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The role of baseline suitability in assessing the impacts of land-use change on biodiversity

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ABSTRACT

We examined differences in species richness between reference and impacted sites to illustrate the extent to which estimated impacts of land-use change on biodiversity can be affected by the degree of baseline suitability (intactness of reference sites) and the species assemblage under consideration. We mist-netted birds at five continuous Amazonian forest sites and 33 land-bridge forest islands (0.63–1699 ha) within a large hydroelectric reservoir. We then produced a gradient of baseline suitability based on forest area of five sets of reference sites, namely *continuous forest*, *1000 ha*, *500 ha*, *250 ha* and *100 ha*, and contrasted these with all smaller islands combined considering two types of species assemblages. The first comprised only species captured at reference sites (*baseline species assemblage*), whereas the second comprised all species captured at all sites (*overall species assemblage*). We also examined biodiversity complementarity to define the minimum set of forest islands retaining the most number of species occurring both at continuous forest sites and across all sites. A focus on the *baseline species assemblage* from the most suitable baseline (*continuous forest*) resulted in an estimated decrease of 67% in species richness at impacted sites. In contrast, a focus on the *overall species assemblage* along with the use of the least suitable baseline (*100 ha*) as a reference condition reversed this trend, resulting in an estimated increase of 43% in species richness at impacted sites. We therefore underline the imperative of considering the intactness of reference sites to accurately assess the impacts of land-use change on biodiversity and establish conservation strategies.

1. Introduction

The 'shifting baseline syndrome' is a concept introduced by Pauly (1995) to explain how depletion in fisheries resources may be overlooked as a change in people's perceptions of what constitutes a suitable pre-existing baseline to evaluate future changes. Accordingly, fisheries scientists accept the stock size and species composition that occurred at the onset of their careers as a baseline, thereby lowering the baseline suitability generation after generation (Pauly, 1995). Since its conceptualization, several studies on this issue have focused on gathering evidence of divergence between 'perceived changes' and actual 'biological changes' (Papworth et al., 2009), particularly in fisheries science (Baum and Myers, 2004; Jackson et al., 2001; Saenz-Arroyo et al., 2005). However, to our knowledge, there are no focused quantitative assessments providing a diagnostic of the degree to which degraded or downsized habitat baselines can mask the 'true' effects of land-use change on biodiversity.

In environmental impact assessments, reference sites used to which impacted sites are contrasted should reflect the 'true' state of nature prior to disturbance to properly set standards for ecosystem diagnosis and restoration (Gardner et al., 2009) as well as the imposition of environmental penalties. However, shifting baselines (i.e. changing biological conditions induced by past disturbance; Papworth et al., 2009) may obscure the most severe impacts of land-use change on sensitive species as a result of extinction filters (Balmford, 1996) and local proliferation of disturbance-adapted species (Morante-Filho et al., 2015). This means that shifting baselines may lead to a 'new state' in which species are resilient to or favored by disturbance, thereby resulting in systematic downward-biased impact estimates. Therefore, the credibility of environmental impact assessments largely depends on baseline suitability (Gardner et al., 2009; Ritter et al., 2017), which herein is defined as the reliability of reference sites in resembling some pre-disturbance condition. Accordingly, a continuous primary forest covering tens of thousands of hectares would be a suitable baseline for an adjacent fragmented landscape (Sigel et al., 2010).

If one focuses only on the species assemblage from reference sites, land-use change will almost inevitably result in species losses (i.e. decreases in species richness). Alternatively, a focus on the overall species assemblage may not only result in species losses, but also in species

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turnover whereby any loss of species exclusively found at reference sites is either compensated (Ewers et al., 2009) or even surpassed (Humphreys and Kitchener, 1982) by any gain of species restricted to impacted sites (i.e. either no net loss or increase in species richness). Hence, environmental impact assessments relying on overall species assemblages are likely to yield optimistic but misleading outcomes (Lövei et al., 2006), which can misdirect conservation strategies. For instance, the minimum set problem is a commonly used tool to identify the most cost-effective set of sites (i.e. the maximum number of species retained in the fewest number of sites) to concentrate conservation efforts (Howard et al., 1998). Nevertheless, the possible solutions for the minimum set problem are target specific (Howard et al., 2000), implying that a focus on either the species assemblage typical of the baseline or the overall species assemblage may result in different solutions. Importantly, such issues would only be relevant if conservation and restoration programs target protecting either the 'true' state of nature or those returning to pre-disturbance conditions (Wiens and Hobbs, 2015), which will become increasingly daunting to achieve given the rapid development of 'novel ecosystems' induced by human activities (Hobbs et al., 2009).

