



**Counting niches: Abundance-by-trait patterns reveal niche partitioning in a Neotropical forest**

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	Neotropical woody plants into shrubs, understory, midstory, and canopy layers.

Response to reviewers

12-Jul-2019

Dear Dr. D'Andrea:

Thank you very much for submitting your manuscript "Counting niches: Abundance-by-trait patterns reveal niche partitioning in a Neotropical forest" ECY19-0381 to Ecology. The reviewers and I appreciate the work you have accomplished. We are willing to consider a revised version for publication in the journal, assuming that you are able to modify the manuscript according to the recommendations.

...

Sincerely,

Prof. María Uriarte  
Subject Matter Editor, Ecology  
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**Thank you to the editor and reviewers for their positive responses to our work, and for their constructive comments. We have addressed all of their major concerns, and believe it has resulted in an even stronger manuscript. We now provide a more nuanced discussion of our results, a more thorough discussion of their implications, and potential caveats to our interpretations.**

**Our responses follow below the respective comments, in bold.**

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Reviewer: 1  
Comments to the Author

The article by D'Andrea et al investigates potential for niche structuring of tropical forests, as revealed by clustering of abundance-weighted trait distributions across species. The paper combines measures of size and abundance, taken from long term plot surveys, with trait data for four prominent physiological traits, and new methods for detecting clustering of species along the trait spectrum. The results suggest clustering is present in two of the four traits investigated: maximum height and wood density, but not seed mass or leaf mass per area. For both of the clustered traits, the statistical methods suggest 4-5 clusters; a number which corresponds with traditional groupings of species by experienced botanists into four height types. The existence of clusters is significant also, as earlier theory suggested over dispersion of trait values would be the a signature of niche differentiation. By contrast, more recent theory

Automatic Cluster Choice.

argues in favour of clustering. The authors therefore claim these results provide evidence of niche partitioning in these forests.

I like many aspects of this paper. It is clearly and concisely written, and tests recent developments in theory of niche differentiation at BCI - a location that has been pre-eminent in the debates around forces structuring forests. Notably, BCI has provided some of the strongest evidence for both neutral and niche theories. Building from a theoretical framework that partly integrates these perspectives, the current paper tests an important prediction of the new theory.

**Thank you for these positive comments.**

I have some concerns around the interpretation of the results, particularly of the presence or not of clusters. The authors claim that existence of clusters suggests “that competition for light structures community composition” (In 27 & later). My concerns are two fold. First, can we or should we take clustering as evidence for or against niche partitioning? Is the evidence here stronger than that in the previous theory, where trait over dispersion was the signature of niche differentiation? Other theoretical models (e.g. Leimar et al 2013 (<http://dx.doi.org/10.1016/j.jtbi.2013.08.005>)) show how niche differentiation can lead to a continuous distribution of traits, given a competition kernel with the right shape.

*Presence of greater variability than expected.*

**This is an important question. As the reviewer points out, classical literature predicts that niche partitioning will lead to trait overdispersion, whereas here we interpret trait clusters rather than overdispersion as evidence of niche partitioning. Our work follows up on recent literature drawing attention to the fact that the same models that predict overdispersion in stable equilibrium will predict clusters as transients (e.g. Scheffer and van Nes 2006, D’Andrea et al 2019). Following the initial findings by Scheffer and van Nes, some of us and others have shown that several ecological forces can maintain the clusters indefinitely as a stationary state. Those forces include immigration (D’Andrea et al 2019), appearance of new species through mutation (D’Andrea & Ostling 2016), periodic environments (Sakavara et al 2018), and “hidden niches” (i.e. independent niche axes providing extra intraspecific regulation, Scheffer and van Nes 2006, Barabas et al 2013). The 50-ha plot on Barro Colorado Island is very likely under the influence of one or several of these forces, such as immigration and other niche axes. Based on this theoretical literature, we therefore interpret clusters on BCI as a more general signature of niche differentiation than the stricter circumstances under which one might predict overdispersion. We added text in the Introduction to make clearer the state of theory regarding clusters versus overdispersion (lines 65-75).**

As the reviewer notes, other literature has indicated that kernels of the right shape may allow for coexistence of a trait continuum (Leimar et al 2013). Specifically, the kernel must have a strictly positive Fourier transform, which is not a general property of competition based on trait differences. (For example, in the family of exponential kernels, only those with exponent

$\leq 2$  will satisfy the condition, and small perturbations of these kernels will break the property and lead to cluster formation.) However, in the absence of empirical evidence that the competition kernels on BCI possess those special properties, we believe a more general expectation is for cluster formation rather than a continuum of traits. We now bring this up on lines 218-226.

Also, clustering was only present for two of the traits only - does that mean the other two traits are not involved in niche partitioning? Previous work at this site has provided reasonable evidence that seed mass (less so LMA) influences population dynamics.

Thank you for raising this valuable point, which we now emphasize in our manuscript (lines 275-287). The absence of clustering in LMA and seed mass does not preclude a role for these traits in niche partitioning on BCI. In D'Andrea et al 2018, we show that a loose connection between trait value and niche strategy can mask clustering along the relevant niche axis. Seed mass is linked to dispersal and recruitment ability (Muller-Landau et al 2008) and may reflect a species' position on a niche axis based on a competition-colonization tradeoff, and is therefore a candidate for clustering -- hence its inclusion in our study. However, seed mass alone may be a poor predictor of a species' strategy along this niche axis, due, for example, to the effects of other traits such as drought tolerance and dispersal mode. LMA is theoretically connected to niche strategies (Wright et al. 2010), but there is substantial ontogenetic variation in its predictive ability of growth, with the relationship being stronger in the seedling stage. Eventually, other aspects of physiology become limiting as the plant grows. Hence, LMA may be a noisy predictor of the niche strategy (Wright et al. 2010). We conclude that the lack of clustering in these traits may be due to their loose connection to niche strategies rather than no involvement in niche partitioning.

My other concern is about the method of cluster analysis. To detect significant clustering, the method uses abundance and compares to null communities where abundance's are shuffled across species. But the authors do not report if traits on their own show any evidence of clustering, without considering abundances. If so, how does this impact significance testing? If traits are significantly clustered on their own, I would consider this strong evidence favouring your general hypothesis. Yet, the effect may not appear significant using the methods applied, as the null communities also include this effect.

→ Physicality of traits.

An analysis based on species trait values alone, independent from their local abundances, would require a different null model than the one we currently use in the paper. Whereas our null model randomly shuffles species abundances among the observed trait values at BCI, a null model that ignores species abundances would likely rely on random selections of species drawn from the regional pool. However, trait data for all species in the regional pool, most of which are rare, are not available, making this approach infeasible at this time. Another type of null model focused solely on species trait values could be to randomly choose trait values from the observed ranges.

**However, non-random patterns compared to this null would more likely be the result of an evolutionary process (D'Andrea and Ostling 2016) rather than niche differentiation during community assembly. Preliminary results using a small number of starting points for the k-means analysis suggest the trait values are not significantly clustered compared with this null. Due to the difficulties in generating these alternative null model communities and/or their associated issues of interpretation we did not pursue these analyses further.**

It would also be good to explain further why wood density shows significant clustering but LMA and seed mass do not, as visually, I cannot see the patterns are that different.

**One of the strengths of our statistically-grounded method is that it detects patterns even when they are not visually obvious, and it tells us when we are “seeing” patterns that actually do not exist.**

While the discussion was admirably brief, I feel there was a missed opportunity, particularly given the background knowledge available for this study site. One of my favourite papers on the topic of clusters is Barabas et al 2013 “Emergent neutrality or hidden niches?”, on which D'Andrea & Ostling are co-authors. That article points out that Scheffer & Nes 2006's model, which kicked off the current theory lineage on clustering of traits, involved a strong assumption required to induce the observed clustering. That is it requires differentiation along an additional niche axis. One possible source for such differentiation is in the interaction with pathogens and herbivores. BCI has a long history of research in this area, and it would be a shame not to consider this in relation to the assumptions of the model.

**Thank you for this insightful question and suggestion. As the reviewer notes, Barabas et al 2013 pointed out that additional niche axes, such as investment in defense against herbivores and pathogens, are required to generate permanent clusters in a closed community subject to no temporal variation in the environment. As the reviewer points out, defense is a well-known important niche axis in tropical forests, and as such is likely to contribute to clusters along the trait axes we report in our study, along with immigration (in fact, we believe it likely that our species also cluster by traits related to defense, and are planning a follow-up study along those lines). We now emphasize this point in our revised Discussion (lines 241-253).**

It is also essential to discuss the results further in relation to successional dynamics. Height appears as a clustered trait, but surely there is a big difference between a shade tolerant shrub and a short early successional pioneer?

**Thank you for this insightful comment. The cluster of species at the low end of the max-height trait axis on BCI may indeed comprise a mix of shade-tolerant shrubs and short, early-successional pioneers. These species may have similar light acquisition strategies (the niche axis represented by maximum height) but be niche-differentiated in terms of**

**their successional strategy, which is a niche axis that would be better reflected on other traits such as wood density rather than maximum height.**

**To reiterate the point above, the four maximum height strategies reflect coexistence that could happen without disturbance and successional dynamics, perhaps due to a tradeoff between investment in light acquisition versus investment in recruitment (Kohyama 1993). On the other hand, the coexistence between species with similar height strategies (i.e. those within the same height cluster) requires differentiation along additional niche axes, such as successional dynamics -- which would be reflected in the distribution of wood density values and/or other traits related to successional strategy. We now make this point in the revised Discussion (lines 241-253).**

Minor issues

Method of clustering identifies clusters that “maximizes the difference between within-cluster trait dispersion in the observed and null communities.” (ln 130). This is not straight forward to visualise, hence i recommend a figure to illustrate the concept.

