Inescapable Taxonomists: Workable Biodiversity Management Based on a Minimum Field Work

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Abstract

Assess the fate of Neotropical forests requires to accurately measures are the base of reliable foret monitoring, crucial to assess the fate of neotropical forests in the current changing climate. The costs of botanical inventories and the taxonomic complexity of Neotropical forests make predominant forest inventories in vernacular names, although these hold high botanical uncertainty. Several methods proposed to compensate botanical uncertainties but none allowed reliable neither functional nor fine-scale diversity approaches. Here we offer a polyvalent diversity estimator propagating botanical uncertainties and workable in numerous specific cases. From a large neotropical inventory, we calibrated the stimator and through simulations we determined an ideal inventory protocol optimizing the costs and the accuracy of forest inventories. Our study first highlighted the unavoidable use to real inventories, compared to general vernacular/botanical tables, and the inescapable recourse to taxonomists to ensure robust diversity survey. Then our simulations allowed estimated the minimum sampling size (XX trees) and percentage of species accurately identified (80% of species known) for inventories to allow diversity estimations with a 10% error. The diversity estimator effectively assessed diversity for a variety of pre-logging and experimental forest monitoring, acknowledging the rescourse to taxonomists, and enabled to design optimized inventory protocols.

Keywords

Biodiversity Measurement, Tree Community, Neotropical Forests, Botanical Uncertainty Propagation, Bayesian Estimator

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1. Introduction

The variety of tree species, their assemblages in space and their dynamics in time are determinant of forests productivity and functioning (Cardinale *et al.*, 2012). Preserve tree diversity is crucial to maintain forests functioning and services, specifically in hyper-diverse tropical forests where the biodiversity is as threatened as it is valuable and unexplored (Barlow *et al.*, 2018). Handling the conservation and management of tree diversity requires setting sensible protection areas and sustainable forest management calibrated according to diversity patterns in space and time and their determinants (Margules & Pressey, 2000; Purvis & Hector, 2000; Gibson *et al.*, 2011; FAO, 2014; Sist *et al.*, 2015).

Correctly measure, map and manage forests biodiversity require accurate and large forest monitoring. The precision of forest inventories, though, is often limited by their significant cost in terms of time, money, and logistic (Feeley & Silman, 2011; Baraloto *et al.*, 2012b). Sampling methods were optimized to minimize these costs and maximize inventory accuracy. Some approaches would restrict inventories to some DBH or height classes, to specific taxa, or would opt for inventories at family or genus level. These methods efficiently translated biodiversity patterns at regional scales and along wide ecological gradients (Steege *et al.*, 2000; Higgins & Ruokolainen, 2004; Réjou-Méchain *et al.*, 2011; Pos *et al.*, 2014). However, these methods were either limited to small areas (under 1ha), sometimes remained biased or holding significant uncertainty, and usually proved limited to detect subtle diversity aspects and to desentangle richness from equitability parameters (Phillips *et al.*, 2003; Baraloto *et al.*, 2012b; Guitet *et al.*, 2014, ; Vellend *et al.*, 2008; Prance, 1994). Another approach proposed to use inventories in vernacular names instead of botanical

species. Vernacular names indeed are easier to attribute, more common and usually do not require vouchers collection or posterior botanical identification. The reliability of vernacular names may be high at genus level, but this proved highly variable across tropical regions: while this reliability was estimated around 60-70% in French Guiana (Hawes *et al.*, 2012; Guitet *et al.*, 2014) to ranges from 32% to 67% in Central Africa (Réjou-Méchain *et al.*, 2011). The multiple and variable associations between botanical and vernacular names then entail significant botanical uncertainties that should not be ignored (Oldeman, 1968). Besides, rough vernacular inventories would not allow functional and phylogenetic approaches, that require identification at the botanical species to comply with phylogenetic and functional database. However the approach through vernacular names deserves further attention. First, it gives the opportunity to analyze pre-logging inventories conducted in large areas by logging companies. Second, as exhaustive inventories, they allow some post-process based on vernacular/botanical names association and allow the building of reliable diversity estimators (ter Steege *et al.*, 2006; Feldpausch *et al.*, 2006; Réjou-Méchain *et al.*, 2008, 2011). Following this idea Guitet *et al.* (2014) proposed a framework propagating vernacular names taxonomic uncertainties in diversity measures. The propagation framework was based on Monte-Carlo processes estimating forest diversity from the vernacular-botanical name association. These association combined prior information from both general taxa-abundance correspondence table (Molino *et al.*, 2009) and reference field inventories. The framework successfully rendered the ranking of plots diversity, but remained restricted to large environmental gradient and for highly different communities (Guitet *et al.*, 2014, 2013). In this study we offer to refine this framework and adapt it to diversity estimation at smaller spatial scales. The following diversity estimator is based on the specific case of the studied community and the inventory protocol. The diversity estimator besides suits all inventories whatever the ratio of botanical determination, *i.e.* ratio of vernacular compared to botanical names. It besides suits experimental specific as well as pre-logging inventories where only the commercial or most recognizable species are identified at species level.