Here, we used a gradient of baseline suitability and define two types of species assemblages derived from systematic avifaunal surveys carried out in continuous forest (control) sites and forest islands within an anthropogenic archipelago of central Amazonia. We then examined how the degree of baseline suitability and both types of species assemblages affect the estimated impact of forest fragmentation on species richness. Furthermore, we compared the solutions for the minimum set problem targeting either the continuous-forest species assemblage derived from only control sites or the overall species assemblage derived from both control sites and forest islands. In doing so, we provided empirical evidence that environmental impact assessments and conservation strategies can be severely biased by both the suitability of the baseline and the set of focal species under consideration.

2. Methods

2.1. Study area

This study was carried out within the Balbina Hydroelectric Reservoir (hereafter, BHR; 1°40′ S, 59°40′ W; Fig. 1) and adjacent areas of continuous intact forest, located in the State of Amazonas, central Brazilian Amazonia. The BHR spans ca. 300,000 ha and was formed by the damming of the Uatumã River in 1987 (Fearnside, 2016), creating over 3500 forest islands on higher elevation terrain of the once continuous intact forest (Benchimol and Peres, 2015a). To offset the environmental impacts of the Balbina hydroelectric dam, an area of 940,358 ha was set-aside on the left bank of the former Uatumã River to create the Uatumã Biological Reserve (IUCN category Ia), the largest of its category in Brazil. Moreover, the reservoir on the left bank, including all its islands, is also protected.

The vegetation is comprised primarily of submontane dense ombrophilous (*terra firme*) forest, although seasonally flooded *igapó* forest formerly occurred along the margins of the Uatumã River before damming. Forest islands at the BHR range in size from 0.2 to 4878 ha and are surrounded by a non-habitat open-water matrix for terrestrial species, punctuated by dead tree snags rising above the water level (Benchimol and Peres, 2015a). Both island area and associated edge-mediated disturbance shape forest structure: smaller islands are species-poor and dominated by pioneer tree species, whereas larger islands are species-rich and contain a higher dominance of large-seeded canopy tree species (Benchimol and Peres, 2015a). According to the Köppen classification, the climate is equatorial fully humid (Af), with mean annual precipitation and temperature of 2464 mm and 26.5 °C, respectively (Alvares et al., 2013).

2.2. Sampling design

We selected 38 sample sites, five in continuous forest sites (hereafter, control sites) and 33 in forest islands (Table A1) distributed across an area of over 200,000 ha (Fig. 1). Sample sites were spaced apart by an average distance of 31.1 km (SD = 17.1 km, range = 1.1–82.6 km). Sixteen forest islands and four control sites were on the left bank, whereas 17 forest islands and one control site were on the right bank (Fig. 1). Forest area of surveyed islands was calculated in QGIS software (QGIS Development Team 2016) using a classified image (Collection 2, 2015, Amazon) derived from 30-m resolution LANDSAT imagery downloaded from the Brazilian Annual Land Use and Land Cover Mapping Project (available at http://mapbiomas.org). Forest cover was defined as 'dense forest' (pixel value 3), because other pixel values effectively represent either heavily degraded forests or non-forest land cover types. Accordingly, the forest area of surveyed islands ranged from 0.63 to 1699 ha.

2.3. Avian surveys

Fieldwork was carried out over 12 months from July to December 2015 and 2016. At each sample site, we surveyed birds using 16 mist nets (12 × 2.5 m, *Ecotone* 1016/12) set in the understory along a continuous near-linear ca. 200-m net-line whenever possible. In forest islands smaller than 4 ha, we used a cross-shaped net-line design, thereby ensuring the same sampling effort across all 38 sample sites. Herein, each mist-net line corresponds to one sample site. Mist nets were operated from 06:00 to 15:00 h for two days each year, amounting a sampling effort of 576 net-hours per sample site and 21,888 net-hours in total (16 mist nets × 9 h × 2 days × 2 years × 38 sample sites). Since mist nets capture mainly understory birds and occasionally birds that walk on the ground or that fly above net level (Karr 1981), our inferences are drawn from a subset of the avifauna. To avoid double-counting, we ringed birds with coded aluminum rings and subsequently excluded recaptures. Rings were provided by the Brazilian National Center for Bird Conservation and Research (CEMAVE) under research permits SISBIO 49068 and CEMAVE 3984.

