Climate change reshapes the eco-evolutionary dynamics of a Neotropical seed dispersal system.

Lilian P. Sales\*, W. Daniel Kissling, Mauro Galetti, Babak Naimi, and Mathias Pires

\*Corresponding author’s address

e-mail: lilianpsales@gmail.com

Supplementary information

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Methods

***Species occurrence***

The occurrence records for 32 frugivore bird species (Supplementary Fig. S1a and Fig. S2) considered to be effective and legitimate seed dispersers of the palm *Euterpe edulis* (Pizo & Simão, 2001; De Barros Leite *et al.*, 2012; Galetti *et al.*, 2013) were obtained from ATLANTIC BIRDS, the largest dataset on Neotropical bird distribution (Hasui *et al.*, 2018). We further complemented this dataset with occurrence records from the following online databases: SpeciesLink (splink.cria.org.br), Global Biodiversity Information Facility (GBIF; www.gbif.org), VertNet (www.vertnet.org), Biodiversity Information Serving Our Nation (BISON; www.bison.usgs.ornl.gov), Berkeley Ecoinformatics Engine (Ecoengine; www.ecoengine.berkeley.edu), and iNaturalist ([www.inaturalist.org](http://www.inaturalist.org)). For all species, we followed the IUCN latest consensus on taxonomy and nomenclature of birds (date of search: October 2018). Online databases were downloaded using the function *occ()* and then collapsed into the same string using the function *fixnames()*, both from the R package *spocc* (Scott *et al.*, 2016). Occurrences for *E. edulis* were complemented with information obtained from the National Center for Flora Conservation (*Centro Nacional de Conservação da Flora -* in portuguese, CNCFlora; cncflora.jbrj.gov.br).

All occurrences were thoroughly assessed and quality-checked for their completeness and reliability. Occurrence records located exactly on centroids of municipalities and political polygons were removed from the dataset, as well as duplicates, incomplete coordinates, and those from museums and herbaria, using the suite of *coord()* functions from R package *scrubr* (Chamberlain, 2016). We cross-checked all bird records and the known extent of occurrence using the IUCN range maps (IUCN, 2019 Downloaded on 09 February 2019). Occurrences further than 200km from the border of species’ IUCN range maps were removed from the dataset. This conservative data-cleaning approach allowed us to only keep reliable occurrence records. To minimize spatial autocorrelation, we further thinned occurrences less than 0.5km from each other, using the function *thin()* from the R package *spThin* (Aiello-Lammens *et al.*, 2015). By doing so, we removed a few records to reduce the effect of clustered sampling, while simultaneously retaining sufficient information for modelling species distributions (Aiello-Lammens *et al.*, 2015). All occurrences are available in the Dryad Digital Repository (LINK WILL BE PROVIDED).

***Bioclimatic predictors***

Climate information for the present and future time-periods (Supplementary Fig. S1b) was obtained from different data sources. The present climate was downloaded from WorldClim version 2 (http://worldclim.org/version2), as gridded files of 1 km² spatial resolution, encompassing climate surfaces for global land areas (Fick & Hijmans, 2017). These data encompass the temporal range of the years 1970–2000 and derive from interpolation of information from 9,000–60,000 weather stations, in addition to thin-plate splines with covariates including satellite information, such as elevation and distance to the coast, performed for different regions of the globe (Fick & Hijmans, 2017). Future climate forecasts were obtained directly from the Data Distribution Centre of the 5th Assessment of the Intergovernmental Panel on Climate Change (IPCC-5, www.ipcc-data.org), as NetCDF (network common data format) files. Such NetCDF data are three-dimensional arrays, containing information on latitude, longitude, and gridded climate forecasts on an annual basis for the years 2006–2099. Climate forecasts rely on prospects of anthropogenic emission rates of greenhouse gases, especially CO2 (IPCC, 2014a), and provide information on surface air maximum temperature (*tasmax*), surface air minimum temperature (*tasmin*), and monthly precipitation (*pr*). These temperature and precipitation values are forecasted according to different emission scenarios.

Climate forecasts from IPCC-5 are based on different types of climate models. These models usually rely on different sets of codes with varying initial parameters, although global estimates are relatively similar (Sanderson *et al.*, 2015). We chose future climate projections from five models known to produce divergent forecasts of temperature and precipitation change (Knutti *et al.*, 2013), namely CESM1-BGC, MPI-ESM-MR, MIROC5, IPSL-CM5A-MR, INMCM4. These models were selected using a stepwise elimination procedure applied to the similarity information from a total of 36 climate models compared by the 5th Coupled Model Intercomparison Project (CMIP5) organized by the Working Group on Coupled Modelling (WGCM) of the World Climate Research Programme’s (WCRP). The five selected climate models, therefore, represent a diverse and skillful subset of the uncertainty in future climate change projections (Sanderson *et al.*, 2015). However, we acknowledge that this procedure removes variation on model projections, so our results should be interpreted as an average of predictions of distinct climate forecasts.

Raw climate data may not be appropriate to represent the environmental conditions that most likely affect the survival and persistence of species in the wild. We therefore transformed the raw climate data into *bioclimatic variables*, derived from monthly temperature and rainfall values but converted into more biologically meaningful variables, such as annual trends, seasonality, and/or extreme climatic events (Hijmans *et al.*, 2005). These variables encompass a wide range of climatic conditions that species likely experience in the field and we used those to characterize the climatic niche of species (described below). To calculate bioclimatic predictors, we used the function *biovars()* from the R package *dismo* (Hijmans *et al.*, 2013), with averages of surface air temperature and precipitation as inputs. Bioclimatic predictors were then calculated for both the present (representing years 1970–2000) and the future (decadal means representing years 2015–2025, 2025–2030, …, 2085–2095).

