**Appendix A – Supplementary material**

**Methods for climatic data and ecological niche modeling**

*Species occurrence data*

The 144,375 occurrence data from 796 woody plant species collected from SpeciesLink and GBIF databases were projected in ArcGis and cleaned up. This process consists in excluding problematic and imprecise occurrence data like duplicated and improbable points such as those on the sea and out of the distribution range according to *Flora do Brasil* (http://floradobrasil.jbrj.gov.br/) and *Tropicos* (http://www.tropicos.org/). After cleaning species occurrence data, we applied a spatial filtering procedure to reduce sampling bias. Occurrences from the same species that were closer than 20 km were excluded and we also only considered species that contained a minimum of 10 occurrences points inside South America, after data cleaning and spatial filtering. We opted for 20 km based on assessment of the number of species having a minimum of 10 occurrences. In fact, increasing such filtering distance (e.g., 25 km) would drastically reduce the number of species with at least 10 occurrences in the study, whereas considering smaller distances and species with less than 10 occurrences could lead to biased models (Zwiener et al., 2020). Increasing such filtering distance would drastically reduce the number of species in the study, whereas considering smaller distances and species with less than 10 occurrences could lead to biased models. We used the Maxent implementation in the ‘dismo’ (Hijmans et al.,2012) R package, all feature classes (as the default), raw output, and no clamping. It is important to highlight that for this study, despite that WorldClim 1.4 uses climatic variables from 1960 to 1990, the species occurrences are not restricted to that period of time.

*Climatic data*

Climatic variables were compiled from the WorldClim 1.4 database (Hijmans et al., 2005) at a spatial resolution of 5’. The 19 variables summarize precipitation and temperature tendencies and represent annual seasonal tendencies as well as limiting and extreme environmental drivers (Hijmans et al., 2005). The set of variables for future climate projections was chosen based on the IPCC Fifth Assessment Report. We selected the global climate models (GCM) CCSM4, GISS-E2-R and MIROC5 and two contrasting representative concentration pathways (RCP 2.6 and RCP 8.5) for the year 2050 (the average for 2041-2060). The GCMs were selected based on the variability of climate predictions. We randomly sampled 1,000 pixels of bioclimatic rasters from all GCMs of the CMIP5 (Coupled Model Intercomparison Project Phase 5) RCP 2.6 and RCP 8.5 scenarios, available for 2050 in the WorldClim database, extracted the respective bioclimatic variables and performed a non-metric multidimensional scaling (NMDS) based on Euclidean distances. We selected contrasting GCMs, in terms of predictions, based on the ordination plot of the NMDS. Hereupon, the bioclimatic variables were submitted to principal component analysis (PCA) in order to reduce the dimensionality and collinearity of environmental layers, which was based on a correlation matrix of standardized variables. Finally, we chose the first six principal components axes as a proxy for the climatic variables in the ecological niche modeling, as they account for >95% of the variation. Moreover, despite WorldClim 1.4 uses climatic variables from 1960 to 1990, the species occurrences are not restricted to that period of time.

*Ecological niche modeling*

Ecological niche modeling approach was used to predict suitable areas where each species could naturally occur in the present and in the future, based on 19 WorldClim (Hijmans et al., 2005) environmental variable models and potential dispersal dynamics. Its core assumptions are that environmental conditions are crucial components of a species’ ecological niche and that the equilibrium between them has been reached where they occur (Peterson et al., 2011; Soberón and Nakamura, 2009). Other assumptions are that species interactions play null or little effect on large-scale distributional patterns (Soberón and Nakamura, 2009; but see Anderson, 2017; Inderjit et al., 2017), and that phenotypic plasticity would potentially take place despite the fact it is unlikely to be precisely predicted in order to be incorporated into niche modeling. As dispersal is a pivotal factor in determining species distributions, a calibration area buffer of either 100 or 200 kilometers - for restricted (i.e., regional) and wide (i.e., continental) distributions, respectively – was created around each occurrence point and a convex hull polygon of minimum bounding geometry was drawn in ArcGIS. The resulting polygon represented the M dimension, which depicts the potential areas where the species could physically reach, and was used in the niche modeling.