2.4. Species assemblages

We defined two types of species assemblages based on the species occurrence across all sample sites (n = 38). The first comprises species captured only at reference sites (hereafter referred to as *baseline species assemblage*, although we also use the term *continuous-forest species assemblage* to refer to the species subset from control sites). The second comprises all species captured in both reference and impacted sites (hereafter, *overall species assemblage*). We used two terminologies to distinguish the data used (1) to examine the baseline issue from those used (2) to solve the minimum set problem. For the first aim, we adopted the term *baseline species assemblage* because it changes as we progressively downsize reference sites. For the second aim, we adopted the term *continuous-forest species assemblage* because it is fixed and only comprises those species that were recorded at control sites.

2.5. Estimated impact of forest fragmentation on species richness

We used five sets of reference sites to represent a gradient of baseline suitability, which was based on insular forest area (Table A2). We assumed that the avifauna in control sites was more intact than that in forest islands and that the avifauna on larger forest islands was more intact than on smaller ones (Aurélio-Silva et al., 2016). Accordingly, the avifauna of each set of reference sites comprises a different baseline, namely *continuous forest*, *1000 ha*, *500 ha*, *250 ha* and *100 ha* (Table A2). The suitability of each baseline was inspected by comparing the number of species retained and gained in relation to the *continuous forest* baseline, so that the suitability of the *continuous forest* baseline was assigned the maximum biodiversity value (Fig. A1).

A previous study at the BHR landscape reported that bird species richness was remarkably reduced in forest islands smaller than 55 ha compared to larger forest islands of up to ca. 1700 ha (Aurélio-Silva