**What we mean by this language is that for a given number of clusters, we first (i) run the k-means algorithm to find the best assignment of species to clusters on BCI, which is the assignment that minimizes the average distance between species in each cluster; then (ii) repeat this procedure on each of a set of null communities, and take the difference between the BCI value and the mean value of the null communities. This difference we call the gap index for this number of clusters; (iii) we calculate the gap index for a range of numbers of clusters, and select the one that gives us the biggest value. That biggest value is the gap statistic, and the number of clusters that gives us that maximum is the estimate for the number of clusters on BCI.**

**This metric is explained in further detail in D’Andrea, Riolo & Ostling PLOS Comp Bio 2019. Fig 1 in S1 Box in the supporting information of that paper illustrates the concept.**

Are the clusters necessarily equally spaced? In Fig2a, for height, it is clear there is a strong break around 27m, but below this height the distribution looks more even than clustered. In other words, two clusters: one for talon trees, then the rest.

**There is no theoretical reason why the clusters should necessarily be equally spaced, nor is this a requirement for our detection of clustering using our statistic (we now note this on lines 154-155). Small between-species differences at one section of the trait axis may be ecologically similar to large between-species differences at another section of the trait axis. Thus, we do not necessarily expect even distribution of clusters.**

**As for the possibility of there being only two clusters in maximum height, our statistical test reveals that the biggest difference in “clusteredness” (formally, the total abundance-**



weighted within-cluster dispersion) between the BCI community and a set of null communities occurs for four clusters. This means that upon testing for different numbers of clusters, four is the number that gives the strongest signal relative to null expectations. However, this finding does not rule out the possibility of layered height structure, with a larger split into tall trees and the rest subsuming substructure made up of three clusters in the bulk. That said, we think the best approach is to defer to the statistical results provided by our test, rather than visual intuition.

Ln 72 - for what taxa?

Our methodology for detecting clusters developed in D'Andrea, Riolo, & Ostling (2019) is not taxon-specific. The method is shown to detect clusters that arise in a variety of "stochastic niche models", i.e. models that include niche differentiation along with stochastic birth, death, and immigration. This includes the MacArthur-Levins (1967) niche axis model, which is not mechanistic, as well as mechanistic models where niche differentiation is specifically deriving from differences in use of resources (whose dynamics are included in the model), differences in habitat use, and differences along a competition-colonization tradeoff. These mechanisms could be at work for a wide variety of taxa and our models are not constructed in a taxon-specific manner. We considered them in order to demonstrate that niche differentiation produces clustering independently from the details of the dynamics of competitive interactions.

We did not make changes to the text of our manuscript regarding this point as it takes too much space to give a detailed sense of the models used to validate the metric in our other paper, and the reader can refer to it for them.

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Reviewer: 2

Comments to the Author

Dear editor and authors,

D'Andrea et al. assess to what extent the distribution of traits show multiple clusters (i.e. different optimum values) across tropical tree species in BCI. They show that maximum tree height clusters around four optima, wood density around five optima, and leaf mass area and seed mass show no clusters. At the regional scale, only maximum height shows clusters, although much less clearly than for BCI alone.

This is an interesting and well-written manuscript. Nevertheless, some aspects are unclear, and other aspects are rather poorly explained. This limits the ability to see these results in a more general context, rather than a specific site study. Below I provide some suggestions for improvement.



**Thank you for the positive comments about our manuscript. We agree that our manuscript could benefit from additional discussion of the broader implications of our results, and we include several points in the new version of our manuscript (see below).**

- The authors mention that it is unknown whether clustering by size occurs in tropical forests (L65-66), but this seems not true: we know that there are different strata in tropical forests, and the authors themselves provide some of the relevant references for this (e.g. L160-161).

**It is true that conventional descriptions of tropical forest structure have long included references to different strata (sub-canopy, canopy, etc.), but to our knowledge there has never been any quantitative empirical support for their existence. Indeed, we were surprised and excited to see that the number of clusters based on tree maximum height conformed to these conventional descriptions, and we think this actually makes our study more compelling. We now highlight this on lines 208-210.**

- It is unclear to me why only reproductive individuals were included. Their hypotheses underlying the formation of trait clusters should hold for all established individuals, not only for the reproductive individuals. Perhaps the formation of clusters becomes stronger during ontogeny (species with non-optimal traits eventually drop out), which would by itself be interesting to test, and may strengthen the authors' conclusions.

**Current models predicting clusters do not include age structure and essentially only track reproductive individuals. Therefore, their predictions pertain to adults. If it could be assumed that the number of non-reproductive individuals is proportional to the number of adults, then our census restriction is indeed unnecessary. However, this is probably too strong an assumption for trees on BCI. Further work should confirm that age-structured models predict clusters for all individuals.**

**We did not add further analysis with non-reproductive individuals to our manuscript because these analyses are computationally demanding and would have taken us longer than the allowed time frame for revision. We see this as an important question to explore in future work.**

- At regional scales, only one peak for maximum height is found, and the authors say that this may "arise through physiological constraints against extreme height". This, however, does not explain why there would be no clusters at smaller maximum height.

**The reviewer is correct that constraints against extreme height do not explain why there would be no clusters at smaller maximum height. In fact, while our statistic identifies a single cluster, it also reveals four clusters subsumed within this larger cluster (see lines 190-193 and caption to Table 1).**

**The single regional peak reflects a unimodal abundance trend along the maximum height axis, with trees in the second height cluster being consistently the most abundant in**

Definition  
of  
Cluster!

**their communities. This abundance trend may result from an interplay of higher light incidence at larger heights and the potential for a larger number of smaller-sized trees in a given area. We now point this out on lines 193-198.**

- The results for height are intuitive and agree with the canopy strata that we are familiar with. However, the results for wood density are not clear and not well explained. Why would there be clusters around .35, .5, .58, .65 and .8? What is so special with these values that species tend to cluster around them? Also, why is this not visible at regional scale? Does that mean that immigration might be weaker (and therefore clusters more apparent) in BCI compared to all other plots? And if so, then perhaps we would not expect strong clusters in larger continuous stretches of forest? It would be good if the authors could elaborate on this.

**Thanks for bringing this up. The positions of the clusters generally have many causes: the available pool of traits, external filtering from the environment, resource availability, and the shape of the competition kernel (the function specifying how species compete given their trait values). In the case of maximum height, it is possible that the optimal heights are determined by the distribution of light below the canopy (the sunfleck model, lines 228-232). In the case of wood density, given its connection to the successional niche, the distribution of light gaps in the forest may possibly determine the positions of the niches. The number of clusters may also be influenced by the rate at which competition drops between species of disparate wood density: the faster the drop, the more niches are allowed. We now mention this in the Discussion (lines 260-264).**

**As for the regional pool, we hypothesize that differences in environmental or ecological conditions across the region may have led to different trait optima (cluster centroid values) in different communities, which led to the erosion of cluster structure when these communities are combined (lines 199-202).**

- No explanation is given as to why no clustering is found for leaf mass area and seed mass. It is important to understand not only the 'significant' results, but especially also the non-significant ones. What does this mean?

**We hope our response to a similar question raised by the other reviewer (page 3 of this letter, lines 275-287 on the manuscript) satisfactorily answers this question.**

A few minor comments:

- L44-45: this sentence is unclear. It seems to me that you have just specified testable predictions?

**By this phrase we meant the lack of model-validated quantitative predictions for trait-based impacts of niche-based competition beyond intuitive ideas of greater-than-chance trait differences. We rephrased for clarity (lines 44-45).**

- L52-53: it is not clear why a potential invader will have higher fitness when it is similar to one of the residents.

**This is borne out of the calculation of the total competition faced by the invader from both residents. Essentially, the increase in competition with the closer resident is more than compensated by an even stronger decrease in competition with the other resident. We now mention this on lines 54-55.**

- L107: usually height (also maximum height) is a highly skewed variable that would be good to log-transform.

**In our study we use maximum potential species height, not individual height. We tested all traits for a skewed distribution and found that only LMA and seed mass were significantly skewed, hence our choice to log-transform these two traits but not maximum height or wood density.**

- L118: what happened with the other two plots?

**In the remaining two plots, all individuals with maximum DBH > 10cm were censused in the entire plot. We now mention this on lines 135-136.**

- L173: may  $K=1$  not just refer to environmental filtering?

**In the case of height, our intuition is that the environment would not filter for one single intermediate height. One would expect filtering for the maximum biologically possible height, or according to the sunfleck model, for different height layers where the incidence of light has local maxima. Our most likely explanation for the presence of a single large cluster in the regional pool is an interplay of higher light incidence at larger heights and the potential for a larger number of smaller-sized trees in a given area (lines 196-198).**

**Counting niches: Abundance-by-trait patterns reveal niche partitioning in a Neotropical forest**

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**Author contributions.** RD and AO conceptualized the study; SJW and RC provided the data; RD, JG, HF, and AO analyzed the data; RD and JG wrote the manuscript; RD, JG, and AO contributed to revisions of the manuscript. RD and JG contributed equally to the execution of this manuscript.

