



A new spin on a compositionalist predictive modelling framework for conservation planning: A tropical case study in Ecuador



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ABSTRACT

Knowledge about spatial biodiversity patterns is a basic criterion for reserve network design. Although herbarium collections hold large quantities of information, the data are often scattered and cannot supply complete spatial coverage. Alternatively, herbarium data can be used to fit species distribution models and their predictions can be used to provide complete spatial coverage and derive species richness maps. Here, we build on previous effort to propose an improved compositionalist framework for using species distribution models to better inform conservation management. We illustrate the approach with models fitted with six different methods and combined using an ensemble approach for 408 plant species in a tropical and megadiverse country (Ecuador). As a complementary view to the traditional richness hotspots methodology, consisting of a simple stacking of species distribution maps, the compositionalist modelling approach used here combines separate predictions for different pools of species to identify areas of alternative suitability for conservation. Our results show that the compositionalist approach better captures the established protected areas than the traditional richness hotspots strategies and allows the identification of areas in Ecuador that would optimally complement the current protection network. Further studies should aim at refining the approach with more groups and additional species information.

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1. Introduction

A common strategy in conservation planning is the design of reserve networks with the final aim of preserving the most unique and biodiverse areas *in situ* (Possingham et al., 2006; Margules and Pressey, 2000; Myers et al., 2000; Prendergast et al., 1999). Conservation strategies vary, but the main trouble in biodiversity conservation is not really related to gaps in knowledge or technical complexities, but to budgetary difficulties: conservationist and governments cannot afford assisting all species under threat, especially for lack of funding in the most biodiverse countries (Bruner et al., 2004). Protected-area systems must ideally represent regional biodiversity and provide conditions to separate it from processes that threaten its persistence (Margules and Pressey, 2000). Conservation efforts should be based on biodiversity richness, density of unique species (i.e., endemics) and threat patterns, rather on

percentage of area officially included in protected-area systems (Rodrigues et al., 2004). In recognition of the need for more representative protected areas and the limited resources that government and conservationist can usually allocate to implement them, systematic approaches to conservation planning have been developed in recent years (Moilanen et al., 2009; Margules and Sarkar, 2007; Margules and Pressey, 2000; Pressey et al., 1993). Unfortunately, direct knowledge about the distribution of organisms is usually scarce. When spatial patterns of biodiversity are not accurately known, reserve designers and conservation managers must use indirect measures of biodiversity patterns, such as those derived from aerial photography and remote sensing sources, or other environmental indicators based on climate, topography, geology and soil attributes (Ferrier et al., 2007.; Margules and Pressey, 2000; Wilson et al., 2005).

A complementary strategy is to use the data stored in natural history collections (Gaubert et al., 2006; Graham et al., 2004; Loisele et al., 2003; Newbold, 2010), which are now available through public databases, such as TROPICOS (www.tropicos.org), or distributed search engines, such as the Global Biodiversity Information Facility network (GBIF, <http://www.gbif.org/>). However,

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these databases also have disadvantages, such as defective spatial coverage, and spatial and taxonomic bias (Ferrier, 2002). A worldwide networking effort is currently under way to reduce the bias in these global biodiversity data (Bisby, 2000; Guralnick et al., 2007; Soberón and Peterson, 2004), but this effort will require many years before robust data sets of complementary biodiversity data will be available, especially in tropical zones (Cayuela et al., 2009). These sampling issues can lead to underestimate the true species distributions. In other words, an error of omission occurs because a species may inaccurately appear absent from a section of its real distribution because the area has not been sampled (Underwood et al., 2010). This defective spatial coverage of biodiversity data could be overcome, however, using species distribution models.

Species distribution models (SDMs; Guisan and Zimmermann, 2000) have become widely used in conservation biology. They allow the expression of habitat suitability as a function of various ecologically meaningful environmental predictors across large spatial coverage. Predictive modelling is a growing discipline and many modelling techniques and approaches have been proposed (Elith and Leathwick, 2009). To cope with this wealth of options, a recent improvement to SDMs has been to ensemble models built with different initial data, modelling techniques or environmental change scenarios into a single, final prediction (Araújo and New, 2007; Grenouillet et al., 2011; Marmion et al., 2009). These improved species predictions – and associated uncertainty – can then be combined to make community predictions (Ferrier and Guisan, 2006). By summarising individual ensemble species distribution models (S-SDMs; Guisan and Rahbek, 2011), one can, for instance, predict potential species richness (Dubuis et al., 2011; Mateo et al., 2012), which can then be used to represent the distribution of richness hotspots in an area (Parviainen et al., 2009) and support the design of reserve networks (Araújo et al., 2004). Predicting richness hotspots is only one of many possible SDM applications in conservation, but other types of predictions at the species, community or landscape levels (e.g., predicted complementarity) are preferred or required to reach specific conservation goals (Whittaker et al., 2005), which may also use SDM predictions as inputs.