Such diversity estimator allows maximizing the accuracy of diversity measures while minimizing the sampling effort, *i.e.* the size of inventoried communities and the number of accurately identified species. In this perspective we thought to calibrate an ideal inventory protocol optimized in terms of sampling effort and determination degree. From a real inventory, with complete vernacular and botanical identifications, we simulated ranges of sampling efforts and identification degrees along which we examined the bias and variability of the diversity estimator.

In this study we *(i)* redesigned a diversity estimator based on a Bayesian framework accounting for both general taxa-association tables and specific field inventories, and *(ii)* applied the estimator to a real Neotropical forest inventory to determine the sampling effort and determination degree of an ideal inventory protocol.

2. Methods

2.1 Study community

We based our analyses on the inventory of a Neotropical rainforest, from the Paracou Research Station in French Guiana (5°18'N and 52°53'W). The experimental site stands in a lowland tropical rainforest with a flora dominated by *Fabaceae*, *Chrysobalanaceae*, *Lecythidaceae* and *Sapotaceae* families. Mean mean annual temperature is 26°C. and the mean annual precipitations average $2980 mm.y^-1$ (30-y period) with a 3-months dry season ($< 100 mm.months - 1$) from mid-August to mid-November and a one-month dry season in March (Wagner *et al.*, 2011). Elevation ranges between 5 and 50 m and soils correspond to thin acrisols over a layer of transformed saprolite with low permeability, generating lateral drainage during heavy rains (IUSS Working Group WRB, 2015). We used the 2015 inventory of six permanent plots of undisturbed forest (6.25ha each, 37.5ha inventoried in total). During inventories trees are identified first with a vernacular name assigned by the forest worker team, and afterward with a scientific name assigned by botanists during regular botanical campaigns. The community inventoried ancompasses 22 904 trees belonging to 375 species and 63 families, identified by 290 different vernacular names. The initial taxonomic uncertainty was 3% of the community, *i.e.* the proportion of trees not identified with a botanical name.

2.2 Diversity measures

Among the large panel of diversity indices we examined here the family of q-generalized (Tsallis) entropy, widely adopted to assess all aspects of taxonomic, functional and phylogenetic diversities. The Tsallis diversity indices derive from a general formula, modulated by an order q emphasizing species frequency (1).

$$^qD = \sum_{i=1}^{N} \left(p_i^q\right)^{\frac{1}{1-q}} \tag{1}$$

In the diversity formula, species relative abundance p_i in a community of N species is raised at the power q that is the order of the diversity. The higher the order q, the higher the emphasis on common vs. rare species, so browsing a range of order q corresponds assess a gradient balance between richness and evenness. The formula retrieves species richness for $q = 0$, Shannon diversity for $q = 1$ where richness and evenness are equally accounted for and Simpson diversity, that can be undestood as the diversity of common species, for $q = 2$. The Tsallis diversity indices would eventually be converted into equivalent number of species in our framework. The conversion in equivalent number of species, through Hill transformation, allows understandable analysis and comparisons among communities (Hill, 1973; Keylock, 2005; Jost, 2006).

2.3 Diversity estimator

The estimation framework is based on the diversity distribution measured on theoretical, fully determined communities. Theoretical inventories are simulated 1 000 times from the real incomplete inventory, through the replacement by

a Monte-Carlo scheme of vernacular names by botanical ones.