## Abstract

Tropical forests challenge us to understand biodiversity, as numerous seemingly similar species persist on only a handful of shared resources. Recent ecological theory posits that biodiversity is sustained by a combination of species differences reducing interspecific competition and species similarities increasing time to competitive exclusion. Together, these mechanisms counterintuitively predict that competing species should cluster by traits, in contrast with traditional expectations of trait overdispersion. Here, we show for the first time that trees in a tropical forest exhibit a clustering pattern. In a 50 ha. plot on Barro Colorado Island in Panama, community trait values exhibit clusters in two traits connected to light capture strategy, suggesting that competition for light structures community composition. Notably, we find four clusters by maximum height, quantitatively supporting the classical grouping of Neotropical woody plants into shrubs, understory, midstory, and canopy layers.

**Keywords.** niche differentiation, trait-based clustering, self-organized similarity, emergent neutrality, competition, tropical forests, Barro Colorado Island, community structure.

## Introduction

A basic principle of community ecology is that coexistence requires niche differentiation, i.e. species differences that stabilize communities by reducing interspecific competition. However, the high diversity and seemingly continuous phenotypic variation of trees in tropical forests raises questions about the importance of niche differentiation as a contributor to species co-occurrence and patterns of diversity, relative to other community assembly processes such as dispersal and ecological drift (Hubbell 2001, Levine and Murrell 2003, Mouquet and Loreau

2003, Chase and Myers 2011). Indeed, neutral models reflecting chance events provide a good fit to the distribution of species abundances in tropical forests (Hubbell 2001, Volkov et al. 2003), although other studies have found evidence of niche differentiation (Kraft and Ackerly 2010, Götzenberger et al. 2012). One likely reason for these mixed results is a lack of model-validated quantitative predictions for how niche-based competition shapes community trait structure.

Classical theory posits that only species whose trait differences are large enough to sufficiently lower interspecific competition will stably coexist. Hence, attempts to find evidence of niche differentiation in nature typically look for greater-than-chance differences in trait values among species (Chase and Leibold 2003, Kraft et al. 2008, Lake and Ostling 2009, Kraft and Ackerly 2010, Götzenberger et al. 2012, D'Andrea and Ostling 2016). However, competition can produce counterintuitive patterns. If two resident species are not distant enough from each other in trait space to allow a third species with an intermediate trait value to invade, the potential invader has higher fitness if it is similar to one of the residents than if it is maximally different from both (MacArthur and Levins 1967). This is because the increase in competition with the close resident is more than compensated by the decrease in competition with the other resident. When this phenomenon is extrapolated to multispecies communities, species are competitively excluded at rates inversely related to trait distance from the nearest trait optimum (D'Andrea and Ostling 2017). As competition among species proceeds, a transient pattern arises characterized by distinct clusters of species with similar traits, centered around locally optimal ecological strategies (Scheffer and van Nes 2006). While competition among species in each cluster eventually leads to exclusion of all but the most competitive species, the similar strategies among the species renders their dynamics near-neutral; indeed, clusters can persist indefinitely under

restorative forces such as immigration (D’Andrea et al. 2019), environmental fluctuations (Sakavara et al. 2018), and specialist enemies (Scheffer and van Nes 2006, Barabás et al. 2013).

In other words, while classical literature predicts that niche partitioning will lead to trait overdispersion, more recent literature suggests trait clusters rather than overdispersion as evidence of niche partitioning. We note that the same models that predict overdispersion in stable equilibrium will predict clusters as transients (Scheffer and van Nes 2006, D’Andrea et al. 2019). Furthermore, it has been shown that several ecological forces can maintain the clusters indefinitely as a stationary state. Those forces include immigration (D’Andrea et al. 2019), periodic environments (Sakavara et al. 2018), and “hidden niches”, i.e. independent niche axes providing extra intraspecific regulation such as specialist enemies (Scheffer and van Nes 2006, Barabás et al. 2013). Given the widespread influence of these forces in nature, we expect clusters to be a more general signature of niche differentiation than the stricter circumstances under which overdispersion might arise.

Clustering by organismal size has been reported in animal (Scheffer and van Nes 2006) and phytoplankton communities (Sakavara et al. 2018), but is not known to occur in tropical forests – a focal point for the development and tests of coexistence theory. Furthermore, previous efforts to detect species clusters have typically ignored species abundances and/or relied on arbitrary binning of trait space (Scheffer and van Nes 2006, Yan et al. 2012) or temporal data to distinguish between occasional and permanent species (Vernon et al. 2009). However, recent work has proposed a parameter-free method which uses trait and abundance data to identify and count the clusters, which was validated using population dynamic models of competition with immigration (D’Andrea et al. 2019).



Here we use this approach to test for trait clustering in the 50-ha Forest Dynamics Plot on Barro Colorado Island, Panama (Condit 1998, Hubbell et al. 1999, Condit et al. 2012a) (BCI). We quantify species strategy using four morphological traits: seed mass, maximum tree height, wood density, and leaf mass per area (LMA). Seed mass is thought to reflect strategies along a tolerance-fecundity tradeoff axis (Muller-Landau 2010), whereby large-seeded species specialize in surviving stressful environmental conditions at the cost of low fecundity and vice-versa. Maximum tree height, wood density, and LMA are associated with competition for light (Kunstler et al. 2016), and as such may reflect plant strategies related to partitioning light availability gradients both vertically (i.e. among forest canopy layers) and horizontally (i.e. across forest patches at different stages of succession). Such partitioning of light access is central to the forest architecture hypothesis (Kohyama 1993) and the related successional niche hypothesis (Grime 1979, Tilman 1988).

Trait pattern indicative of a niche mechanism will likely only become evident at a spatial scale above that of any spatial heterogeneity involved in the mechanisms (Kraft and Ackerly 2010, D'Andrea and Ostling 2016). Therefore, we look for signatures of niche partitioning at the whole plot (50 ha) scale, large enough to encompass the spatial heterogeneity in patch-age since disturbance involved in these niche mechanisms (Hubbell et al. 1999). Because immigration can reinforce local clustering if surrounding forests have species clustered around the same trait-based niche optima, or mask local clustering if surrounding forests have species clustered around different trait-based niche optima, we compare results at the plot-scale with results from a combined pool of 40 census plots within 30km of BCI (Condit et al. 2013, 2016) (Fig. 1).

## Methods

The Barro Colorado Island Forest Dynamics Plot is a 1,000-by-500 meter tract of tropical forest on Barro Colorado Island in Panama (Hubbell et al. 1999, Condit et al. 2012b) (Fig. 1). The plot has been censused for stems above 1 cm diameter at breast height (DBH) in 1982, 1985 and every five years through 2015. The plot contains approximately 210,000 stems with DBH  $\geq$  1 cm, and about 300 tree species. Results shown in the main text pertain to the 2000 census; however, results are consistent across all available censuses (Appendix S1: Table S1, Figs. S3-S6).

We used four traits related to plant architecture, leaf structure, and seed size. Trait data, drawn from Wright et al. (2010), were based on the following protocols: 1) Maximum height was estimated as the mean height of the six largest (by DBH) individuals, measured using a rangefinder. 2) Wood density ( $\text{g}/\text{cm}^3$ ) was measured after drying at 60°C. 3) Leaf mass per area ( $\text{g}/\text{m}^2$ ) was measured on leaf laminae, excluding petioles and petiolules, averaged across six individuals. For species that reach the canopy we used leaves exposed to direct sunlight --- i.e. sun leaves. For all others we used shade leaves collected from the crowns of the tallest individuals in the 50 ha plot. 4) Seed mass (g) refers to endosperm plus embryo only and was measured after drying at 60°C. Traits with skewed distributions (LMA and seed mass) were log-transformed to reduce the skew. Palms were excluded from wood and leaf trait analyses, due to their substantial differences in physiology from dicots.

We looked for clustering among reproductive individuals (adults), since population dynamic models producing emergent clusters do not consider population structure. We consider individuals to be reproductive when their DBH exceeds half the maximum DBH observed for its

species, a relationship that explains over 80% of interspecific variation in reproductive size thresholds (see Visser et al. 2016: Fig. S9). Maximum DBH was estimated as the average of the six largest individuals in the BCI plot in 2005, and an additional 150 ha of mapped tree plots located within 30 km and mostly within 10 km of BCI (Visser et al. 2016).

The regional pool consists of 40 1-ha sampling sites within 30km of BCI (Condit et al. 2013, 2016). In 38 of these sites, individuals with maximum DBH > 1cm were censused in 40m-by-40m internal subplots, while individuals with DBH > 10cm were censused in the entire plot. In the remaining two plots, all individuals with maximum DBH > 10cm were censused in the entire plot. Hence, we standardized the counts by the respective sampling area to estimate densities in these sites. Of the circa 850 species contained in these sites, trait data were available for those also found on BCI (see Table 1, caption to Fig. 1). While lack of pattern among this subset of species in the regional pool does not rule out clustering among all species, it shows that the pattern on BCI is not simply mirroring regional-scale pattern inherited via immigration.