***Soil predictors***

Although the importance of climate for defining species range limits has strong empirical support (Sexton *et al.*, 2009), plants are also constrained by edaphic features because germination and seedling establishment require suitable soil conditions (Mod *et al.*, 2016). For that reason, the inclusion of soil predictors improves the accuracy of species distribution models for tropical plants (Figueiredo *et al.*, 2018). In addition to the bioclimatic predictors, we therefore incorporated edaphic features (soil predictors) to the distribution models of the palm *Euterpe edulis*. We included soil features known to be ecophysiologically meaningful to plants, namely: absolute depth to bedrock, bulk density, cation exchange capacity, clay content, sand content, soil organic carbon content, and pH(Mod *et al.*, 2016; Figueiredo *et al.*, 2018). These data were obtained from SoilGrids (www.soilgrids.org), which is a 3D worldwide information system on soil properties at different depths (Hengl *et al.*, 2014, 2017). We downloaded soil information from SoilGrids at 1km² spatial resolution for the upper soil layers up to 30cm in depth, which are known to encompass most of the root system of the *Euterpe edulis* palm (Bovi *et al.*, 1978). For each 1km² cell, we derived averages over the 0–30cm depth from the weighted average of the soil features within the depth interval with a numerical trapezoidal rule, as suggested by Hengl *et al.* (2017).

***Ecological niche models***

To establish the relationship between environmental conditions (soil and/or climate) and species occurrences, we fitted ecological niche models to occurrence data (Supplementary Fig. S1c). We maximized the performance of our ecological niche models by limiting species-specific background extents and including only regions that are probably accessible to species via migration (Barve *et al.*, 2011). This was done by limiting the background to a bounding box of the most extreme geographical coordinates from the occurrence records, plus an additional 10 degrees to each boundary, a value close to the predicted maximum dispersal in 100 years for several species (Schloss *et al.*, 2012). Environmental layers were then cropped to adjust them to this study extent and 10,000 background/pseudo-absence points were sampled (one per cell, with no replacement) (Barbet-Massin *et al.*, 2012). For the palm, we then compared ENMs with only the climate predictors or with both climate and soil predictors using the Akaike Information Criterion (AIC) (Akaike, 1974) (Table S1).

Prior to calibrating the models for each species, we tested for multicollinearity among predictor variables (Graham, 2003) using a hybrid approach (Naimi *et al.*, 2014) that involves quantifying the variance inflation factor (VIF) (Marquardt, 1970) and pairwise correlation tests. The approach, implemented in the *usdm* R package (Naimi, 2014), uses a stepwise procedure to measure VIF for all variables, calculates correlations between pairs of variables, and then identifies the pair with the highest correlation value. A specific correlation greater than a certain threshold (here: *r* = 0.6) is a sign of collinearity, and the variable that shows a greater VIF in the pair is then excluded. This procedure was repeated until all strongly correlated variables were excluded, resulting in a total of four to six predictor variables for each species (Supplementary Table 1).

The species distributions predicted from ENMs were evaluated for their accuracy (Supplementary Fig. S1d) using a repeated sub-sampling procedure where 25% of the records were drawn randomly and used to measure the performance of the models fitted using the remaining 75% of the records. This procedure was replicated 100 times for each modelling method and each species. We used two metrics to measure the accuracy: the true skill statistic (TSS) (Allouche *et al.*, 2006), and the area under the receiver operating characteristic curve (AUC) (Fielding & Bell, 1997). While AUC is a threshold-independent metric, measuring TSS relies on selecting a probability of occurrence threshold where a presence is discriminated from an absence. Both AUC and TSS provide a single value of model performance varying from 0 to 1, and -1 to 1, respectively. An AUC value of 0.5 (and a TSS value of 0) implies random discrimination between presence and absence, and the values greater and lower than this value imply a discrimination capacity better and worse than chance, respectively. A value of 1 indicates perfect discrimination by both metrics. For each model, we selected a threshold that maximized TSS (Liu *et al.*, 2005). In addition to measuring TSS, we used this threshold to convert the continuous predictions of habitat suitability into binary (suitable/unsuitable) maps. Our species distribution predictions had overall good accuracy (TSSmean = 0.70 ± 0.07, AUCmean = 0.87 ± 0.04) (Table S1).

We then used an ensemble forecasting procedure to generate a consensus prediction for each species by combining the predictions from different models (Supplementary Fig. S1d, e). We used a weighted mean function for this procedure where the TSS predictive performance was used as the weighting parameter. The idea behind the ensemble approach is that a combined multiple-model prediction is more accurate than at least half of the original models (Araújo & New, 2007) and it reduces uncertainty in regard to model type (Araújo *et al.*, 2019). We used the ENM modelling workflow to forecast the ensemble distribution of each species in the future between the years 2020 and 2090 on a decadal basis (i.e. centered on years 2020, 2030, 2040, etc.). This allowed us to track the climatic niche of each species between successive time intervals (Littlefield *et al.*, 2017).