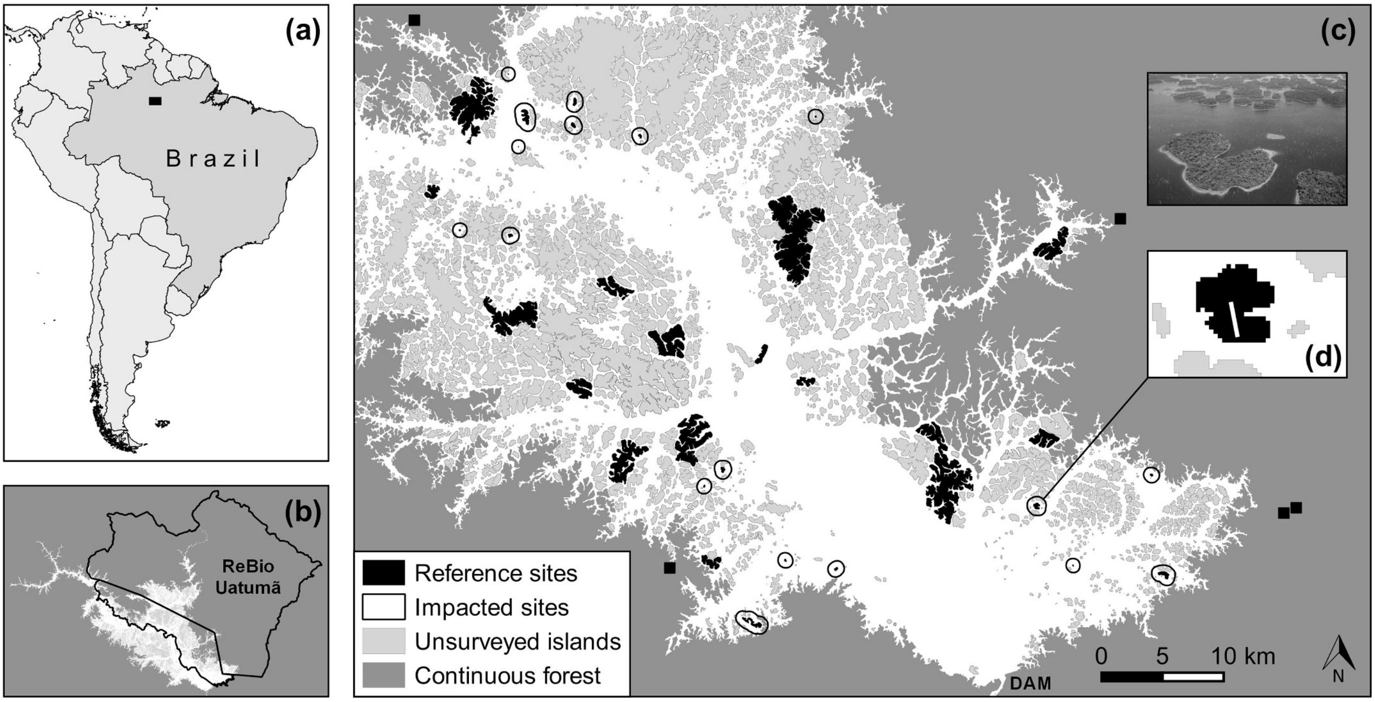

Fig. 1. (a) Location of the study area in central Brazilian Amazonia, indicated by a solid rectangle containing (b) the Balbina Hydroelectric Reservoir (BHR) landscape (water in white, forest in gray), showing the boundaries of the Uatumã Biological Reserve, a strictly-protected area safeguarding most of this landscape; (c) larger inset map showing the spatial distribution of the 38 sample sites within the BHR landscape, including all surveyed islands and continuous forest sites; and (d) detail of an understory mist-net line (white line) used to sample the avifauna. Reference sites correspond to continuous forest sites and forest islands larger than ca. 100 ha, whereas impacted sites correspond to forest islands smaller than 55 ha (Fig. A2 and Table A1). Photo credit: Eduardo M. Venticinque.

et al., 2016). Therefore, surveyed islands smaller than 55 ha (n = 18; Table A1) were regarded as impacted sites due to forest fragmentation – the landscape process involving both forest loss and the breaking apart of forest (Fahrig, 2003).

Having defined the gradient of baseline suitability and the impacted sites, we compared the species richness of all 18 impacted sites combined to that of each of the five baseline levels (Fig. A2) for both the *baseline* and the *overall* species assemblage. To accomplish this, we used the iNEXT package (Hsieh et al., 2016) in R (R Core Team, 2018) to calculate the rarefied number of species based on equal completeness (i.e. sample coverage) instead of equal size (i.e. number of individuals), because species-rich sites require a greater number of individuals to be fully characterized than species-poor sites (Chao and Jost, 2012). Next, we calculated the proportional difference in species richness between the impacted sites combined and each of the five baseline levels to assess to what extent our estimated impacts of forest fragmentation are affected by the degree of baseline suitability and the composition of focal species assemblages. Estimated impact was measured as one minus the proportional difference between impacted and reference sites, so the higher the value, the more severe the estimated impact. Accordingly, if reference sites harbor 10 species and impacted sites 4 species, the estimated impact is 0.6 [1 – (4/10)] or a 60% reduction in species richness.

2.6. Minimum set problem

We used a biodiversity complementarity approach to determine the minimum number of forest islands (i.e. the 'solution' for the minimum set problem) that retained the maximum combined number of species (Howard et al., 1998) for both the *continuous-forest* and the *overall* species assemblage captured across the entire set of 33 surveyed islands. To do so, we used an algorithm that first selects the forest island containing the highest number of species and then sequentially selects the forest islands that add the highest number of previously unrepresented species (Howard et al., 1998). In the event of a tie, the more species-rich island was selected, and if that tie persisted we selected the largest island. This procedure was repeated until all species captured in the entire set of 33 forest islands were represented by at least one individual. We then quantified the differences between the solutions for the minimum set problem targeting both the *continuous-forest* and the *overall* species assemblage.

3. Results

Considering all 38 sample sites, we captured a total of 2115 birds representing 130 species, 103 genera, and 38 families. At the five continuous forest control sites, we captured 614 birds representing 86 species, 71 genera and 30 families; the number of individuals per control site ranged from 75 to 165 (mean [SD] = 122.8 [37.9]), and the number of species from 28 to 54 (42.8 [10.5]; Table A1). At the 33 forest islands, we captured 1501 birds representing 109 species, 90 genera and 35 families; the number of individuals per forest island ranged from 5 to 121 (45.5 [28.3]), and the number of species from 3 to 43 (16.1 [9.7]; Table A1).

3.1. Estimated impact of forest fragmentation on species richness

The estimated impact of forest fragmentation on species richness, measured as the contrast between reference and impacted sites, was affected by both the degree of baseline suitability and the species assemblage under consideration (Fig. 2). Accordingly, the estimated impact was gradually reduced as a function of decreasing baseline suitability. Yet forest fragmentation significantly depressed the species richness of the *baseline species assemblage*, regardless of the degree of baseline suitability (Fig. 2; Table 1). In contrast, a focus on the *overall species assemblage* revealed a negative effect of forest fragmentation only when the most suitable baseline (*continuous forest*) was used as the reference condition (Fig. 2; Table 1). Furthermore, the *overall* species