Our clustering metric has two foundations: the k-means clustering algorithm (MacQueen 1967), an optimization procedure which assigns species to clusters by minimizing the average trait distance between individuals in the same cluster; and the gap method (Tibshirani et al. 2001), which compares the observed data against null distributions, and selects the number of clusters that maximizes the difference between within-cluster trait dispersion in the observed and null communities. Specifically, given a candidate number of clusters,  $k$ , the k-means algorithm finds the arrangement of species into  $k$  clusters that minimizes within-cluster trait dispersion:  $D_k$

$= \frac{1}{k} \sum_C \sum_{i,j \in C} n_i n_j d_{ij}^2$ , where  $C$  refers to a cluster ( $1 \leq C \leq k$ ),  $n_i$  is the abundance of species  $i$ ,

and  $d_{ij}$  is the trait distance between species  $i$  and  $j$ . The algorithm starts with randomly chosen

trait values in the local community as possible cluster centers, then puts species into the cluster

whose center is the closest to them, then recalculates cluster centers, and so on until the algorithm converges or changes in  $D_k$  fall below a specified threshold. Because the result can depend on the starting set of cluster centers, the procedure is repeated with different starting sets, and the final cluster arrangement with the lowest  $D_k$  across all sets is selected (note that the clusters need not be equally spaced). We use enough starting sets that larger numbers do not lower within-cluster dispersion further (typically between 1,000 and 10,000). We then apply this k-means algorithm to 1,000 null communities, and the difference in within-cluster trait dispersion  $D_k$  between the observed community and the mean null value is the gap index for  $k$  clusters,  $G_k = D_k - \bar{D}_{k,\text{null}}$ . Finally, we find the number of clusters that maximizes the gap index. This maximal value -- corresponding to the peak in the gap curves in Figs. 2, 3 -- is the gap statistic,  $G = \max (G_k)$ , and the value of  $k$  at which it occurs is the estimated number of clusters  $K$ .

We obtain a null distribution of gap statistics by performing the above routine on each of the null communities, and from this distribution we extract significance (p-value) and standardized effect size (z-score). The z-score is  $Z = (G - \mu)/\sigma$ , where  $\mu = \frac{1}{1000} \sum_{\text{nulls}} G_{\text{null}}$  is the mean of the null gap statistics and  $\sigma^2 = \frac{1}{1000} \sum_{\text{nulls}} (G_{\text{null}} - \mu)^2$  is the variance. The p-value is the proportion of null communities with a higher gap statistic than the observed community,  $P = \frac{1}{1000} \sum_{\text{nulls}} I(G_{\text{null}} > G)$ , where the indicator function  $I$  is 1 if its argument is true, and zero otherwise. Our null communities contain the same set of observed trait values and abundances, with abundances randomized across the traits. We therefore test for a nonrandom association between traits and abundances, as opposed to a nonrandom set of traits or abundances.

**Results**

We found significant clustering of species on BCI based on species maximum height (Fig. 2A; Fig. 2E). There were four height-based clusters, falling at approximately eight-meter intervals. Intriguingly, the pattern aligns well with the historical division of humid Neotropical forests into four strata of about ten meters each: shrubs, understory, midstory, and canopy (Paul W Richards 1952, Terborgh 1985, Condit et al. 1995) (Fig. 3, Appendix S1: Fig S1). We also found a significant pattern of five clusters based on wood density on BCI (Fig. 2F). Notably, species on BCI were also significantly clustered around a single wood density optimum. This occurred because species with intermediate wood densities were more common than those with extremely low or high wood densities (Fig. 2B), potentially indicating physiological costs or environmental filters against extreme trait values. We found no evidence for clustering based on LMA or seed mass.

The similar number of clusters by maximum height and wood density led us to ask if the two trait-based patterns reflected the same underlying niche axis. Even though maximum height and wood density did not correlate significantly (Pearson's  $\rho = -0.10$ , p-value = 0.06), maximum height clusters correlated with wood density clusters ( $\chi^2$ -test p-value = 0.02, Cramér's  $V = 0.20$ ), supporting this tentative hypothesis.

We found significant clustering by maximum height at the regional scale, with the highest gap index occurring at  $K = 1$  cluster, and a secondary but still significant peak at  $K = 4$  clusters (Appendix S1: Fig. S2A, B). The existence of four height-based clusters at both local and regional scales suggests a consistent organization of species into the same four niches across many tropical forest communities. However, a key difference between local and regional height-

based patterns is the presence of a significant single cluster at the regional scale. This single regional peak reflects a unimodal abundance trend along the maximum height axis, with trees in the second height cluster being consistently the most abundant in their communities. This abundance trend may result from an interplay of higher light incidence at larger heights and the potential for a larger number of smaller-sized trees in a given area.

As for lack of clustering by wood density in the regional pool, we hypothesize that differences in environmental or ecological conditions across the region may have created different trait optima (cluster centroid values) in different communities, leading to the erosion of cluster structure when the communities are combined.

## Discussion

Our results underscore competitive partitioning of light as a major driver of tropical forest community structure. Specifically, we found cluster-based evidence for niche partitioning by maximum height, a trait associated with light capture, and wood density, a trait associated with shade tolerance (Wright et al. 2010). Conventional descriptions of tropical forest structure have long included references to different strata (sub-canopy, canopy, etc.), but to our knowledge there has never been any quantitative empirical support for their existence.

Testing for trait-based clustering is an appealing approach for the detection of niche partitioning because it conceptually unites the notions of stable species coexistence via differences and transient species coexistence via similarity (Holt 2006). Perhaps counterintuitively, it is precisely because species with similar strategies compete more strongly, and experience similar competitive effects from the rest of the community, that clusters emerge

(D'Andrea et al. 2018). In other words, clusters reflect the simultaneous advantages of differing from others while being similar to those favored strategies.

We note there are special cases where competition could allow for coexistence of species with any trait value (Leimar et al. 2013). Specifically, the function specifying the relationship between competition and species traits (often referred to as the competition kernel) must have a strictly positive Fourier transform, which is not a general property of competition based on trait differences. For example, in the family of exponential kernels, only those with exponent  $\leq 2$  will satisfy the condition, and small perturbations of these kernels will break the property and lead to cluster formation. However, in the absence of empirical evidence that the competition kernels on BCI possess those special properties, a more general expectation is for cluster formation rather than a continuum of traits.

The mechanistic origin of clustering may involve environmental selection favoring certain traits over others. For example, according to Terborgh's sunfleck model (Terborgh 1985), light availability below the canopy may peak at various vertical strata due to intersection of light cones originating from gaps in the canopy. Latitudinal parameters which affect the angle of incidence, combined with the shape of tree canopies in tropical forests, predict three such strata below the canopy, for a total of four optimal tree heights based on light availability.

Alternatively, the height-based clusters we identified may arise through tradeoffs between the light-related advantages of being tall and shading others, and the budgetary constraints that investment in height impinges on reproductive growth, such as through losses in recruitment or shade tolerance (Kohyama 1993, Kohyama and Takada 2009). These tradeoffs may result in an effective relationship between interspecific competition and height similarity. In such a case, the number of clusters would relate to how quickly competition drops with increasing separation in



maximum height. Regardless of the mechanism, the height-based clusters reflect the existence of multiple light-related niches, as well as stabilization via light-related niche partitioning.

The existence of four clusters by height suggests that only four species can coexist on BCI based on differences in height alone, but it does not mean that only four species can stably coexist on BCI. Additional niche axes may support higher coexistence, and in fact may be responsible for the maintenance of the observed clusters. Barabás et al. (2013) pointed out that additional niche axes, such as susceptibility to different herbivores and pathogens, are required for the permanence of clusters in a closed community subject to no temporal variation in the environment. Though recent empirical studies report a good deal of overlap in enemy host use, models suggest that small differences in susceptibility to enemies between tree species may still contribute significantly to diversity maintenance (Sedio and Ostling 2013). Hence, they likely also contribute to the permanence of clusters along the trait axes we report in our study. Another example additional niche axis is the successional niche (Tilman 1988): trees sharing the same height niche may niche-differentiate by shade tolerance. This could be reflected in the distribution of wood density values and/or other traits related to successional strategy.

Wood density in Barro Colorado Island tree species has been found to be a good predictor of species niche strategies along a tradeoff axis between survival under stressful conditions and rapid growth under optimal conditions (Wright et al. 2010). Therefore, the clustering we found in wood density suggests niche partitioning along a growth-mortality tradeoff axis, i.e. the successional niche (Tilman 1988). The precise positions of the clusters could have many interacting causes: the available pool of traits, external filtering from the environment, resource availability, and the shape of the competition kernel. In the case of wood density, given its connection to the successional niche, the distribution of light gaps in the forest

may possibly determine the positions of the niches. The number of clusters may also be influenced by the rate at which competition drops between species of disparate wood density: the faster the drop, the more niches are allowed.

The wood density results are not fully independent from our maximum height results, as indicated by the correlation between height and wood density clusters. To fully delineate the niche space driving pattern on BCI, a multivariate trait treatment would be required. However, such an approach raises questions of how to best convert trait values along different trait axis into a good predictor of competition. Moreover, traits could combine in different ways to form multidimensional niche space (D'Andrea et al. 2018); for example, Euclidean distance may be a poor predictor of competition, and therefore not be useful for detecting clustering. Determining how competition maps to multivariate trait space requires mechanistic niche models going beyond the existing theoretical literature, which typically focuses on contributions of individual traits.

The absence of clustering in LMA and seed mass does not preclude a role for these traits in niche partitioning on BCI. D'Andrea et al. (2019) showed that a loose connection between trait value and niche strategy can mask clustering along the relevant niche axis. Seed mass is linked to dispersal and recruitment ability (Muller-Landau et al. 2008), and is therefore a candidate for clustering along a niche axis characterizing a competition-colonization tradeoff – hence its inclusion in our study. However, seed mass alone may be a poor predictor of a species' strategy along this niche axis, due for example to the effects of other traits such as drought tolerance and dispersal mode. LMA is theoretically connected to niche strategies (Wright et al. 2010), but there is substantial ontogenetic variation in its predictive ability of growth, with the relationship being stronger in the seedling stage. Eventually, other aspects of physiology become

limiting as the plant grows. Hence, LMA may be a noisy predictor of the niche strategy (Wright et al. 2010). We conclude that the lack of clustering in these traits may be due to their loose connection to niche strategies rather than no involvement in niche partitioning.