***Forest loss thresholds***

Forest cover interacts synergistically with climate change to determine climate-driven migrations of species across fragmented landscapes (Sales *et al.*, 2019). In addition to creating migratory routes through which forest specialists might track their changing climates (Lawler *et al.*, 2013), the amount of available forest cover sets habitat thresholds for the persistence of several Neotropical bird species (Melo *et al.*, 2018). Here, we used the percent of forest cover to simulate: 1) the species responses to habitat loss and 2) the barriers to the dispersal of specialist species (Supplementary Fig. S1g, h, i). We used global projections of future tree cover loss based on spatially-explicit forecasts and historical trends on tree cover loss (Hewson *et al.*, 2019). These forest cover projections use a variety of bio- and geophysical characteristics of landscapes, such as biomes and soil drainage, in addition to forest accessibility (e.g. distance to railroads, airports) and agricultural opportunity costs (such as distance to markets, economic rents for croplands, etc.), with observed historical trends of forest loss from years 2000 to 2014, to explain the cell-based land-use transition. These models forecast tree cover loss for the next 15 years, assuming a *Business-as-usual* scenario of tree cover loss (Hewson *et al.*, 2019).

We focused on the projected distribution of tree cover for the year 2030. We did not consider further land use changes until 2090 because land-use and land-cover are affected by decisions and political agendas that are difficult to predict. In Brazil, recent political decisions led to a turnaround of environmental law regarding protected areas and riparian vegetation (Abessa *et al.*, 2019), dramatically affecting trends on deforestation and land conversion, so that the future of forests is now even more uncertain and unpredictable (Ferrante & Fearnside, 2019). We, therefore, took a conservative approach and assumed that the observed trends of forest cover loss of the recent past will continue to drive forest loss in the near future (2030), assuming no further forest loss between the years 2030 and 2090.

To simulate response thresholds of species to forest loss, we converted the 1km² binary raster file of the presence/absence of tree cover into the percent of tree cover remaining at a 10km² resolution (landscape scale). We thus created a 10km² resolution file containing the expected percent of forest cover remaining in the year 2030 for each grid cell across the whole of South America because several frugivores have geographic distributions that extend beyond the Atlantic forest of Brazil. The cell size of 10km² was chosen because some of the large-bodied Neotropical frugivorous birds threatened by extinction require at least this amount of forest cover to hold viable populations (Bonfim *et al.*, 2019). This cell size is, thus, a good proxy for the minimum habitat requirements of these species. For each species, we applied habitat thresholds of response to the loss of forest cover, according to species-specific knowledge about habitat preferences and responses to habitat fragmentation in the Atlantic forest. Habitat preferences of frugivorous birds were obtained from several books and other sources (Stotz *et al.*, 1996; Hoyo *et al.*, 2015; Vale *et al.*, 2018; IUCN, 2019). Our classification of habitat preference was based on forest cover because the palm *Euterpe edulis* requires preserved forests to hold viable populations (Pizo & Simão, 2001; De Barros Leite *et al.*, 2012). Therefore, within our study frugivore subset, if a bird species occurs exclusively in forest-like habitats it was assigned as a *forest specialist*. If a bird also occurs in open habitat (e.g. savanna, shrubland, grassland, wetlands, and artificial terrestrial environments), it was assigned as a *generalist*.

In addition to these habitat preferences, we used the conservation status from the national red list (Brazil Red Book of Threatened Species of Fauna (2016)) and the international red list (The IUCN Red List of Threatened Species (2019)) to classify species into several response groups. Our classification scheme, therefore, included habitat use type and the known vulnerability of species to forest loss, as a function of the category of the threat of each species, and encompassed: (i) *extreme forest specialists*; (ii) *moderate forest specialists*; and (iii) *habitat generalists* (Supplementary Fig. S2). Extreme forest specialists were those forest specialists that are threatened, i.e. critically endangered (CR), endangered (EN), or vulnerable (VU), by either the national or international red list. This included species such as the large-bodied frugivores *Crax blumenbachii* (Red-billed Curassow) and the *Pipile jacutinga* (Black-fronted Piping-Guan).

As a conservative estimate, we considered those extreme forest specialists to require at least 50% forest cover in a 10km² landscape (Bonfim *et al.*, 2019). These species are targeted for hunting in landscapes with less forest cover (Galetti *et al.*, 2013; Bovo *et al.*, 2018) and their persistence is usually restricted to landscapes with high forest cover, such as the largest Atlantic forest remnants of the Serra do Mar and Serra do Espinhaço (Hasui *et al.*, 2018). We considered moderate forest specialists to be those forest specialists that are currently not threatened according to the national or international red list of threatened species, i.e. birds classified as near threatened (NT) and least concern (LC). This included most medium-sized species such as toucans and toucanets. These species are usually able to tolerate some degree of habitat fragmentation but are depleted from landscapes with less than 30% forest cover (Boesing *et al.*, 2018; Melo *et al.*, 2018; Martensen *et al* 2012; Crouzeilles *et al*, 2014). Finally, we considered habitat generalists to be species that can thrive in other than forest-like habitats and which are not considered threatened by the national and international red list of threatened species. Thresholds of tree cover were not applied for those generalists because most of them are able to survive and reproduce in human-dominated landscapes regardless of tree cover (Galetti *et al.*, 2013; Boesing *et al.*, 2018; Bovo *et al.*, 2018).