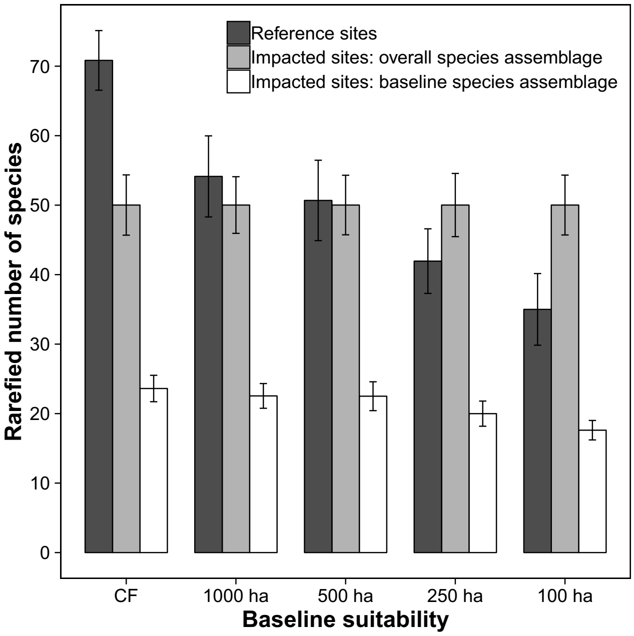

Fig. 2. Comparisons between the rarefied number of understory bird species at reference and impacted sites across a gradient of baseline suitability for two types of species assemblages. The bar plot shows the contrast between reference and impacted sites from the most (CF – continuous forest) to the least suitable baseline (100-ha forest islands), thereby affecting the estimated impact of forest fragmentation on species richness of both types of species assemblages. Rarefied number of species were standardized by sample coverage (0.927). Error bars indicate the 95% confidence intervals.

Table 1
Estimated impact of forest fragmentation on understory bird species richness measured for five reference sites (Fig. A2), representing a gradient of baseline suitability from the most (continuous forest) to the least suitable (100-ha forest islands). The significance of differences in species richness between reference and impacted sites was determined by comparing rarefaction curves and their associated 95% confidence intervals. Differences were considered significant whenever the 95% confidence intervals did not overlap. Asterisks (*) denote a significant difference in species richness between reference and impacted sites. Higher values indicate more severe impacts of forest fragmentation on species richness (see Fig. 2).

Reference sites	Species assemblage	
	Baseline	Overall
Continuous forest	0.67*	0.29*
1000 ha	0.58*	0.08
500 ha	0.56*	0.01
250 ha	0.52*	−0.19
100 ha	0.50*	−0.43*

richness at impacted sites was significantly higher than that at the least suitable baseline (*100 ha*; Fig. 2; Table 1), which could be interpreted as a positive effect of forest fragmentation on species richness. Note that the terms ‘positive’ and ‘negative’ are used here to describe relationships between variables, and *not* to assign whether effects are either ‘good’ or ‘bad’ to meet conservation goals.

3.2. Minimum set problem

Considering the *continuous-forest species assemblage*, the solution for the minimum set problem included 12 forest islands (36.4% of 33 islands; 69.7% of the aggregate area), which harbored 65 out of 86 species (75.6%; Fig. 3a). Considering the *overall species assemblage*, the solution for the minimum set problem included 21 forest islands (63.6% of 33 islands; 72.0% of the aggregate area), which included 109 out of 130 species (83.8%; Fig. 3b). Thus, a focus on the *continuous-forest species assemblage* would reduce conservation investments in terms of the number of forest islands to be protected from 21 to 12, and also in terms of the aggregate area. Nevertheless, even the entire set of 33 forest islands surveyed failed to include 21 species that were only represented at continuous forest sites.

4. Discussion

Biodiversity comparisons between reference and impacted sites are likely to be severely biased if reference sites are significantly degraded or reduced in extent, rather than represented by a relatively suitable baseline of continuous primary habitat. As a result, shifting baselines reduce the contrast between reference and impacted sites, leading to unduly optimistic diagnostics of the magnitude of impacts as we have shown here (Fig. 2). For instance, the amphibian species richness of a ca. 250-ha forest reserve in a southern Costa Rican landscape was not significantly different from that of either countryside forest elements (e.g. small forest fragments, live fences, hedgerows, riparian strips) or crop fields and pastures (Mendenhall et al., 2016). In contrast, the amphibian species richness of primary forest sites larger than 1 Mha (i.e. suitable baseline) in northeastern Brazilian Amazonia was higher than that in either secondary forests or eucalypt plantations retaining a native understory (Barlow et al., 2007). Apart from the role of suitable baselines to properly assess the scale of impacts, the authors of two meta-analyses have either considered sites larger than 100 ha as ‘minimally altered forests’ (Mendenhall et al., 2016) or have not defined their minimum size (Mendenhall et al., 2014). Nonetheless, forest intactness (i.e. baseline suitability) depends not only on levels of habitat disturbance (Barlow et al., 2016), but also on its overall spatial extent (Potapov et al., 2017), since protected areas larger than 1 Mha are required to support full complements of species (Thiollay, 2002, 1989) and landscape-scale ecological processes in tropical forests (Laurance, 2005; Peres, 2005).