Our study provides a new line of evidence that niche differentiation shapes tropical forests, notwithstanding neutral theory's success at fitting species abundance distributions (Rosindell et al. 2012). Yet, our results go further by identifying specific numbers of niches and their associated trait optima. Future extensions of clustering analysis could look at other traits related to defense chemistry or abiotic preferences, further delineating the niches contributing to coexistence in tropical forests.

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## Tables and Figures

**Table 1: Clustering results for the 50-ha plot and regional pool.** For each header, the left column refers to the 50-ha BCI plot (“50 ha.”), and the right column refers to the regional pool (“Region”). The total number of species for which trait data were available is listed under “Species”, and the total number of individuals represented is listed under “Individuals.” The number of clusters  $K$  is the value at which the gap index peaks. z-scores and p-values were obtained by comparing the gap statistic against 1,000 null communities. In the case of maximum height, in addition to the peak at  $K = 1$  listed below, the regional pool also had a significant subpeak at  $K = 4$  ( $Z = 2.0$ ,  $P = 0.03$ ).

	<u>Species</u>		<u>Individuals</u>		<u>Clusters (K)</u>		<u>z-score (Z)</u>		<u>p-value (P)</u>	
	50 ha.	Region	50 ha.	Region	50 ha.	Region	50 ha.	Region	50 ha.	Region
Maximum height	259	242	20,620	13,743	<b>4</b>	<b>1</b>	<b>2.3</b>	<b>3.4</b>	<b>0.01</b>	<b>0.02</b>
Wood density	229	219	17,139	9,273	<b>5</b>	20	<b>2.1</b>	1.6	<b>0.02</b>	0.06
Leaf mass/area	250	234	18,368	9,528	3	3	0.2	1.5	0.40	0.07
Dry seed mass	185	177	18,259	10,667	15	3	0.2	1.0	0.38	0.16

**Figure 1. Field site.** Intact tropical forest covers 20% of Panama. Our regional pool is an aggregate of 40 sampling sites within 30km of BCI. Combined, these sites comprise approximately 850 species, of which trait data were available for 242 species (max height), 219 (wood density), 234 (leaf mass per area), 177 (seed mass), comprising between 9,528 and 13,743 adult trees. Barro Colorado Island, spanning roughly 16 km<sup>2</sup>, sits in an artificial lake in the Panama Canal. The 50-ha Forest Dynamics Plot, located near its center, is a 1,000m by 500m patch of forest containing 300 tree species and 21,000 adult trees.

**Figure 2. Results.** Stem plots show trait distribution in the 50-ha plot on BCI for maximum height (**A**), wood density (**B**), leaf mass per area (**C**), and seed mass (**D**). Each stem represents a species, with its trait value plotted on the abscissa and abundance on the ordinate. Data shown for the 2000 census. The corresponding gap curves (**E-H**) plot the gap index against the potential number of clusters. The gap statistic is the highest point on the curve, with the red line indicating the 95<sup>th</sup> quantile of the expected gap statistic under no pattern, obtained from 1,000 null sets. The peaks above the red line in (**E**) and (**F**) reveal clustering by maximum height, with four clusters, and wood density, with five. The alternating colors in the respective stem plots show cluster membership of each species.

**Figure 3. Height layers.** Visual representation of the forest on Barro Colorado Island, highlighting the four height-based groups identified by our metric: shrubs ( $61 \pm 2$  species;  $8,071 \pm 712$  adult individuals), understory treelets ( $71 \pm 3$ ;  $7,308 \pm 165$ ), midstory trees ( $61 \pm 1$ ;  $2,957 \pm 114$ ), and canopy trees ( $64 \pm 1$ ;  $2,836 \pm 82$ ), where the numbers represent mean and standard deviation across the 7 censuses. Horizontal lines show maximum height of the dominant (most abundant) species in each group.