The effect of thresholds of forest loss on the persistence of frugivorous birds was then simulated by overlaying the predictions of climate suitability of each species (i.e. decadal binary maps derived from ecological niche models) onto the resulting gridded file of minimum forest cover (calculated from species-specific forest cover thresholds). Cells with unfavorable climate conditions and/or cells with less than the minimum forest cover required for species persistence were both attributed as “unsuitable”. Hence, each cell predicted as “suitable” for a species exhibited suitable climate conditions and had enough forest cover to sustain viable populations of the bird. These suitable cells, however, may be out of reach of current populations if a species cannot disperse to these areas. We, therefore, simulated the dispersal of each species on top of climate suitability and habitat thresholds of each grid cell (see below).

***Dispersal-restricted potential distribution of frugivores***

To allow for a spatially-explicit simulation of climate-driven movements of frugivorous birds within fragmented landscapes, we additionally simulated dispersal constraints among occupied grid cells (Supplementary Fig. S1i). We did this by simulating the dynamics of occupied cells (i.e. those with suitable climate and minimum forest cover, see above) across space (with a spatial resolution of 10km² cell size) and time (with a temporal resolution of decadal time steps) using a cellular automata model. The initial distribution of each species was defined by the set of occupied cells at time *t*initial. The dynamics of occupancy for each species were then defined by the projected environmental niche (based on climatic suitability and habitat thresholds) and the species’ ability to colonize newly suitable environments. Occupied cells remained occupied by a particular species when the projected environmental conditions remained suitable across decadal time steps (*t*initial, *t* +1, *t* + 2, …, *t*final). In cases when the environment (of a grid cell) became unsuitable, occupied cells were decolonized and became empty. Colonization of empty target cells could occur if (i) the cell became suitable at a given time step, and (ii) barriers did not prevent the movement from a potential source cell. Hence, an unsuitable cell in time *t* (target) could be colonized if environmental conditions (climate, forest cover) became suitable in time *t+1* and if it was within the reach of a suitable (source) cell (Engler *et al.*, 2012). This required the definition of species-specific dispersal abilities and potential barriers for dispersal within fragmented landscapes (see below).

From an animal’s perspective, the absence of trees can be a barrier to dispersal, depending on species ability to move across open or fragmented landscapes (Tucker *et al.*, 2019). Here, we use Hewson et al (2019)’s model of tree cover, idem as explained in the previous section *Forest loss thresholds*. In the context of this cellular automatamodel, barrier cells can be defined as being permanently unsuitable and hampering dispersal across the landscape (Engler *et al.*, 2012). Since the absence of trees does not affect species movement equally across species(Tucker *et al.*, 2019), we distinguished the effect on *extreme forest specialists* (which may rely heavily on trees to move across landscapes) from that on *moderate forest specialists* (which may eventually cross open areas) (Bovo *et al.*, 2018). Hence, the absence of trees was considered a strong barrier to the dispersal of *extreme forest specialists*, for which simulated dispersal kernels only allowed movement between adjacent suitable cells. However, the absence of trees was considered only a weak barrier to the dispersal of *moderate forest specialists*, where we allowed movement across two diagonally adjacent barrier pixels, so that no distance greater than two consecutive barrier cells could be crossed (Engler *et al.*, 2012). These dispersal constraints were applied stepwise to all decadal files containing information on occupied cells, i.e. from the present (initial distribution) to the future (the year 2090) using the 10-year projections of suitable climates and forest cover for each species (Supplementary Fig. S1k). Note that the suitability of an area for the frugivore is not assumed to be conditional on the suitability for the palm, since none of these frugivore species are dependent exclusively on *E. edulis.*

The outcome of this cellular automaton model is a map of potential distribution restricted by dispersal, where cells can be partitioned according to occupancy dynamics. We defined *climate refugia* cells as those projected to be suitable and occupied in both the present and future. *Potential migration* cells were those cells that became newly suitable (in time *t+1*) and which were also accessible via dispersal from source cells (from previous time steps). Cells that became suitable but not accessible were defined as *dispersal limitation* cells. Finally, we defined *local extirpation* cells as those that were suitable in the present but became unsuitable in the future, i.e. areas that expose current populations to future climatic conditions that likely exceed the amplitude and seasonality to which species populations are currently adapted to (Williams & Jackson, 2007; Ribeiro *et al.*, 2016).

***Palm seed dispersal scenarios***

For frugivores, we considered species’ movements in response to environmental change as a result of their own physiological tolerance and climatic niche tracking (Tingley *et al.*, 2009; La Sorte & Jetz, 2012). However, in sessile organisms like plants, seed dispersal is the only mechanism by which plants track their changing environments (González-Varo *et al.*, 2017). To incorporate the effect of seed dispersers on the colonization of analog climates of the palm tree *Euterpe edulis*, we created two dispersal scenarios, namely *passive* and *frugivore-based* dispersal. In the *passive* dispersal scenario, palm populations can only persist where they are not exposed to non-analog climates (*climate refugia* cells). The rationale behind this approach is that non-zoochorous seed dispersal mechanisms restrict seed deposition to a 100–250m radius, as suggested by the structure of genetic differentiation (Carvalho *et al.*, 2015) and seedling recruitment (Pizo *et al.*, 2006) in palm populations of defaunated sites, which is smaller than the 1km² size of our cell. Thus, whenever fruits are not carried away by frugivores, it is likely that palm seeds remain in the same cell in the consecutive time step. Therefore, cells forecasted to be suitable in the future were only projected to remain occupied if the cell was already occupied in previous time steps.