The maximum entropy (Maxent) method was used to construct niche models (Phillips et al., 2006). It was chosen over other available modeling methods given its high performance and suitability for presence-only data (Elith et al., 2006; Peterson et al., 2011). The settings were: five bootstraps replications, raw output and a threshold of 5% lower values of training presences over the mean estimate to produce binary predictions (Merow et al., 2013; Peterson et al., 2011). Other settings were kept as the default.

The geographical distribution estimates for each species in the future were derived from overlaying the thresholded projections of the three global circulation models and selecting only the areas where the three models overlapped. The climatic data and ENM processing were performed with the package 'dismo' (Hijmans, et al., 2012) and scripts available at <https://github.com/narayanibarve/ENMGadgets>. All analyses in this work were performed in R (R Core Team, 2017).

To evaluate models, we randomly split the data into training (70%) and testing (30%) datasets. Due to lack of true absence data, we used omission error as a performance metric using the function ‘kuenm\_omrat’, implemented in the R package ‘kuenm’ (https://github.com/marlonecobos/kuenm) with default parameters (threshold = 5). We only considered models that presented error rate ≤ 5% on testing data. Final models were calibrated with all occurrences and applied in the subsequent biodiversity analyses.

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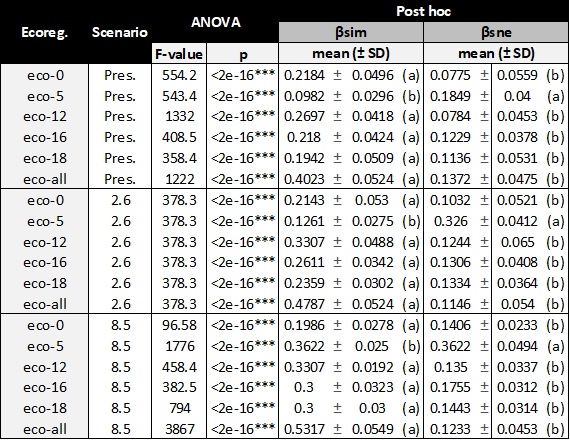
Soberón, J., Nakamura, M., 2009. Niches and distributional areas: concepts, methods, and assumptions. Proceedings of the National Academy of Sciences, 106(Supplement 2), 19644-19650, <https://doi.org/10.1073/pnas.0901637106>.

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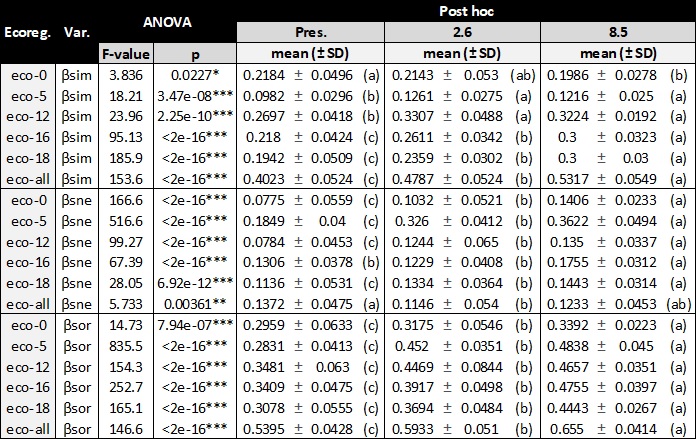
**Figures and tables**

 **Fig. S1.** Temporal pairwise comparison boxplots for each ecoregion in each present-future scenario pair.

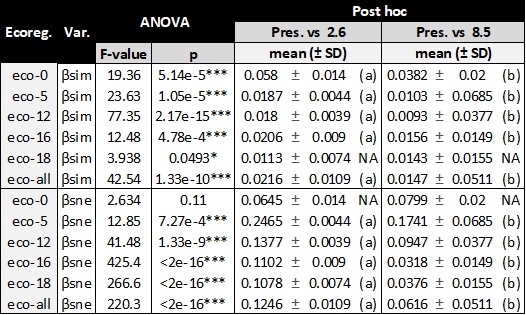
**Table S1.** βsim and βsne comparison in each scenario ANOVA (DF = 1) and Fisher's LSD (post hoc) results in each ecoregion ('ecoreg') and scenario. Significance codes: 0 (\*\*\*), 0.001 (\*\*), 0.01 (\*) and 0.05 (٠).