A remarkable example of a terrestrial shifting baseline is the La Selva Biological Station (ca. 1600 ha), an intensively studied tropical forest reserve in Costa Rica. Decades of research have revealed that both the richness and abundance of habitat-sensitive species are expected to decline, whereas those of disturbance-adapted species are expected to increase, thereby resulting in a shift in community structure (i.e. changes in species composition and population sizes) with some relict species populations. At La Selva, such shifts in community structure have been attributed to forest shrinkage and isolation induced by surrounding land-use change (dung beetles, Escobar et al., 2008; birds, Sigel et al., 2006), and climate-driven reduction in microhabitat resources (amphibians and reptiles, Whitfield et al., 2007). Therefore, some authors have cautioned against the use of La Selva as an ‘intact’ tropical forest baseline for neighboring modified habitats, given its declining biodiversity conservation value over 35–40 years (Escobar et al., 2008; Sigel et al., 2006).

We caution against the naïve use of the ‘best’ locally available reference sites whenever those are not representative of a suitable baseline (Cardinale et al., 2018). This claim is supported by our results, which provide the first quantitative evidence that the estimated impact of forest fragmentation on species richness is gradually reduced from the most to the least suitable baseline (Fig. 2; Table 1). We also emphasize the need to describe in future studies the size and the level of structural and/or compositional habitat disturbance of reference sites. For example, Hannah et al. (2007) found no differences in bird species richness and composition between fragments (<300 ha) and reference sites (2500–40,000 ha) of eucalypt woodlands in Australia. However, these authors acknowledged that almost their entire study area had been subjected to about 150 years of habitat disturbance primarily associated with pastoralism, and that the species assemblage they sampled likely represented a relatively resilient subset of the once