In the *frugivore-based* dispersal scenario, we simulate the effect of frugivores on the colonization of novel climates by the palm. To do so, we assume that co-occurrence precedes the biotic interaction, by projecting pairwise shared environmental correlations into geographical space (Colwell & Rangel, 2009). In other words, we superimposed the map of the potential distribution of each frugivore to the palm distribution, within the same time step (centered on years 2020, 2030, …, 2090). These spatial matches defined suitable conditions for both partners and where the biotic interaction could take place if dispersal limitations did not prevent occupancy. Then, we applied frugivore-specific dispersal constraints into that shared unit, because the frugivores are the agents of dispersal or the ones who actively navigate through the landscape.

***Model assumptions***

Our models assume that seed dispersers can only effectively disperse the seeds of the palm tree from source to target cells if these cells are suitable for both species, according to dispersal limitations defined by the perspective of the movement agent (i.e. the animal). In addition, we assume that the colonization of analog climates by the palm tree is an opportunistic event at a macroecological scale, resulting from the climatic niche tracking by the seed disperser itself. Therefore, our model assumes a mechanistic redundancy on the response of interacting species to climate change, so that: i) species-specific responses to climate change are driven by physiological tolerances and dispersal-mediated climate niche tracking (i.e. *climate change affects species distributions*); but ii) seed dispersal at a geographical scale affects colonization patterns of the least-mobile interaction partner (i.e. *biotic interactions affect species response to climate change*).

***Evolution of seed size***

To evaluate the potential evolutionary consequences of novel frugivore assemblages for seed size evolution of the palm *Euterpe edulis*, we simulated the selection each frugivore could pose on seed size over time. (Supplementary Fig. S1). To do so, we combined genetic information on seed size heritability from previous work (Galetti *et al.*, 2013) with a simple evolutionary model of trait evolution. The expected evolutionary changes in seed size were thus modeled as:

*Zt*+*1*= *Zt* + *h2* (*Pf* - *Zt*)

in which *Zt* is the expected maximum seed size at generation t, *h2* is the mean heritability of seed size, *Pf* is the maximum seed size each frugivore species can swallow, given gape size allometric limitations, and *h2* (*P* - *Zt*) is the response to selection at generation *t*. Mean heritability of seed size (*h2* = 0.35) was obtained from Galetti *et al*. (2013), who estimated it from the relationship between seed size and genetic relatedness among palms, controlling for environmental patchiness under isolation by-distance assumptions. We focus on maximum seed size because small frugivore species cannot disperse the large seeds, whereas large frugivore species can ingest and disperse seeds of varying sizes. Therefore, selection acts against the large seeds constraining the large end of the seed size distribution. The known generation time of 18.7 years for this palm (Franco & Silvertown, 2004) was used to parameterize the simulation time frame. We acknowledge that seed size is subjected to multiple evolutionary pressures related to environmental factors and other types of interactions (REF). Thus, our simulations are not aimed at providing estimates of the future seed size but to explore the potential differences in the pressures exerted over seed size by the varying frugivore assemblages occurring across the palm distribution.

Empirical data on ingested seed size were only available for a subset of frugivores (*n* = 7) that disperse the palm *Euterpe edulis*. However, it is known that several morphological traits are phylogenetically preserved in birds (Böhning-Gaese & Oberrath, 1999), including forage-related cranial attributes, so that dietary niche shapes the tempo and mode of phenotypic evolution in birds (Felice *et al.*, 2019). We therefore assumed that the trait of interest (i.e. the maximum seed size each bird can ingest) is phylogenetically preserved due to allometric constraints on gape size and used, phylogenetic imputation, a powerful tool for dealing with missing information in functional trait datasets (Molina-Venegas *et al.*, 2018) to infer maximum ingested seed sizes (*Pf*) for the remaining species. We built phylogenetic eigenvector maps using the bird phylogenetic tree proposed by Jetz *et al* (2012). Phylogenetic eigenvector maps allow transforming phylogenetic relationships of trait values into explanatory variables (eigenvectors), which can then be used to model trait values for target species (Guénard *et al.*, 2013). Target species are those for which trait values are unknown, but whose position within the phylogeny of the group is known, so that phylogenetic eigenvector maps allow estimating trait values for those species with missing data (Guénard *et al.*, 2013). The resulting scores enable empirical predictions of trait values for the target species, based on the observed trait values for the species in the phylogeny (Table S3). Here, we used the maximum seed size ingested by seven seed disperser bird species (Galetti *et al.*, 2013), in addition to their time-calibrated position in the phylogeny (Jetz *et al.*, 2012), as our training dataset, to estimate the trait values for the remaining 25 target bird species for which measurements of the ingested maximum seed size are missing. Phylogenetic eigenvector maps were estimated using the *MPSEM* R package (Guenard & Legendre, 2013).

