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Research Letters

Spatial conservation priorities for top predators reveal mismatches among taxonomic, phylogenetic and functional diversity



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ABSTRACT

Systematic conservation planning is traditionally based on biological features, sometimes representing a single biodiversity component, such as top predators. However, few studies have tested the efficiency of traditional spatial prioritizations to capture the phylogenetic and functional diversity of entire faunas. Here, we evaluated (1) the congruence among spatial prioritization analyses based on taxonomic, phylogenetic and functional diversity for mammals and birds occurring in Brazil; and (2) the congruence among outputs of spatial priorities for carnivores and birds of prey and priorities for conserving the phylogenetic and functional diversity of all mammal and bird species. Priority sites differed among taxonomic groups as well as among biodiversity aspects, with low congruence among them. Overall, both strategies – full group and top predators – were not efficient and have not captured even half of all variation in phylogenetic and functional diversity existing in the groups.

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Introduction

Systematic conservation planning – the prioritization of sites due to their natural values and implementation of strategies to secure the survival and maintenance of biodiversity – is usually based only on the diversity of taxa (Margules and Pressey, 2000). However, taxonomic diversity is often

considered a less meaningful biological diversity measure because it ignores the differences among species (Rodrigues et al., 2011). Some authors have shown that taxonomic diversity does not necessarily overlap the distribution of other important components of biodiversity, such as the phylogenetic and functional diversity (Faith, 1992; Devictor et al., 2010; Strecker et al., 2011). Phylogenetic diversity quantifies the relatedness among species, based on their evolutionary

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histories (Pavoine and Bonsall, 2011). Meanwhile, functional diversity reflects the ecological relationships among species, considering their life history strategies and the roles that they play in the ecosystem (Pavoine and Bonsall, 2011). Given that extinction of species has led to non-random loss of evolutionary information (Purvis et al., 2000) and underlying ecological functions (Flynn et al., 2009), it is fundamental to test whether current conservation plans are efficient in capturing these biodiversity aspects.

Systematic conservation planning is also a complementarity-based site selection method accounting for both the biological attributes of sites, and inter-site similarities in order to represent all features without much duplication (Kukkala and Moilanen, 2013). Further, a comprehensive conservation plan should address the use of limited conservation resources efficiently beyond maximizing biodiversity features (Margules and Pressey, 2000). Spatial mismatches between taxonomic, phylogenetic, and functional patterns have been evidenced (e.g. Safi et al., 2011), but there are still few studies including the multifaceted nature of biodiversity in conservation planning (Devictor et al., 2010; Strecker et al., 2011) and they encompass only single groups. Top predators, for example, have long been considered a good conservation surrogate by conservation biologists that are faced with time and logistic constraints (Sergio et al., 2008). This group has been commonly employed as tool when identifying areas to conserve spatial heterogeneity (Sergio et al., 2008), a proxy of biodiversity.

However, to date there is no study investigating whether spatial priorities defined on the basis of top predators is efficient to capture the phylogenetic and functional diversities of entire faunas. Here, we used geographic distribution data of mammal and bird species – including top predators of both groups (carnivores and birds of prey, respectively) – for all terrestrial biomes of Brazil. We compared traditional spatial prioritization approaches, which are based on taxonomic diversity with approaches considering phylogenetic and functional components of biodiversity. Also, we explored the congruence between spatial prioritization based on top predators and those different facets of biological diversity. More specifically we tested: (1) the congruence (i.e. spatial overlap) between the priority sites based on taxonomic diversity of all mammals and birds and the phylogenetic and functional diversity of all these species, and (2) the congruence between the priority scenarios based on taxonomic diversity of carnivores and birds of prey and the phylogenetic and functional diversity of all mammal and bird species.

Materials and methods

Species distribution models

We modeled the potential distribution of Brazilian mammals ($n=515$ species) and birds ($n=1581$ species) as a function of abiotic variables using the extension of occurrence provided by IUCN (www.iucnredlist.org) and BirdLife International (www.birdlife.org). Because species distribution maps have, in general, coarse resolution we chose to model each species distribution instead of using its extension of occurrence. This

has been used to provide finer resolution estimates of species occurrences for spatial planning analyses (e.g. Loiselle et al., 2003).

We mapped each species in a grid of 3057 cells with 0.5×0.5 of latitude/longitude (about of 55,200 m in Ecuador Line) covering all Brazilian territory. We built a presence-absence matrix from overlapping the species distribution maps and cell grids. Species were considered as present in a cell when their range covered more or at least 50% of the cell. We also built a matrix of abiotic variables: altitude and climatic variables (Mean Temperature of Warmest Quarter, Mean Temperature of Coldest Quarter, Annual Precipitation and Precipitation Seasonality). We obtained these variables from WorldClim database (www.worldclim.org) interpolating climate data from 1950 to 2000 periods.

Projections coming from alternative species distribution models can be variable and, in addition, the sensitivity of each species to the models is unknown (Diniz-Filho et al., 2009). Therefore, as we were interested in a large number of species, with different range characteristics and sensibilities unknown, we modeled the species distribution applying an ensemble forecasting approach in which different methods of ecological niche model were combined (Araújo and New, 2007). This procedure provides a more robust consensus forecast reducing uncertainties (Araújo and New, 2007) that may mislead conservation actions making them less cost-effective (Loiselle et al., 2003). We chose the following ecological niche models (ENM) methods: Generalized Linear Models (GLM), Generalized Additive Models (GAM), and Multivariate Adaptive Regression Splines (MARS). We used such methods because their predictions are intermediate between commission and omission error if compared with distance and machine-learning methods (see Rangel and Loyola, 2012).

To build each ecological niche model we randomly partitioned the species data in calibration data (75%) and validation data (25%) replicating this process for 50 times (cross-validation test). We used true skill statistics (TSS, Allouche et al., 2006) as a measure of model performance, given by:

$$TSS = \text{sensitivity} + \text{specificity} - 1$$

where sensitivity is the proportion of species presences correctly identified and specificity is the proportion of the correctly identified species absences (both calculated from the validation subset). Models with TSS lower than 0.5 were excluded from analyses. Species occurrences resulting from ecological niche models were expressed as frequencies of occurrence at which they appear at each cell. We also calculate presence-absence at each cell applying a majority consensus rule cutting estimated frequencies of occurrence at 50%.

Phylogenetic and functional analyses

For each cell grid we quantified the phylogenetic and functional diversity of (i) carnivores, (ii) birds of prey, (iii) all other mammals (except carnivores) and (iv) birds (except birds of prey) of Brazil based on the species composition resulted of ecological niche models. To quantify the phylogenetic and functional diversity of groups we used the Mean Pairwise Distance (MPD), a measure independent of taxonomic diversity (Webb, 2000). Originally, MPD was developed for estimating

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