The vernacular-botanical replacement are based on the association probability between each vernacular names and the botanical names inventoried. For each vernacular name the association model follows a multinomial distribution $M([s_1, s_2, \ldots, s_N], [\alpha_1, \alpha_2, \ldots, \alpha_N])$, with $[\alpha_i]$ the association probability of botanical name s_i with the vernacular name.

The association probability vectors $[\alpha_v]$ were determined with a Bayesian framework based on the combination of botanical expertise and observed associations. First, the estimation of $[\alpha_v]$ accounted for prior information from experts' knowledge in the form of a general taxa-association table listing all botanical names likely corresponding to the vernacular name v. From this general table, the probability $\lambda_i = {}^1/m_v$ was attributed to each of the m_v botanical names with a confirmed association with v. When no association was established the probability $\lambda_i = {}^\varepsilon/_{N-m_v}$ was attributed to the botanical name, with ε standing for a background noise set to 0.01 here. Second, the estimation of $[\alpha_v]$ accounted for observed inventories giving real association frequencies ϕ_i between v and the m'_v botanical names with observed association. Similarly, the association probability $\lambda_i = {}^\varepsilon/_{N-m'_v}$ was attributed to botanical names with no observed association. The final $[\alpha_v]$ distribution was modeled by a Multinomial-Dirichlet scheme combining the two vectors $[\lambda^v]$ and $[\phi^v]$ (McCarthy, 2007).

To test the relevance of the general table and observed inventories information, we tested a range of weighting w. Assuming a distribution of $[\phi^v]$ conditionally to $[\alpha^v]$ the weighting returned the formula (2).

$$[\alpha_i^v] : \left[\alpha_i^v |_{(1-w)\lambda_i^v, w.\phi_i^v}\right] = Dirichlet\left((1-w)\phi_i^v + w.\lambda_i^v\right) \quad (2)$$

When $w = 0$ only observed inventories were considered, when $w = 0.5$ both information were equally accounted for and when $w = 1$ only the general taxa-association table was considered.

2.4 Simulation of determination and sampling effort gradients

The simulation of a determination effort gradient, *i.e.* an increasing proportion of vernacular names among all identifications, allowed to (i) examine the diversity estimator response to the determination effort and (ii) determine the best input balance w between general table and observed inventories for the estimator. The indetermination gradient was simulated by ignoring an increasing number of botanical identifications in the reference inventory. As rare species had more chance to be undetermined (Kendall test, $\tau = -0.46, p < 10^{-16}$), the trial of ignored determination followed botanical names abundance ($p_{undetermined} = f_i^{-0.1}$, with f_i botanical name frequency).

The simulation of a sampling effort gradient, *i.e.* an increasing number of trees inventoried to compute the observed association probability, assessed the response of the

diversity estimator to sampling effort. The simulated gradient ranged from 500 to 22 000 trees randomly selected in the reference inventory.

Along both indetermination and sampling effort gradient we examine the estimator bias, *i.e.* the difference between the estimation and the real diversity (Baltanas, 2009), the estimator variability, *i.e.* 95% confidence interval.

3. Results

3.1 The reponse to determination effort, and the design of an ideal framework

Along the indetermination gradient, when considering both general taxa-association table and observed inventory the diversity was increasingly overestimated (Fig. 1*(a)*). This overestimation increased with the order of diversity q, while it was not significant for the richness ($q = 0$), the overestimation reached 45% of the real diversity for Shannon diversity ($q = 1$) and it reached 57% of the real diversity for the Simpson diversity ($q = 2$).

When only considering the general taxa-association table (Fig. 1*(b)*) the richness ($q = 0$) was underestimated (reaching a 50% underestimation), while both Shannon and Simpson diversities were overestimated (respectively reaching underestimations of 67% and 125%).

When only confidering the observed inventory (Fig. 1*(c)*) the estimator remained slightly biased but it did not exceed 15% of the real diversity for any order of diversity.

A bootstrap of the 100 simulations for each specific case and diversity order showed a stabilization of variances after 60 simulations.

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3.2 Calibrating the sampling effort

Along the sampling effort gradient from 500 to 22 000 trees, the richness estimation remained underestimated but the estimator confidence interval did not exceed 7%. The Shannon and Simpson were less biased, for 2 000 trees inventoried the Shannon diversity bias fell to 15% while the bias of Simpson estimator fell to 6% (Fig. 2.