***Hotspots of selective pressure for the reduction of seed size***

The expected selection effect of individual frugivorous birds (in future assemblages) on seed size of the palm (*Zfi*) was calculated as the difference between the initial maximum seed size (*Zt* = 12.8mm, i.e. the average seed size in non-defaunated sites (Galetti *et al.*, 2013)) and the final maximum seed size (see below) expected for each local palm “population” (i.e. within a grid-cell) under size-specific selection using:

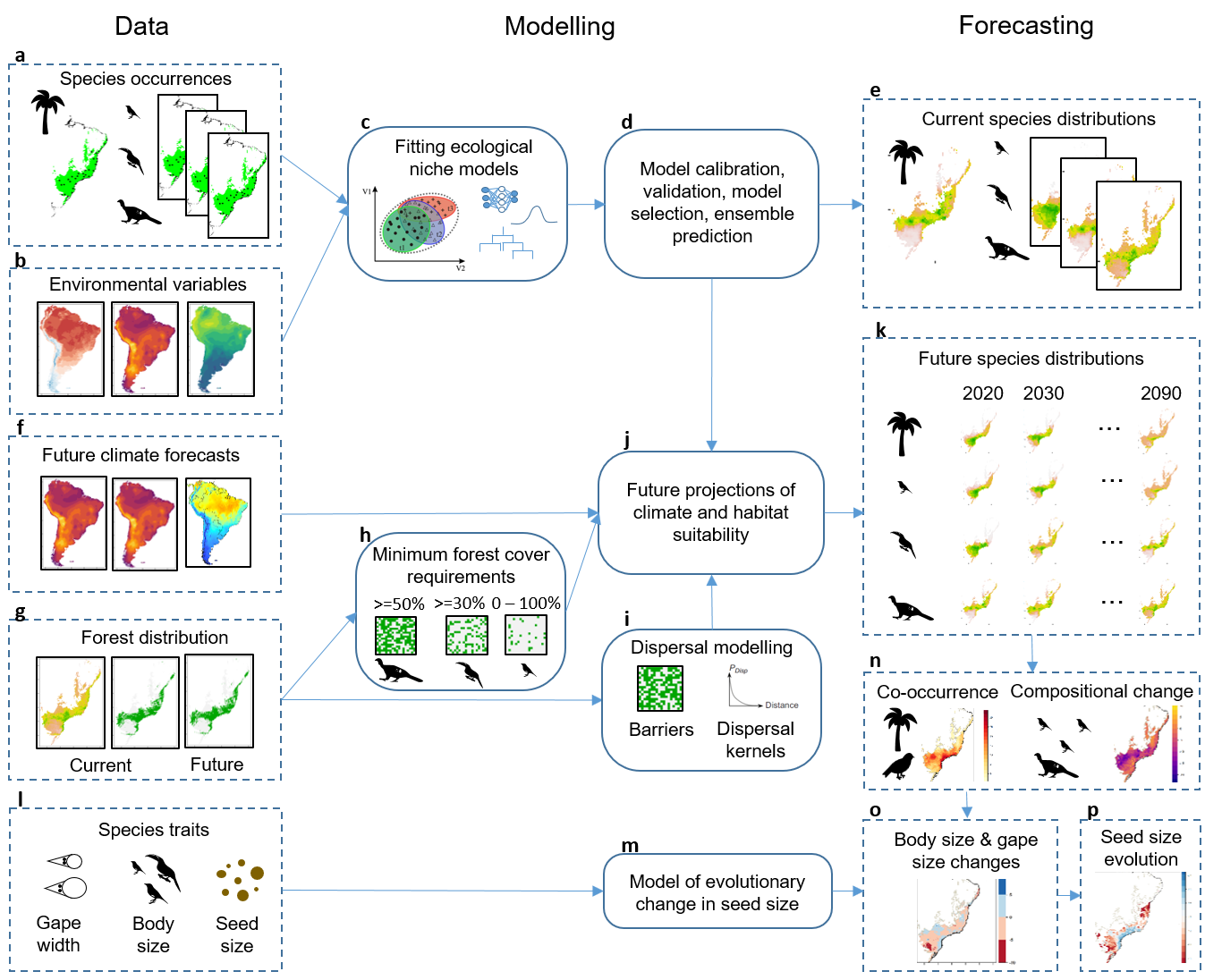
*Zfi* = (*Zt**- Zt*+*n*) × *f*

where *Zt* is the initial seed size and *Zt*+*n* is the expected seed size after *n* generations of the palm and under selection by frugivore *i* (Supplementary Fig. S1m). Negative values thus indicate the magnitude of potential selection towards smaller seed sizes, considering the initial maximum seed size found in most non-defaunated areas (12.8mm) (Galetti *et al.*, 2013). In addition, we weighted the expectations of change in seed size by *f*, a “frugivory score” based on the relative contribution of fruits to each bird’s diet, whose values range from 1 (sporadic frugivory), 2 (moderate frugivory) to 3 (extensive frugivory). This model therefore assumes that gape size limitations of frugivorous birds in a local community can cause a directional selective force on palm seed (as empirically suggested by Galetti et al. 2013), weighted by the impact of frugivory intensity on food resources (i.e. the reliance of a frugivore on fruits of *Euterpe edulis*). To quantify the overall trend on seed size evolution in a given grid cell, and as the result of climate-driven redistributions of frugivorous seed dispersers, we averaged the *Zf* value of all species (weighted by their frugivory score) that were present in novel assemblages, i.e. based on the species composition of frugivores in the final grid cells (the year 2090). In other words, the resulting selection force on seed size (Ƭ), for every cell, was the sum the *Zfi* of the species predicted to occur in each cell, divided it by the sum of their *f* values, as in:

Ƭ=

We finally highlight especially those regions that are expected to suffer the greatest reductions in seed size as a function of the redistribution of seed dispersers, i.e. hotspots of selective pressure (Supplementary Fig. S1p). The contribution of each frugivore species to selection certainly depends on species abundances. Yet, there is not enough information or well-grounded methods to reliably estimate abundances for these frugivore species across space and over time. Therefore, these estimates offer only a baseline that would certainly be altered by differences in relative abundance. Because the smaller-sized frugivore species considered here tend to be locally more abundant than the large ones, our estimates are conservative and the pressure for reducing seed size is likely greater in magnitude than these baseline estimates we report here.