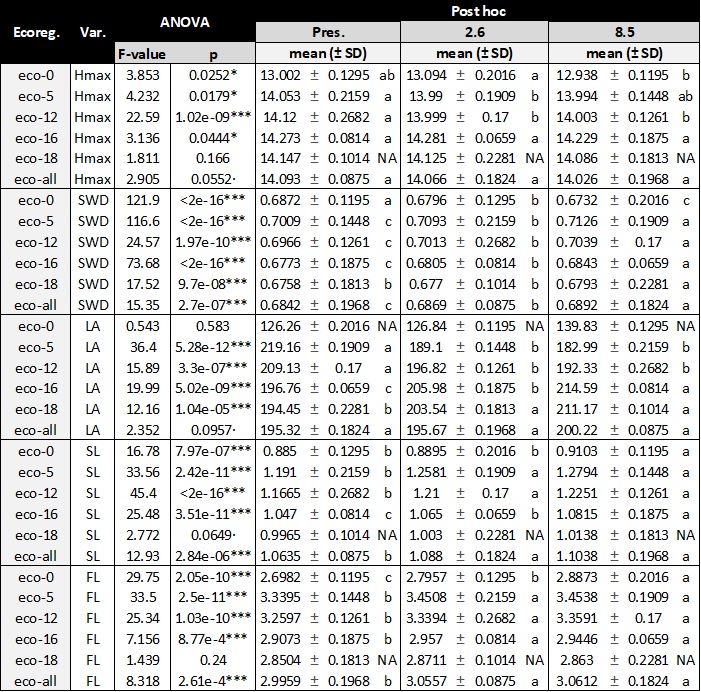
**Table S2.** ANOVA (DF = 2) and Fisher's LSD (post hoc) results of βsim, βsne and βsor comparison among all three scenarios, with each variable ('var.') in each ecoregion ('ecoreg.'). Significance codes: 0 (\*\*\*), 0.001 (\*\*), 0.01 (\*) and 0.05 (٠).



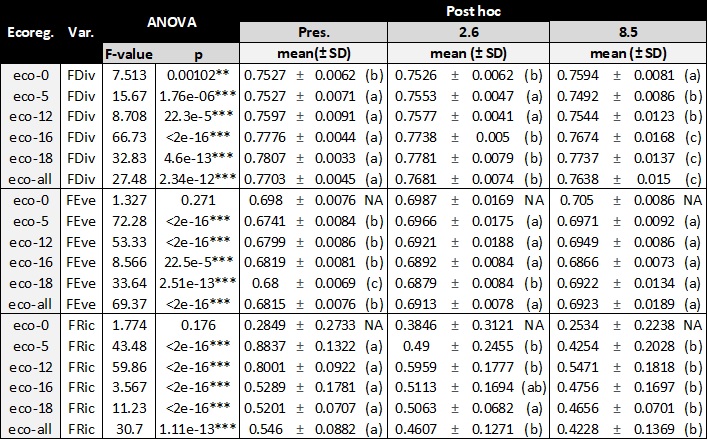
**Table S3.**  ANOVA (DF = 1) and Fisher's LSD (post hoc) results of the temporal βsim and βsne comparison among the pairwise scenarios, with each variable ('var.') in each ecoregion ('ecoreg'). Significance codes: 0 (\*\*\*), 0.001 (\*\*), 0.01 (\*) and 0.05 (٠).



**Table S4.** ANOVA (DF = 2) and Fisher's LSD (post hoc) results of the community-weighted means comparison among all three scenarios, with each variable ('var.') in each ecoregion ('ecoreg.'). Significance codes: 0 (\*\*\*), 0.001 (\*\*), 0.01 (\*) and 0.05 (٠).



**Table S5.** ANOVA (DF = 2) and Fisher's LSD (post hoc) results of the functional diversity indices comparison among all three scenarios, with each variable ('var.') in each ecoregion ('ecoreg.'). Significance codes: 0 (\*\*\*), 0.001 (\*\*), 0.01 (\*) and 0.05 (٠).



**Table S6.** Number of species in each range category for the study area in the climatic scenarios.



**Phylogenetic tree**

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