4. Discussion

4.1 Inescapable taxonomists

The method developed in the line of Guitet *et al.* (2014) to propagate the taxonomic uncertainty of vernacular names in diversity mesures provided a reliable estimator for diversity indices of different order. The use the general taxonomic-association table proved to systematically overestimate the diversity. Indeed in the general table vernacular/botanical association probability were independent of botanical names abundance, so rare vernacular were indifferently replaced by rare or abundant botanical names. Randomly along the
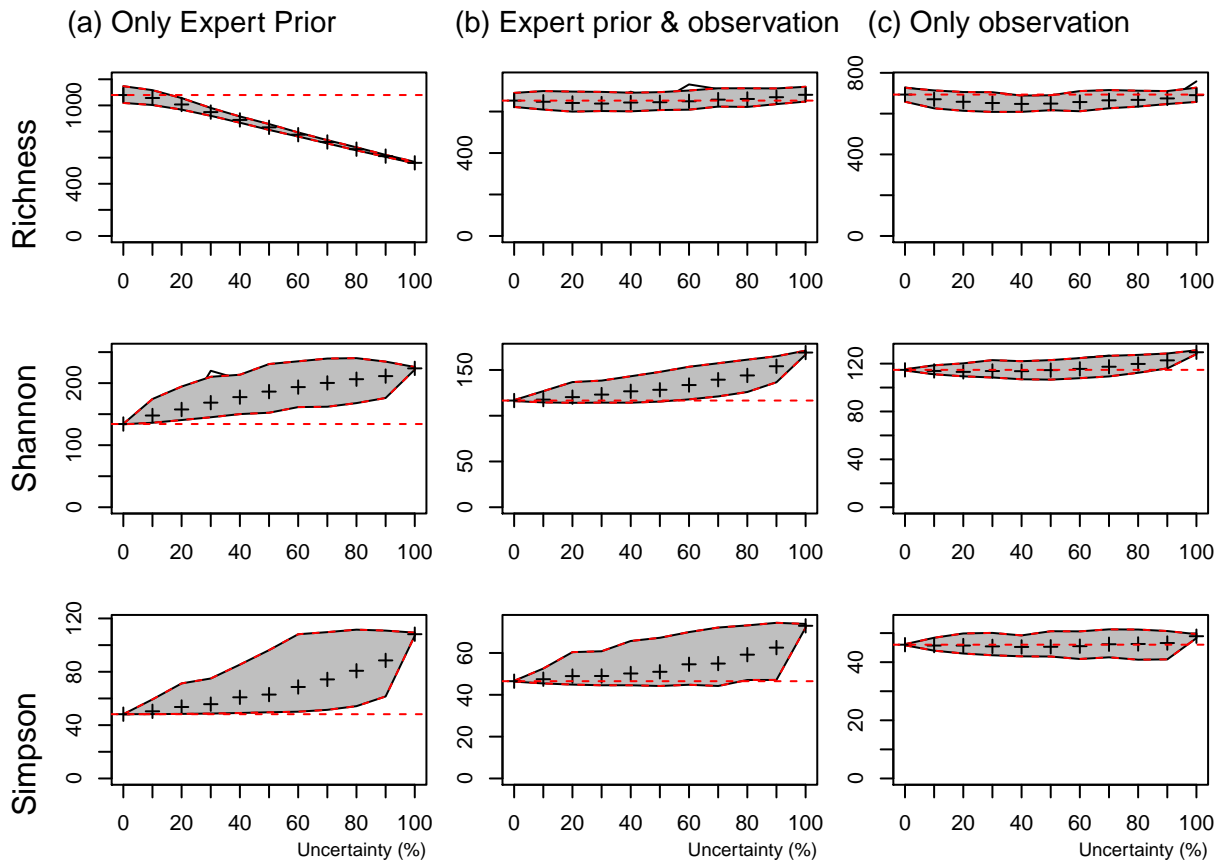
Figure 1. Indices degradation along a taxonomic uncertainty gradient. 95% envelopes of the Richness, Shannon and Simpson indices calculated through our propagation method along an uncertainty gradient from 0 to 100% of undetermined species. In (a) Only expert prior is considered to compute the association frequencies, in (b) both expert and observation prior are equally accounted for in the propagation method and in (c) only the observation prior is considered.
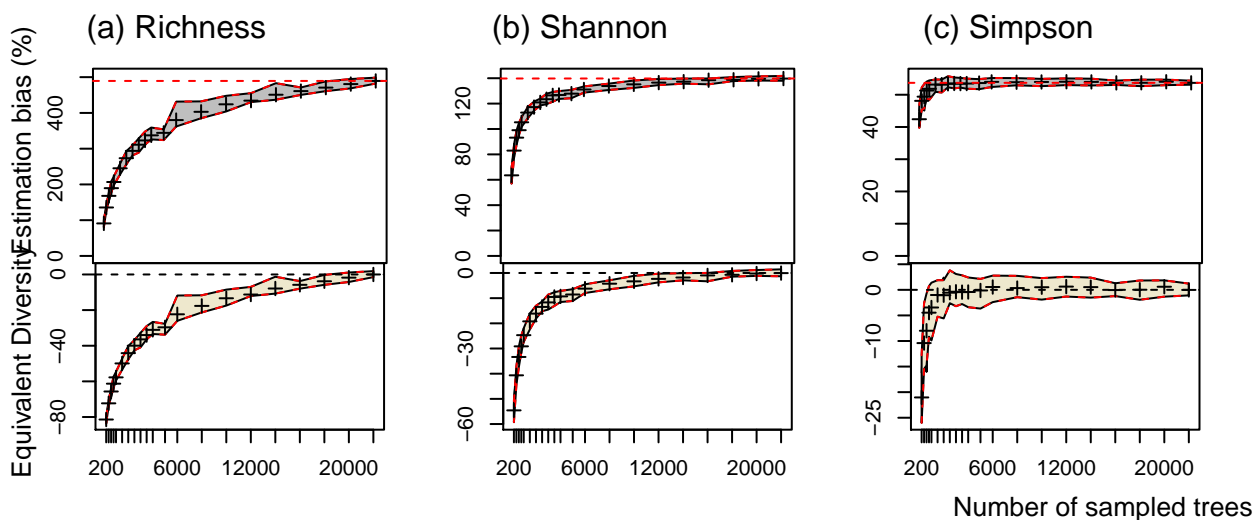
Figure 2. Degradation along a sampling effort gradient of the Richness, Shannon and Simpson diversities estimated for the reference inventory in vernacular names. The propagation method to estimate the diversities is only based on the reference field inventory. Above plots correspond to the estimated diversity in equivalent number of species and below plots correspond to the relative bias of the estimation compared to the value of the reference field inventory. For both dashed lines represent the value of the reference field inventory and crosses and red lines respectively represent the mean, 0.05 and 0.95 quantiles estimated after 1000 iterations.