Supplementary Figures



**Supplementary Fig. S1. Summary of the workflow representing key parts related to data preparation, modelling, and forecasting.** Species occurrences (a) and, soil and/or current climate variables (b) were used in ecological niche models (c) which, after calibration, validation, and ensemble procedures (d), allowed predicting current species distributions (e). The combination of future climate forecasts (f) and tree cover (g) (via minimum forest cover requirements; h), while incorporating landscape barriers (i) allowed to make future projections of the climate and habitat suitability of species (j), allowing the forecast of future species distributions for both the palm and its animal seed dispersers (k). In addition, species traits (l) and a model of evolutionary change in seed size (m), via changes in the forecasted composition and co-occurrence of species in novel assemblages (n) allowed to estimate the changes in body mass and gape size of novel frugivore communities (o) and subsequently to make spatially-explicit predictions of seed size evolution (p).

Uma imagem contendo pássaro, rebanho, em pé, livro

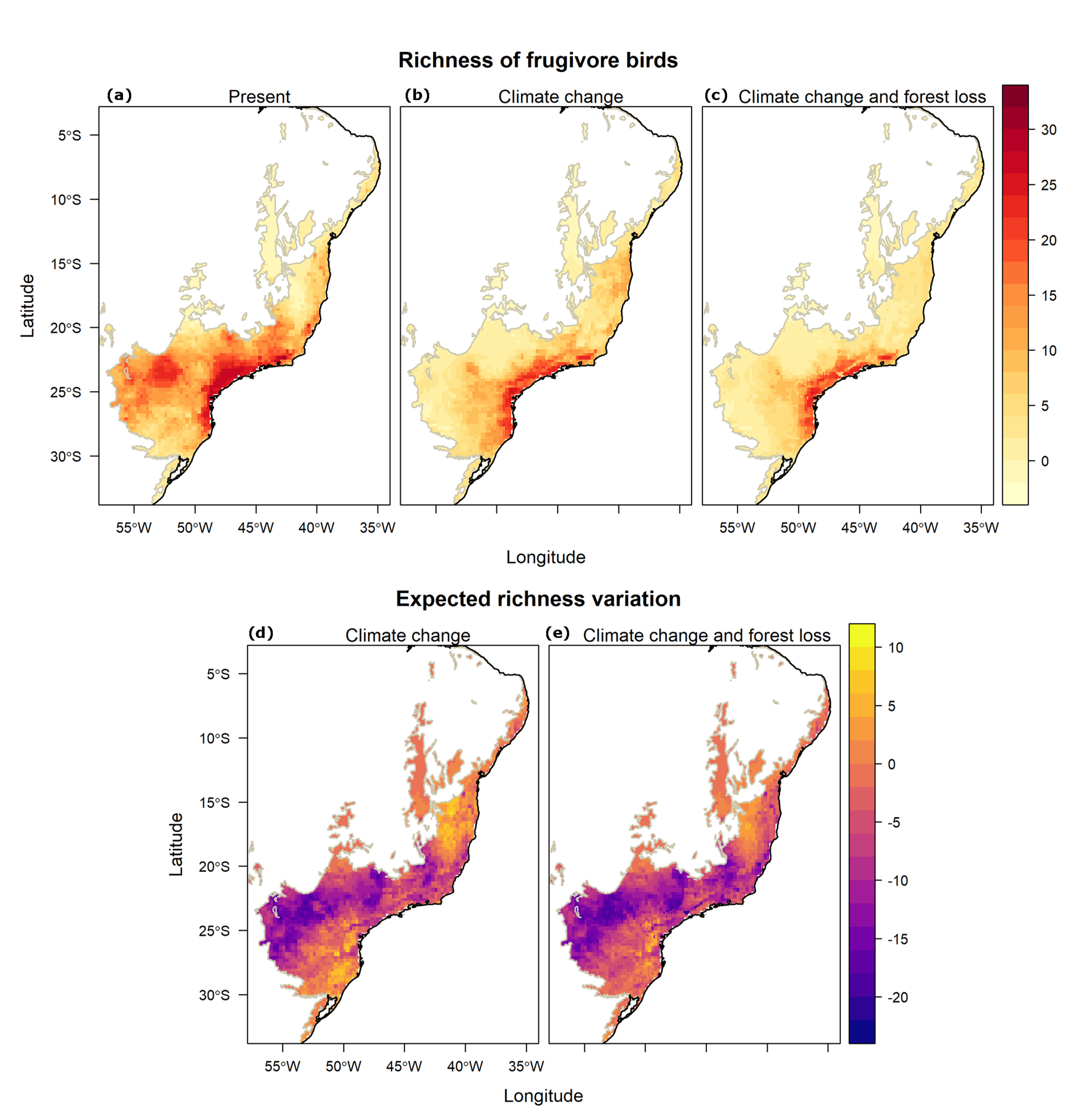
Descrição gerada automaticamente

**Supplementary Fig. S2.** Frugivorous bird species that disperse the seeds of the palm *Euterpe edulis*. From a total of 32 effective and legitimate dispersers. In reading order, species are: *Myiodynastes solitarius* (Chalk-browed Mockingbird)*, Pitangus sulphuratus* (Great Kiskadee)*, Carpornis cucullate* (Hooded Berryeater)*, Carpornis melanocephala* (Black-headed Berryeater)*, Procnias nudicollis* (Bare-throated Bellbird)*, Mimus saturninus* (Chalk-browed Mockingbird)*, Lipaugus lanioides* (Cinnamon-vented Piha)*, Lipaugus vociferans* (Screaming Piha)*, Lipaugus ater* (Black-and-gold Cotinga)*, Pyroderus scutatus* (Red-ruffed Fruitcrow)*, Baryphthengus ruficapillus* (Rufous-capped Motmot)*, Celeus flavescens* (Blond-crested Woodpecker)*, Tityra braziliensis* (Black-tailed Tityra)*, Turdus amaurochalinus* (Creamy-bellied Thrush)*, Turdus flavipes* (Yellow-legged Thrush)*, Turdus leucomelas* (Pale-breasted Thrush)*, Trogon rufus* (Black-throated Trogon)*, Trogon surrucura* (Surucua Trogon)*, Trogon viridis* (White-tailed Trogon)*, Selenidera maculirostris* (Spot-billed Toucanet)*, Ramphastos ariel* (Ariel Toucan)*, Ramphastos dicolorus* (Red-breasted Toucan)*, Pteroglossus aracari* (Black-necked Aracari)*, Pteroglossus bailloni* (Saffron Toucanet)*, Turdus subalaris* (Eastern Slaty Thrush)*, Turdus rufiventris* (Rufous-bellied Thrush)*, Turdus albicollis* (White-necked Thrush)*, Pipile jacutinga* (Black-fronted Piping-Guan)*, Crax blumenbachii* (Red-billed Curassow)*, Penelope obscura* (Dusky-legged Guan)*, Penelope superciliaris* (Rusty-margined Guan)*,* and *Aramides cajaneus* (Gray-necked Wood-Rail).

Pássaro colorido num galho mato no fundo