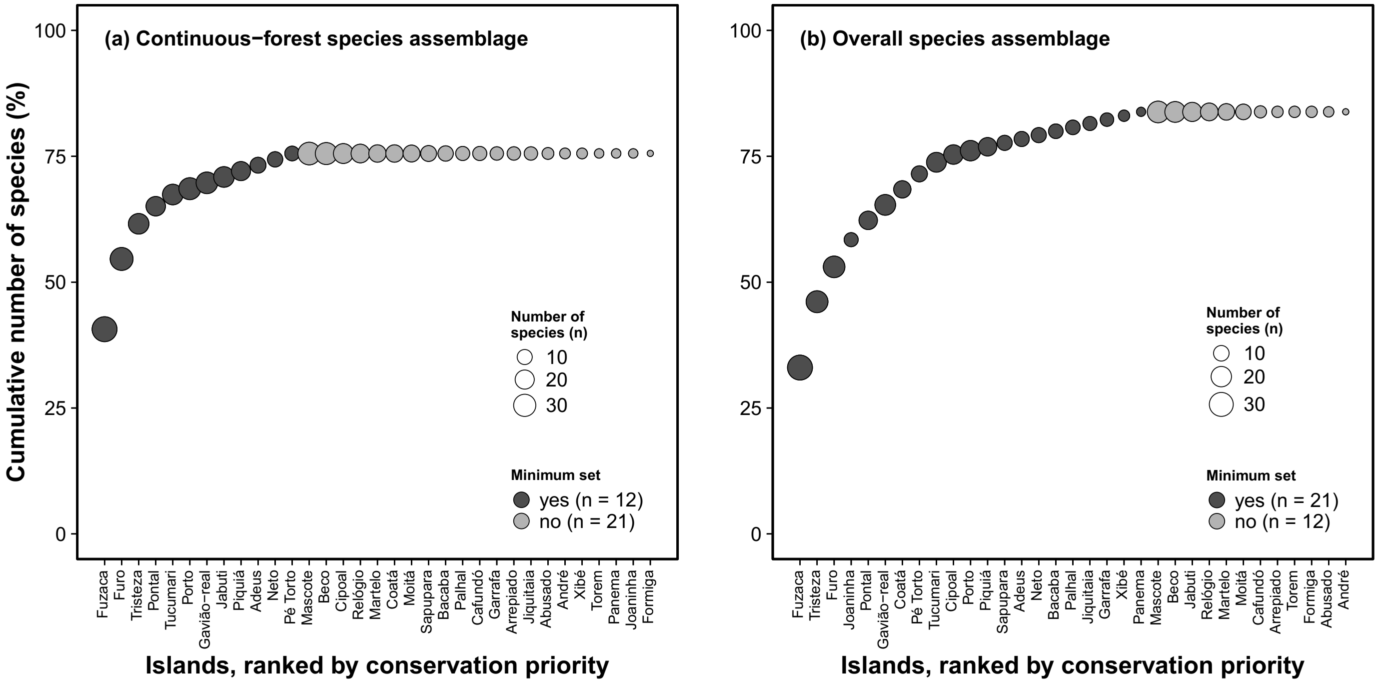

Fig. 3. Cumulative number of understory bird species occurring on forest islands considering both the (a) *continuous-forest* and the (b) *overall* species assemblage. Forest islands are ranked from those adding the largest to the smallest number of unrepresented species in the entire metacommunity. Dark gray circles represent forest islands included within the solution of the minimum set problem: a set of forest islands whose avifauna complement each other and collectively capture the largest number of species within the fewest number of forest islands. Light gray circles represent forest islands that fail to add new species to the metacommunity.

'intact' species assemblage. In other words, environmental impact assessments should be explicitly interpreted by considering the condition of the baseline.

Another potential source of bias in environmental impact assessments is the proximity of reference from impacted sites, wherever spillover effects occur (Gilroy et al., 2014). This exchange of species between reference and impacted sites could substantially reduce their divergence in community structure (Hatfield et al., 2019), thereby affecting impact estimates. However, spillover effects are particularly evident soon after forest fragmentation (e.g. first six months; Bierregaard, Jr and Lovejoy, 1989) and facilitated by more permeable matrix habitats (e.g. coffee plantations in contrast with castle pastures; Boesing et al., 2017). Given that we surveyed land-bridge islands ca. 30 years post-isolation, and the surrounding matrix is a vast body of open water, we believe that spillover effects for the vast fraction of forest vertebrates are at best minimal (see Benchimol and Peres, 2015b; Palmeirim et al., 2018).

Given the pace of habitat loss and degradation across the globe, most remaining suitable reference sites will likely become shifting baselines (Watson et al., 2018), ultimately preventing realistic assessments of the impacts of land-use change on biodiversity. As previously pointed out, "what we need are datasets that have clear baselines that tell us what expected values of biodiversity are" (Cardinale et al., 2018). We therefore urge prioritizing biodiversity surveys in the last remaining undisturbed areas of any biome to establish solid baselines prior to anthropogenic disturbance (Bobrowiec and Tavares, 2017; Ritter et al., 2017), especially in the tropics where an unknown but vast number of undescribed species exist, and large forest tracts still remain intact (Watson et al., 2018). However, wherever suitable baselines are unavailable or located far away from impacted sites, baseline species assemblages can be coarsely inferred using data from natural history collections (Lister, 2011); both formal and gray literature, and species databases (e.g. Bogoni et al., 2018); species distribution range maps, interviews with local people, and expert information (e.g. Canale et al., 2012). Alternatively, we recommend environmental impacts to be estimated from species groups of high conservation concern (e.g. habitat specialists, sensitive to disturbance, threatened with extinction).

We considered only species captured at reference sites (i.e. *baseline species assemblage*) to calculate the number of species that was retained at impacted sites (hereafter referred to as *number of species retained*) as a response variable. This avoids the non-trivial task of assigning species specificity to different habitat types and the nuisance of including disturbance-adapted species that often proliferates at impacted sites. The *number of species retained* is still a measure of species richness, with several advantages: it is simple to collect, intuitive to interpret, and easy to compare across studies (Banks-Leite et al., 2012). To some extent, this measure also accounts for community composition and allows the sampling effort to be statistically controlled for in comparative studies. In particular, we showed a significant difference between reference and impacted sites if the *number of species retained* is used as a biodiversity measure, regardless of the baseline condition (e.g. continuous forest and larger islands). In contrast, by focusing on the *overall species assemblage*, the negative effect of forest fragmentation on species richness was only apparent if continuous forest sites were used as the baseline (Fig. 2). A combination of shifting baselines and the inclusion of disturbance-adapted species from impacted sites can lead to a higher perceived conservation value for impacted sites than for reference sites, if species richness is used as a biodiversity measure (Fig. 2). For example, Blake and Loiselle (2001) found an overall higher number of understory bird species (including disturbance-adapted species) in young second-growth at La Selva Biological Station, northern Costa Rica, compared to neighboring old-growth forest. We reanalysed their data using the *number of species retained* as the response variable to compare young second-growth, old second-growth and old-growth forests at La Selva. In doing so, we found that old-growth forest retained the highest number of species compared to either age classes of second-growth forest patches (Fig. A3). Essentially, the *number of species retained* is a measure of species richness lost from reference sites, which by definition holds the maximum biodiversity value. Therefore, we believe the *number of species retained* is a reliable and straightforward biodiversity measure to quantify the conservation value of human-modified habitat patches in anthropogenic landscapes (Fig. 6 in Gardner et al., 2009), even when reference sites that could be deemed as intact are simply unavailable.