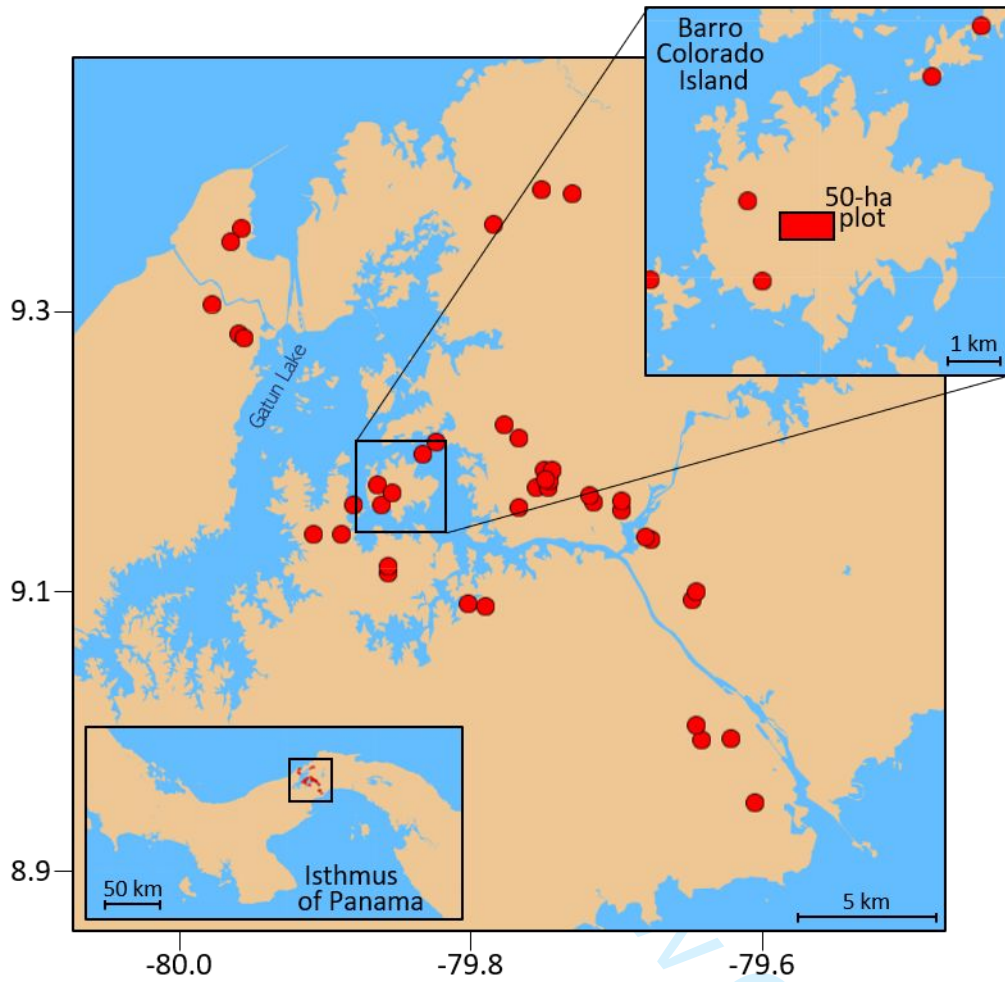
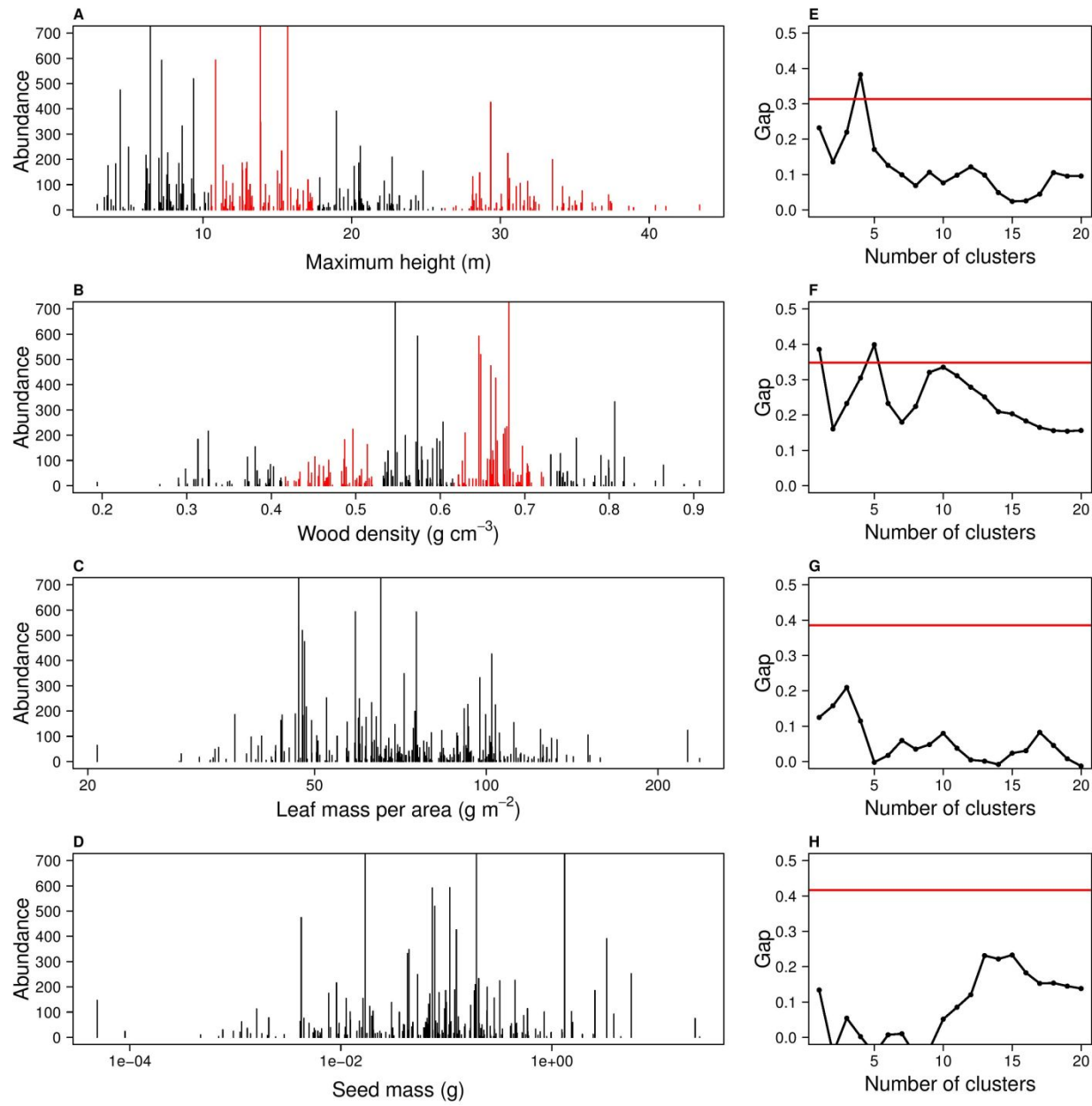
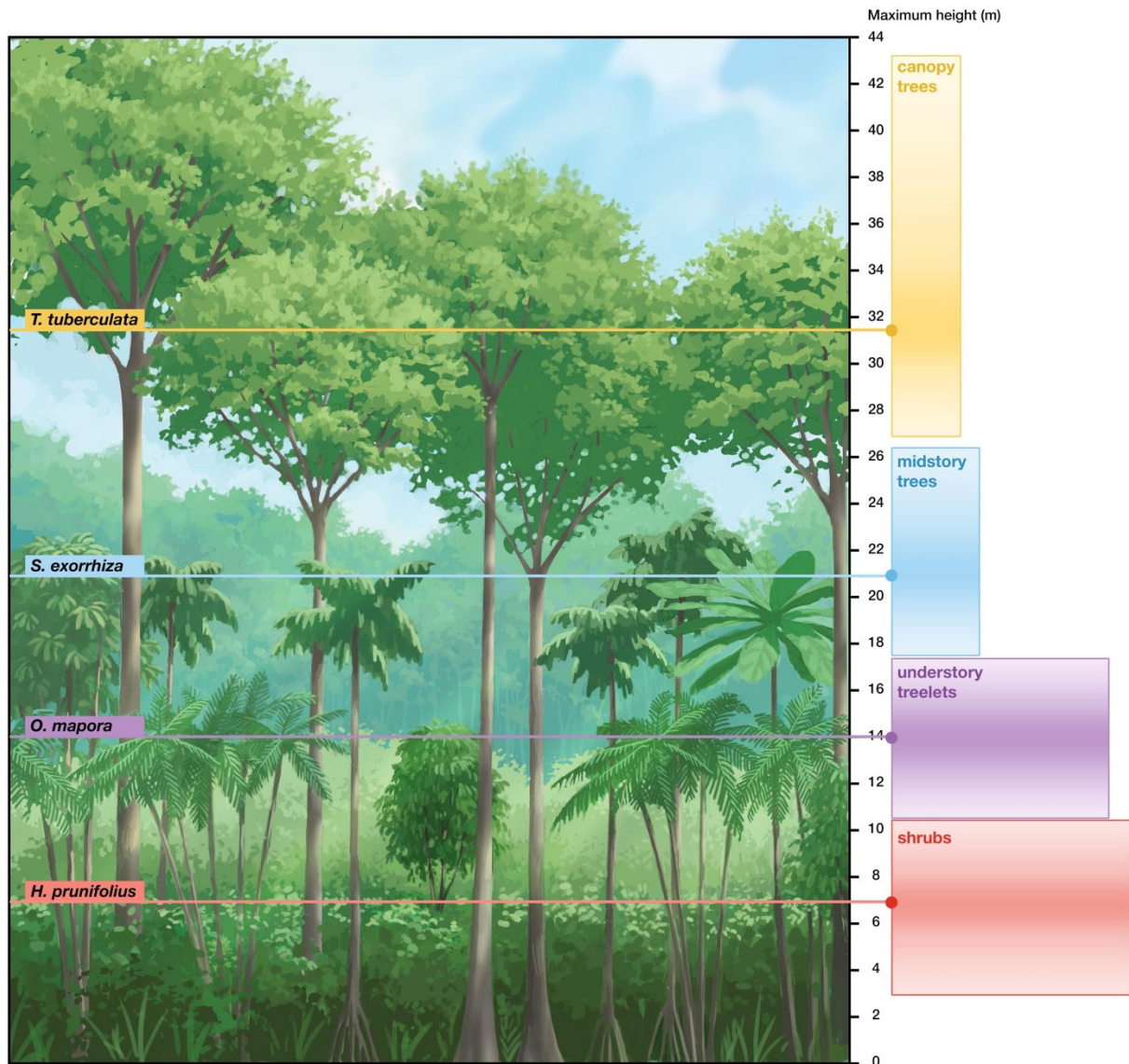


Figure 1.



**Figure 2.**



453

454 Figure 3.

**Appendix S1: Supplementary tables and figures to Counting niches:  
Abundance-by-trait patterns reveal niche partitioning in a Neotropical forest**

**Journal: Ecology**

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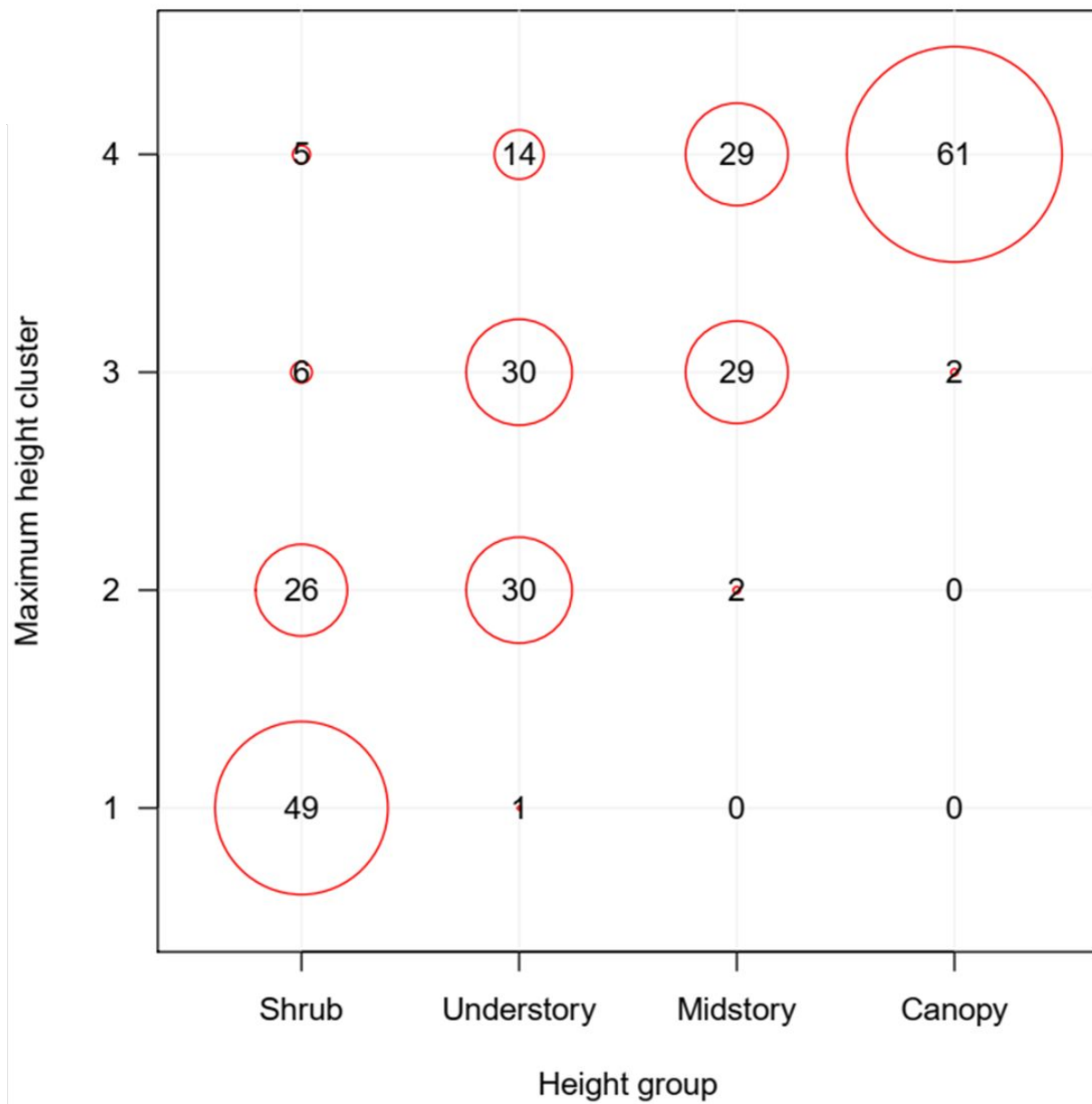
**Table S1.** Clustering results are consistent across censuses. To save computational resources, traits with insignificant results were tested every two censuses. RP: regional pool. RGR: relative dbh growth rate. MRT: mortality.

