within a phylogenic group (e.g., Tribe), when data deficient species are included, the status of the species previously assessed will probably change slightly. For example, if we are able to include in our analyses *R. chui* it will probably have high PI (based on existing life history data), thus lowering some of the PI values of the already assessed species.

Despite the remarkable variation in the life history traits included in the Ecological Oddity (EO) calculation (body size, fecundity, dietary breadth, and habitat breadth), these factors seem to be conserved in most of the tribe representatives, resulting in high EO values for few species that differ from the average morphological and/or ecological phenotype. Thus, two thirds of the 39 pseudoboines evaluated for this factor had relatively low values for this index, while only three species had very high EOs (*Clelia hussami* because of its narrow habitat breadth, and *Drepanoides anomalus* and *Rhachidelus brazili* due to their diet specialization on lizard eggs and bird eggs, respectively; Alencar et al. 2013; Gaiarsa et al. 2013). Indeed, this pattern would be expected in any clade with a great amount of phylogenetic inertia. Unlike expected (Cadotte et al. 2009; Redding et al. 2010), EO and PD were not correlated (Table A5), indicating that among pseudoboines higher distinctiveness in ecological or morphological features are not necessarily restricted to more phylogenetically distinct species. In addition, although some factors have been used twice in different indices (like body size and mean fecundity, both used in IVE and EO), none of the indices used were correlated (Table A3). This result also reinforces the importance to use prioritizing methods based on several factors (Grammont & Cuarón 2006; Mace et al. 2007). Finally, another benefit of our approach is its flexibility and the fact that it can be easily updated to include other factors and/or metrics.

In the present age of extinction with worst-case scenarios indicating extinction rates that would qualify as the sixth mass extinction (Barnosky et al. 2011) we are faced by the "agony of choice" (Vane-Wright et al. 1991) and have to decide which species are saved and which are not targeted with any conservation action (Heard & Mooers 2000; Posadas et al. 2001). Most strategies focus on the most endangered or threatened species (Wilson et al. 2006). Thus, in order to aid species prioritization, the approach used herein considers not only the vulnerability to extinction of species (EVE and IVE; e.g., Filippi & Luiselli 2000; IUCN 2001), but also the evolutionary history of the lineage studied (PD; e.g., May 1990; Vane-Wright et al. 1991) as well as the degree of ecological uniqueness of species within a lineage (EO; cf. Redding et al. 2010). Although it is not possible to compare values obtained in studies with different clades (the indices generated are clade-specific), when extended to more inclusive lineages within a group of organisms we hope this approach can contribute to a more comprehensive prioritization framework, enhancing the quality of future prioritization processes.

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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.2015.01.006.

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