simulations the abundance of rare species were inflated at the expense abundant ones.

In contrast the use of observed inventories proved more reliable as it accounted for botanical names abundance. The rescourse to taxonomists and pre-inventories proved unavoidable to correctly estimate and therefore manage forest biodiversity.

4.2 Calibration of an optimized inventory protocol

The response of the diversity estimator bias and variability allowed determining the inventory protocol minimizing the determination ratio and sampling effort while maximizing the estimator bias and variability. The real richness proved difficult to assess whatever the sampling and determination effort, as already suggested in previous analysis comparing several inventory methods (Higgins & Ruokolainen, 2004). Still, although the richness estimation remained biased the variation remained low and allowed preserving communities ranking of with similar indetermination ratio (Vellend *et al.*, 2008).

Conversely, the Shannon and Simpson diversity estimations proved less biased, and this key given their power to detect small time and spatial scale diversity variations (Baraloto *et al.*, 2012a; Berry *et al.*, 2008; Cannon, 1998; Plumptre, 1996). From 2 000 pre-inventoried trees the Shannon and Simpson estimators respectively displayed 12% and 1% uncertainty.

5. Conclusion

In this paper we developed a diversity estimator developed in this paper propagating vernacular names' taxonomic uncertainty to the measure tropical forest diversity. It proved reliable to estimate forest diversity for all diversity order and highlighted the inescapable rescourse to taxonomists and minimum real inventories. The response of the estimator bias and variability along a sampling effort gradient allowed optimizing an ideal inventory protocol. With an initial reference botanical inventory of 2 000 trees Shannon and Simpson diversities were estimated within 10% and 1% confidence intervals. The diversity estimator allows integrating the specificity of the working team and local forest structure and is thus adaptable to all specific case.

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