Université de Montréal

Évaluation de l'unicité écologique sur des échelles spatiales étendues et continues

par

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Mémoire présenté en vue de l'obtention du grade de

Maître ès sciences (M.Sc.)

en Sciences biologiques

19 avril 2021

Université de Montréal

Faculté des arts et des sciences

Ce mémoire intitulé

Évaluation de l'unicité écologique sur des échelles spatiales étendues et continues

présenté par

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a été évalué par un jury composé des personnes suivantes :

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Résumé

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Abstract

...summary and keywords in english...

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Liste des sigles et des abréviations

KQ-Methode   Méthode des moindres carrés, de l'allemand *Methode der kleinsten Quadrate*

MCMC   Monte Carlo par chaînes de Markov, de l'anglais *Markov Chain Monte Carlo*

MSE   Erreur quadratique moyenne, de l'anglais *Mean Square Error*

NDR   Retract d'un voisinage, de l'anglais *Neighbourhood Deformation Retract*

OLS   Moindres carrés ordinaires, de l'anglais *Ordinary Least Square*

ZFC   Théorie des ensembles de Zermelo-Fraenkel avec l'axiome du choix

Remerciements

...remerciements...

Introduction

Introduction

La diversité bêta, définie comme la variation dans la composition en espèces entre les sites au sein d'une région géographique d'intérêt (Legendre et al., 2005), est une mesure essentielle pour décrire l'organisation de la biodiversité dans l'espace.

Méthodes

Nous avons mesuré comment l'unicité compositionnelle varie sur des échelles spatiales étendues et continues. Nous avons utilisé *Julia v1.5.3* (Bezanson *et al.*, 2017) pour la majorité des analyses et *R v4.0.2* (R Core Team, 2020) pour certaines étapes spécifiques. Tous les scripts utilisés pour les analyses sont disponibles au site `https://github.com/gabrieldansereau/` `betadiversity-hotspots.`

Données d'occurrence

Nous avons restreint nos analyses à la famille des parulines du nouveau monde (*Parulidae*) en Amérique du Nord (Canada, États-Unis, Mexique) à l'aide de la librairie *R* `auk`.

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First Article.

Titre de l'article

by

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This article was submitted in Une revue.

The main contributions of Gabriel Dansereau for this articles are presented.

— Calcul de telle chose;

— Vérification de telle équation;

— Idée pour telle définition;

— Démonstration de tel théorème.

Le coauteur1 a suggéré telle chose.

Le coauteur2 a fait telle calcul.

RÉSUMÉ. Le résumé en français.

Mots clés : Mots clés

ABSTRACT. The english abstract.

Keywords: Key words

1. Introduction

Beta diversity, defined as the variation in species composition among sites in a geographic region of interest (Legendre et al., 2005), is an essential measure to describe the organization of biodiversity though space. Total beta diversity within a community can be partitioned into local contributions to beta diversity (LCBD) (Legendre and De Cáceres, 2013), which allows the identification of sites with exceptional species composition, hence unique biodiversity. Such a method, focusing on specific sites, is useful for both community ecology and conservation biology, as it highlights areas that are most important for their research or conservation values. However, the use of LCBD indices is currently limited in two ways. First, LBCD indices are typically used on data collected over local or regional scales with relatively few sites, for example on fish communities at intervals along a river or stream (Legendre and De Cáceres, 2013). Second, LCBD calculation methods require complete information on community composition, such as a community composition matrix Y; thus, they are inappropriate for partially sampled sites (e.g. where data for some species is missing), let alone for unsampled ones. Accordingly, the method is of limited use to identify areas with exceptional biodiversity in regions with sparse sampling. However, predictive approaches are increasingly common given the recent development of computational methods, which often uncover novel ecological insights from existing data (Poisot et al., 2019), including in unsampled or lesser-known locations, as well as larger spatial scales. Here, we examine whether the LCBD method can assess ecological uniqueness over broad and continuous scales based on predictions of species distributions and evaluate whether this reveals novel ecological insights regarding the identification of exceptional biodiversity areas.

Species distribution models (SDMs) (Guisan and Thuiller, 2005) can bring a new perspective to LCBD studies by filling in gaps and performing analyses on much broader scales. In a community