A cost-effective virtue of focusing on the *continuous-forest species assemblage* is that it reduces the conservation effort that could be allocated to highly complementary priority sites – here represented by the minimum number of forest islands that could be protected to maximize the number of species retained across the entire landscape – compared to the number of target sites prioritized based on the *overall species assemblage*. This can be simply explained by the fact that the former (*continuous-forest*) species assemblage is a subset of the latter (*overall*). Furthermore, solutions for the minimum set problem depend on the target species group (Howard et al., 2000). For example, our smallest surveyed island (Joaninha, 0.63 ha) was ranked as the fourth most important in the minimum set selection based on the *overall species assemblage*, but it was not included in the minimum set based on the *continuous-forest species assemblage* (Fig. 3), essentially because this island failed to retain any species assigned to 'high' forest dependency (sensu BirdLife International, 2018). In other words, the number, identity and conservation priority of the forest islands included in solution of the minimum set problem were all affected by which species assemblage was targeted. However, we underline that even a fragmented forest area larger than 7800 ha (the total area of all 33 surveyed islands) failed to sustain the entire avifauna recorded at our continuous forest sites, reinforcing the notion that there is no substitute for large areas of unbroken primary forest to safeguard primary forest biodiversity (Gibson et al., 2011; Meyer et al., 2015). Notwithstanding, these outcomes support our claim that a focus on species assemblages derived from reference sites provides the best possible impact assessment approach in examining the effects of land-use change on biodiversity, while also establishing conservation strategies to compensate for those impacts.

5. Conclusions

The magnitude of the impacts of land-use change on biodiversity is measured as the extent to which impacted sites deviates from an assumed reference condition (i.e. baseline), with greater deviations leading to higher impact diagnostics. The suitability of the baseline is therefore likely to affect the estimated magnitude of the impacts, thereby resulting in realistic assessments whenever the baseline is suitable, but unduly optimistic assessments whenever the baseline was historically degraded. However, genuine optimistic assessments based on suitable baselines may arise if impacted sites are embedded in biodiversity-friendly landscapes (e.g. primary forest fragments surrounded by old-growth secondary forest; Stouffer et al., 2011) and/or the focal species assemblage is not sensitive to the impact being assessed (e.g. temperate birds are less likely to be negatively affected by forest fragmentation than tropical birds; Lindell et al., 2007).

Although the issue on shifting baselines has already been raised (Gardner et al., 2009), here we provide quantitative evidence on the pivotal role of suitable baselines in deriving reliable assessments of the impacts of land-use change on biodiversity. Accordingly, defining even well-preserved forest islands as large as 1000 ha as a reference condition significantly reduced impact estimates compared to baselines consisting of undisturbed continuous forest. Since suitable baselines are no longer available in most regions worldwide, we emphasize the need to consider the size and level of habitat disturbance of comparable reference sites to interpret the outcomes of environmental impact assessments (Hannah et al., 2007; Ritter et al., 2017). We also showed that a focus on species assemblages derived from reference sites alone, rather than the overall species assemblage, has two consequences. First, there was a negative effect of forest fragmentation on species richness even when we defined the most degraded reference sites (100-ha forest islands) as the comparative baseline. Second, allocation of conservation investments could be considerably reduced if one targets only those species that presumably occupied any given site prior to habitat disturbance, which are likely those of higher conservation concern. We therefore conclude that environmental impact assessments should focus on species assemblages derived from suitable baselines if they are to be reliable.

CRediT authorship contribution statement

Anderson Saldanha Bueno: Conceptualization, Methodology, Formal analysis, Investigation, Writing - original draft, Visualization, Project administration, Funding acquisition. **Carlos A. Peres:** Conceptualization, Methodology, Writing - review & editing, Supervision, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

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