However, SDMs are not free of errors and uncertainty (Carvalho et al., 2010; Underwood et al., 2010), because: (1) the distribution data on which they are based contain errors (see above); (2) they may not include all environmental, ecological and historical factors that affect species distributions (Guisan and Zimmermann, 2000); (3) there might be uncertainty in the environmental variables used to generate the SDMs, either through measurement errors or as a consequence of the resolution at which variables are mapped and (4) these environmental variables may be partially collinear (as likely here to some extent), potentially hampering full models' predicting performance. These errors and uncertainties commonly give rise to an overestimation of species distributions (Segurado and Araújo, 2004). These commission errors – false positives – can have an untoward impact on conservation decisions process, because areas where species do not occur might be selected for conservation effort, resulting in both a waste of funds and an unrecognised failure to achieve a conservation target (Rondinini et al., 2006).

Although hotspots have been used to refer to those areas rich in endemic species, the term has also been applied to areas of high diversity in species, endangerment and rarity (e.g. García, 2006; Godown and Peterson, 2000; Grand et al., 2004; Ortega-Huerta and Peterson, 2004; Rutledge et al., 2000). We refer here to hotspots as high richness areas, i.e. simple stacking of SDMs (or richness models), as most traditionally practiced in the scientific literature (e.g. García, 2006; McClean et al., 2005; Ortega-Huerta and Peterson, 2004; Pineda and Lobo, 2009; Urbina-Cardona and Flores-Villela, 2010). This traditional richness hotspots

methodology is aimed to the conservation of the largest possible number of species in the smallest possible area (Kareiva and Marvier, 2003; Whittaker et al., 2005). However, using richness hotspots to set priorities is questionable when considering a broader range of objectives, such as preserving unique components of biodiversity (rarity, endemism), maintaining functioning ecosystems throughout the world or providing the greatest variety of distinct plant and animal lineages for future evolutionary breakthroughs (Kareiva and Marvier, 2003; Orme et al., 2005). For instance, some authors have already argued for the importance of studying biodiversity “coldspots” within the design of conservation networks (Bohn and Amundsen, 2004; Kareiva and Marvier, 2003; Price, 2002).

One such approach is the compositionalist approach (Callicott et al., 1999; Whittaker et al., 2005; Williams and Araújo, 2000), which considers different pools of species separately (similar biogeographic regions or level of endemism here, see material and methods). Each pool consists of species sharing characteristics that differ from other pools, and represents a different biodiversity value, eventually including the importance of each of these groups in a final map. In the richness hotspots strategy, the importance of these groups is masked by the total set of species. Therefore, the compositionalist approach potentially represents a complementary view to the richness hotspots approach at regional scale, i.e. a spatially more informative approach than for example taking into account information of different biogeographical areas or rates of endemism. For example, despite the extreme conditions of the Ecuadorian páramo, over 1500 species of vascular plants are estimated to be present (León-Yáñez, 2000). This figure means that 10% of the Ecuadorian flora is present in 5% of the territory (Mena-Vásquez et al., 2001). Much endemism is restricted to Páramo formations due to their unique environmental conditions (Young et al., 2002). The richness hotspots approach would presumably predict maximum biodiversity richness in the Amazon basin, the two Andean slopes, and the Chocó biogeographic region. Therefore, this approach is unlikely to identify the unique plant formations from Páramo and will be unable to include information on endemic species. An approach allowing the consideration of individual species or pools of species is required for these tasks. The compositionalist approach, by allowing the representation of compositions of particular species and pools of species, should identify Páramos as optimal areas for conservation.

Both the traditional richness hotspots and the compositionalist approaches require comprehensive species distribution maps, but these are rarely available in a spatially-explicit way, especially in tropical countries (Kareiva and Marvier, 2003). One possible way to overcome this issue is to use model predictions as a surrogate for real distribution data, but there are still few published examples of such model-based approaches that consider biogeographic specificities and endemism to design conservation areas.

Here, we propose such a complementary compositionalist approach based on species distribution models (SDMs) to identify areas of maximised suitability for conservation (AMSC). We illustrate the approach with plants in Ecuador, with focus on the Coastal, Andean, Páramo, Amazonia regions, and endemic species. We take advantage of the most comprehensive plant database compiled so far for Ecuador, with 408 species from herbarium collections.

We use advanced ensemble SDMs based on six modelling techniques for each individual species and subsequently stack them (according to Guisan and Rahbek, 2011) by region and endemism to generate compositionalist maps of species richness. Finally, we evaluate the conservation status of plant diversity in Ecuador using the potential richness maps derived from the simple stacking of all species predictions and the new compositionalist approach considering stacked groups of species. Ultimately, we show how

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