Trait	Census	Species	Individuals	Clusters	Z-score	P-value
Maximum height	1982	252	21,423	4	2.6	0.005
	1985	253	21,670	4	2.6	0.003
	1990	254	22,340	4	2.5	0.003
	1995	257	21,341	4	2.4	0.011
	2000	259	20,620	4	2.3	0.012
	2005	260	20,177	4	2.1	0.024
	2010	260	20,631	4	2.2	0.014
	RP	242	13,743	1	3.4	0.001
Wood density	1982	223	17,332	1	2.8	0.001
	1985	223	17,902	1	2.8	0.001
	1990	224	18,597	1	2	0.025
	1995	227	17,646	5	2.2	0.023
	2000	229	17,139	5	2.1	0.017
	2005	229	16,874	5	1.9	0.035
	2010	229	17,325	5	1.7	0.055
	RP	219	9,273	20	1.6	0.058
Leaf mass per area	1982	243	18,478	18	-1	0.839
	1990	245	19,947	3	-0.4	0.618
	2000	250	18,368	3	0.2	0.396
	2010	251	18,437	3	1	0.15
	RP	234	9,528	3	1.5	0.072
Seed mass	1982	183	18,735	16	-0.2	0.548
	1990	184	19,707	13	0.3	0.396
	2000	185	18,259	15	0.2	0.377
	2010	185	18,154	13	0.2	0.407
	RP	177	10,667	3	1	0.158

**Figure S1. Correspondence between quantitative height clusters and qualitative classification.** Circle sizes are proportional to the numbers within, which show how many species are classified in each combination of our four height clusters and the four qualitative height groups. Largest values are close to the diagonal, indicating a good match between the two classifications. Cramér's  $V$ , which measures the degree of association between two categorical variables, was 0.58 (0 = no association, 1 = perfect correspondence). Data for the qualitative groupings obtained from Wright et al<sup>35</sup>. Note that this classification into height groups (x-axis) was based on typical height of reproductive adults, not the species maximum height. As such, some species are classified one height group below their corresponding maximum-height cluster, hence the bias towards placement above the diagonal.

**Figure S2. Regional pool results.** Results displayed in analogous form to Fig. 2. Only maximum height is clustered, with significance at  $K = 1$  and  $K = 4$ . Wood density and LMA are marginally significant at  $K = 20$  and  $K = 3$ , respectively.

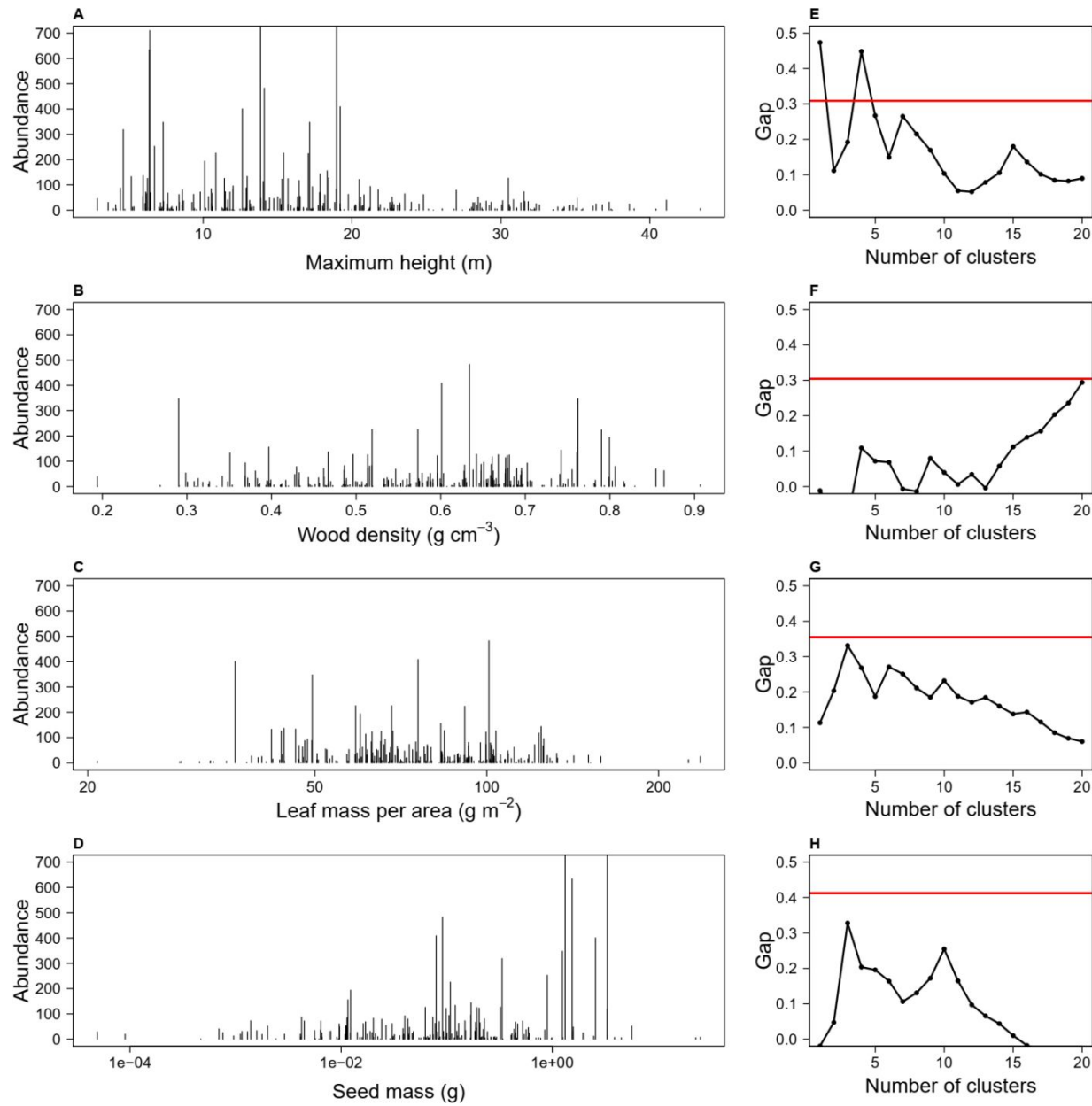
**Figures S3-S6. BCI results for all available censuses.** Pattern was consistent across censuses, especially for maximum height (Fig S4). In wood density (Fig S5), the peak at  $K = 5$  tops  $K = 1$  as the highest gap index over time. LMA (Fig S6) and seed mass (Fig S7) results were obtained for alternate censuses to save computational resources.