matrix Y, such as required for LCBD calculation, ecological communities are abstracted as assemblages of species present at different sites. Viewing communities as such opens the perspective of predicting community composition from predictions of individual species, which is precisely the aim of SDMs. Community-level modelling from SDMs is not an especially novel idea (Ferrier et al., 2002; Ferrier and Guisan, 2006), but it is increasingly relevant with the advent of large-scale, massive, and open data sources on species occurrences, often contributed by citizens, such as eBird and GBIF. At their core, SDMs aim at predicting the distribution of a species based on information about where the species was previously reported, matched with environmental data at those locations, and then make predictions at other (unsampled) locations based on their respective environmental conditions. However, going from single-species SDMs to a whole community is not a trivial task, and many solutions have been suggested, such as stacked species distribution models (S-SDMs) (Ferrier and Guisan, 2006), spatially explicit species assemblage modelling (SESAM) (Guisan and Rahbek, 2011), joint species distribution models (JSDMs) (Pollock et al., 2014), and hierarchical modelling of species communities (HMSC) (Ovaskainen et al., 2017). These alternative methods all have different strengths, but even S-SDM, in a sense the most simple and less community-specific method, has been shown to provide reliable community predictions (Norberg et al., 2019; Zurell et al., 2020). This is important, as in the context of large-scale studies with a high number of sites and species, reducing the model complexity with a simpler yet efficient model such as an S-SDM can reduce the number of computations in an important way. Regardless of the method used, community-level analyses can be applied to the resulting community prediction, but this has been lacking for community measures other than species richness (Ferrier and Guisan, 2006). Notably, the LCBD framework has, to our knowledge, never been applied to SDM results. The computation of local contributions to beta diversity (LCBD) on SDM predictions, however, raises the issue of calculating the uniqueness scores on much larger community matrices than on the typical scales on which it has been used.

The total number of sites will increase (1) because of the continuous scale of the predictions, as there will be more sites in the region of interest than the number of sampled sites, and (2) because of the larger spatial extent allowed for the SDM predictions. A high number of SDM-predicted

sites with a large extent opens up the possibility of capturing a lot of variability of habitats and community composition, but also many very similar ones, which could change the way that exceptional sites contribute to the overall variance in the large-scale community. LCBD scores have typically been used at local or regional scales with relatively few sites (Legendre and De Cáceres, 2013; da Silva and Hernández, 2014; Heino et al., 2017; Heino and Grönroos, 2017). Some studies did use the measure over broader, near-continental extents (Yang et al., 2015; Poisot et al., 2017; Taranu et al., 2020), but the total number of sites in these studies was relatively small. Recent studies also investigated LCBD and beta diversity on sites distributed in grids or as pixels of environmental raster layers, hence continuous scales, but these did not cover large extents and a high number of sites (Tan et al., 2017, 2019; Legendre and Condit, 2019; D'Antraccoli et al., 2020). Niskanen et al. (2017) predicted LCBD values of plant communities (and three other diversity measures) on a continuous scale and a high number of sites (> 25 000) using Boosted Regression Trees (BRTs). However, they modelled the diversity measures directly instead of modelling species distributions first, as we are suggesting here. They obtained lower predictive accuracy for LCBD than for their other diversity measures, mentioning that it highlighted the challenge of predicting LCBD specifically. They also computed LCBD indices at a regional scale, not a continental one, while a using a fine spatial resolution (1 km x 1 km). Therefore, the distribution of LCBD values at broad, continuous scales with a high number of sites and predicted species assemblages remains to be investigated.

Measuring ecological uniqueness from LCBD indices on extended continuous scales also raises the question of which sites will be identified as exceptional and for what reason. The method intends that sites should stand out and receive a high LCBD score whenever they display an exceptional community composition, be it a unique assemblage of species that may have a high conservation value or a richer or poorer community than most in the region (Legendre and De Cáceres, 2013). Both the original study and many of the later empirical ones have shown a negative relationship between LCBD scores and species richness (Legendre and De Cáceres, 2013; da Silva and Hernández, 2014; Heino et al., 2017; Heino and Grönroos, 2017), although other studies observed both negative and positive relationships at different sites (Kong et al., 2017) or quadrats (Yao et al.,

2021). Therefore, this relationship should still be investigated, especially at broad continuous scales, where LCBD indices have not yet been used. Total beta diversity increases with spatial extent (Barton et al., 2013) and is strongly dependent on scale, notably because of higher environmental heterogeneity and sampling of different local species pool (Heino et al., 2015), which could potentially add some variation to the relationship. Neither the previous studies at broad spatial extents (Poisot et al., 2017; Taranu et al., 2020; Yang et al., 2015), on spatially continuous data (Tan et al., 2019; D'Antraccoli et al., 2020), or on a high number of sites (Niskanen et al., 2017) have specifically measured the variations of the richness-LCBD relationship according to different regions and spatial extents. These studies brought forward relevant elements which now need to be combined.

This study shows that species distribution modelling offers relevant LCBD and community-level predictions on broad spatial scales, similar to those obtained from occurrence data and providing uniqueness assessments in poorly sampled regions. Our results further highlight a changing relationship between site richness and LCBD values depending on (i) the region on which it is used, as species-poor and species-rich regions display different uniqueness profiles; and on (ii) the scale at which it is applied, as increasing the spatial extent can merge the uniqueness profiles of contrasting subregions to create a new, distinct one at a broader scale. Hence, our method could prove useful to identify beta diversity hotspots in unsampled locations on large spatial scales, which could be important targets for conservation purposes.

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