45 **Figure S1.**

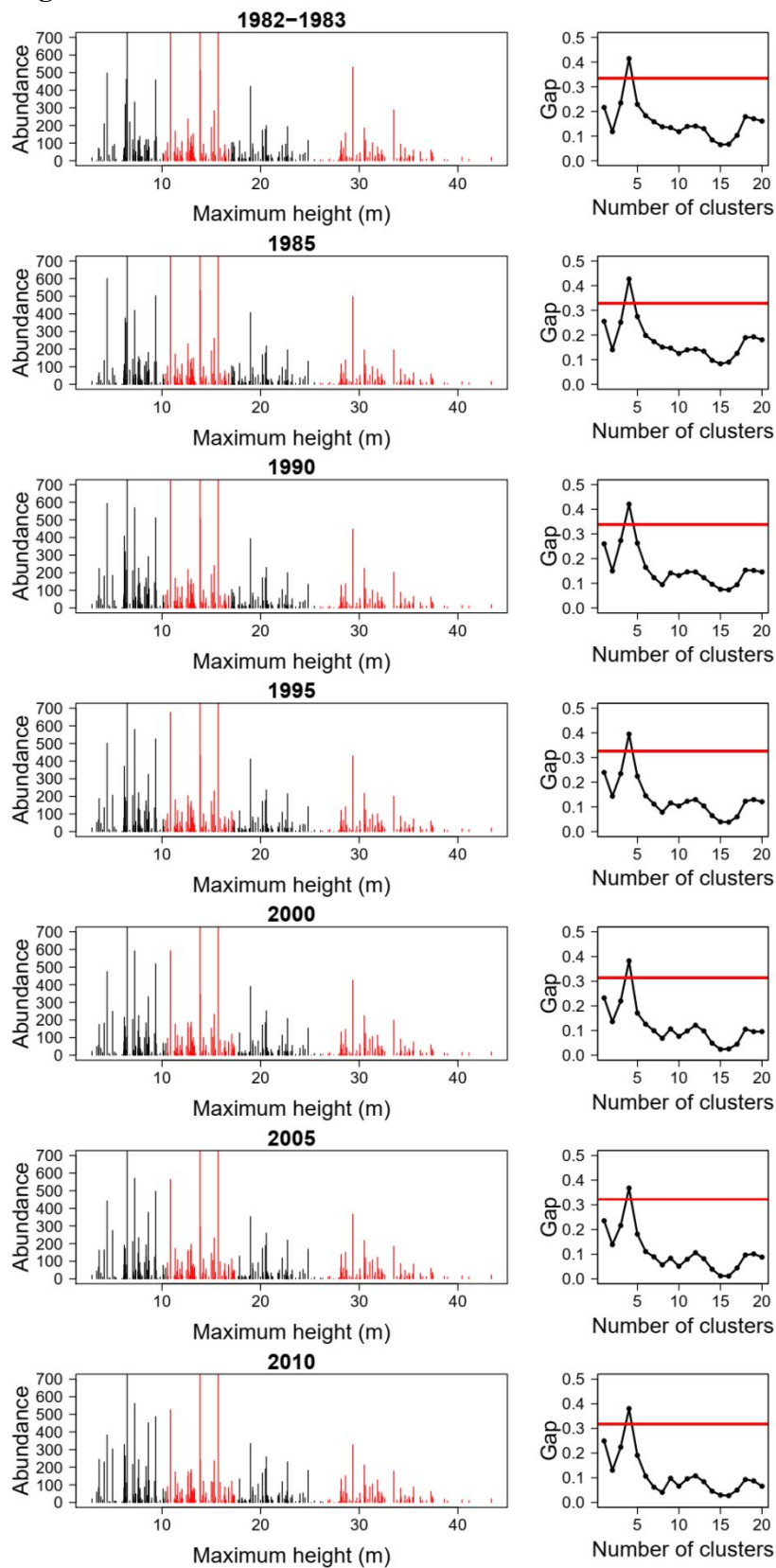
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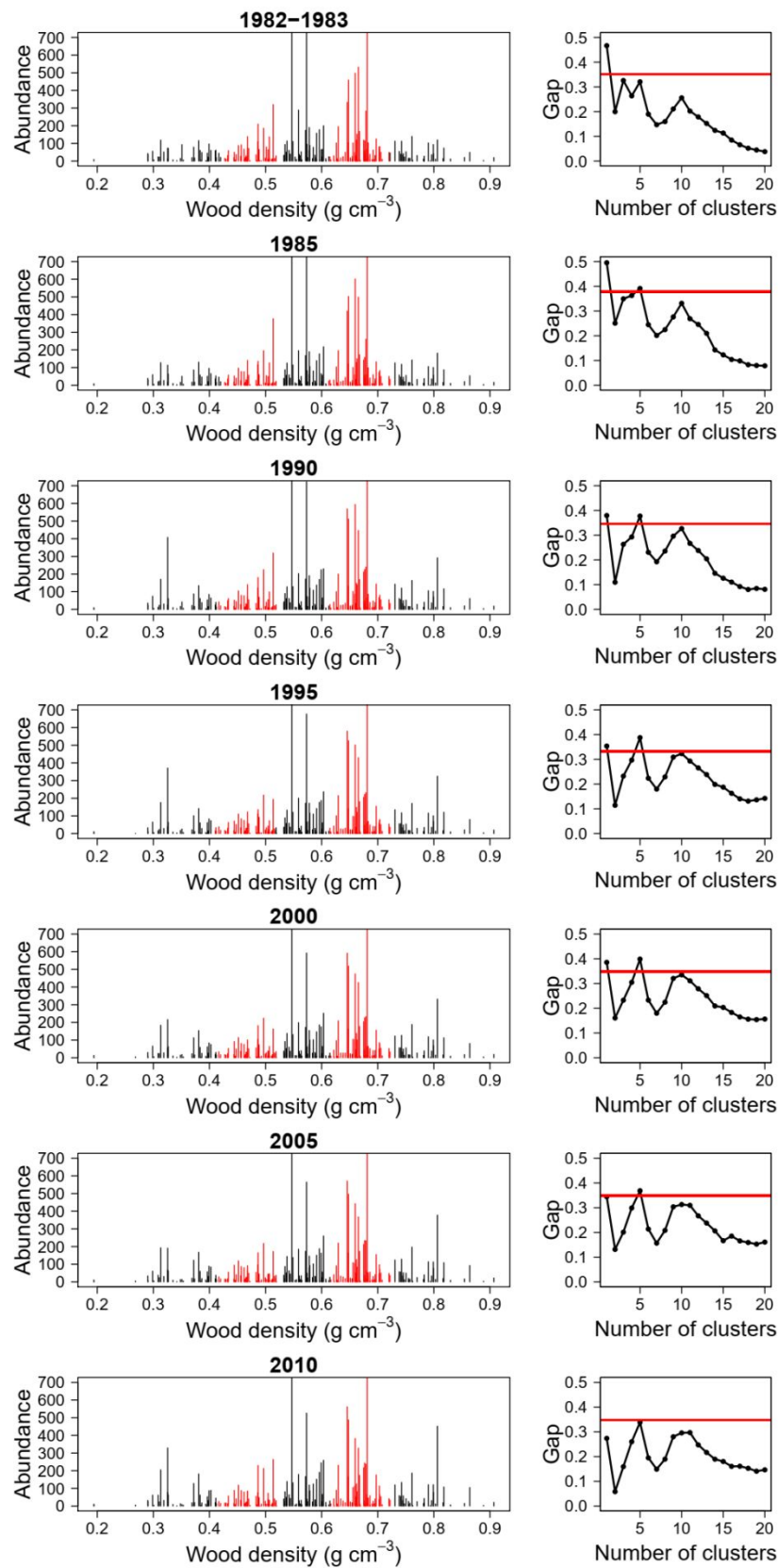
48 **Figure S2.**

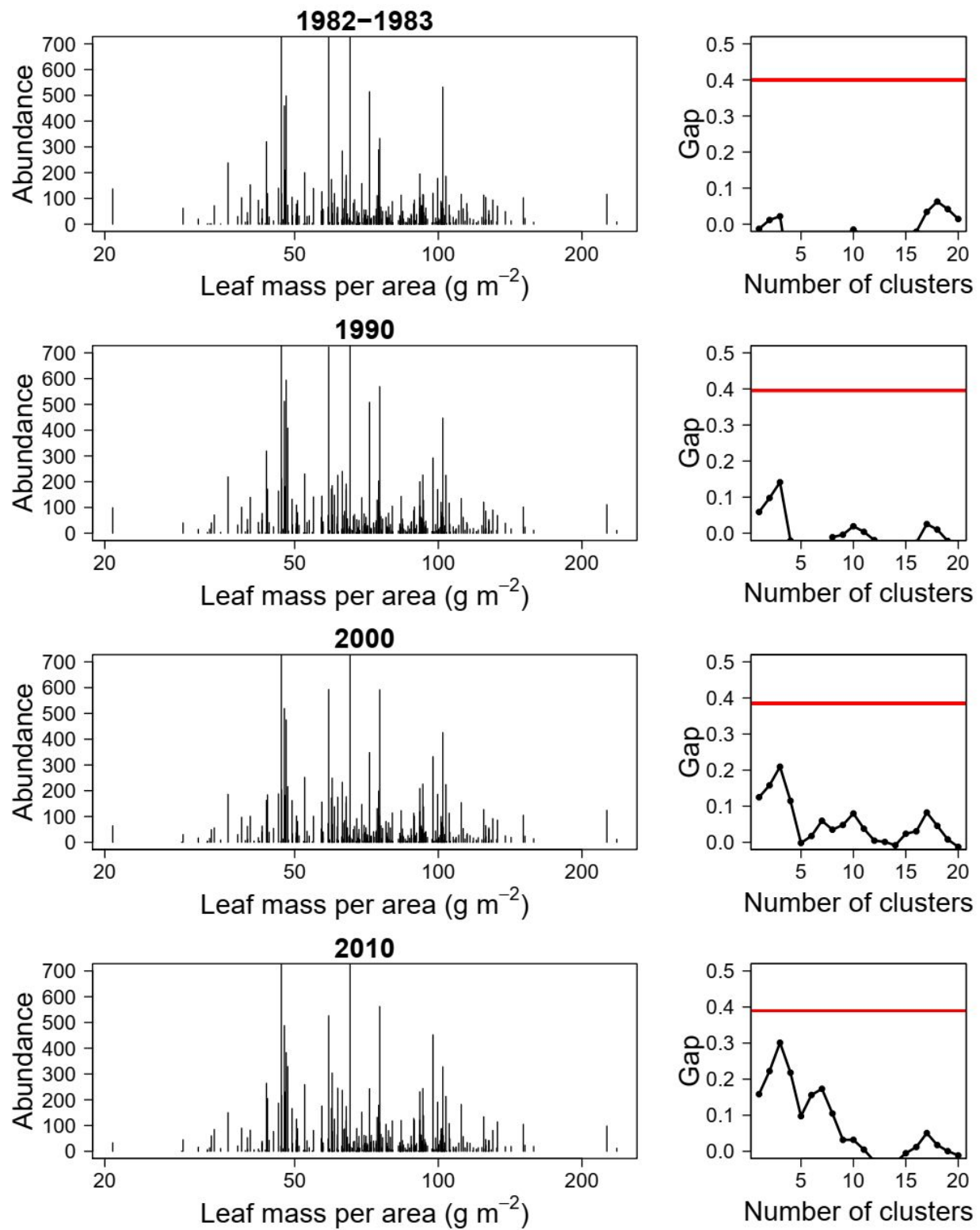


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51 **Figure S3.**

54 **Figure S4.**



56 **Figure S5.**

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59     **Figure S6.**