Descrição gerada automaticamente com confiança baixa

**Supplementary Fig. S3.** The palm *Euterpe edulis* and some of its seed dispersers consuming the palm’s fruits. *Ramphastos dicolorus*, *Ramphastos vitellinus*, *Pipile jacutinga*, *Pyroderus scutatus*, *Turdus flavipes*, *Turdus rufiventris*. Photos by Mathias Pires.

**Supplementary Fig. S4.** Expected distribution of the species richness of frugivores of the palm Euterpe edulis, under a business-as-usual scenario of climate change. Upper panels indicate frugivore richness in (a) the present, (b) year 2090, under climate change alone, and (c) under climate change plus forest loss. Lower panels indicate expected richness change, i.e., the difference between present-day and projected future richness of frugivores for (e) climate change alone and (f) climate change plus forest loss.

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Supplementary Tables

**Supplementary Table S1: Summary of ecological characteristics of the frugivore species studied here.** Behavior indicates whether a species regurgitates (reg) or defecates (def) the ingested seed. Body mass is given in grams (g) and Gape Size in millimeters (mm). Frugivory score relates to the trophic dependency of species on fruits (1 = sporadic, 2 = moderate, and 3 = extensive frugivory). The acronyms IUCN and ICMBio refer to the conservation status as defined by the International Union for the Conservation of Nature and the Chico Mendes Institute for Biodiversity Conservation, respectively (LC = least concern, NT = near threatened, VU = vulnerable, EN = endangered, CR = critically endangered). Classification is the final functional grouping related to the conservation status and forest dependency (ext = Extreme forest specialist, mod = Moderate forest specialist and gen = Generalist)

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species binomial | Common name | Behavior | Body Mass  (g) | Gape Size  (mm) | Frugivory  Score | IUCN | ICMBio | Classification |  |
| *Aramides cajaneus* | Gray-necked Wood-Rail | reg | 397 | 16 | 1 | LC | LC | gen |  |
| *Baryphthengus ruficapillus* | Rufous-capped Motmot | reg | 175 | 17 | 1 | LC | LC | mod |  |
| *Carpornis cucullata* | Hooded Berryeater | reg | 76 | 14 | 3 | NT | LC | mod |  |
| *Carpornis melanocephala* | Black-headed Berryeater | reg | 64 | 17 | 3 | VU | VU | ext |  |
| *Celeus flavescens* | Blond-crested Woodpecker | reg | 201 | 13 | 1 | LC | LC | gen |  |
| *Crax blumenbachii* | Red-billed Curassow | def | 3500 | 26 | 2 | EN | CR | ext |  |
| *Lipaugus ater* | Black-and-gold Cotinga | reg | 80 | 15 | 3 | NT | LC | mod |  |
| *Lipaugus lanioides* | Cinnamon-vented Piha | reg | 95 | 19 | 3 | NT | NT | mod |  |
| *Lipaugus vociferans* | Screaming Piha | reg | 69 | 18 | 3 | LC | LC | mod |  |
| *Mimus saturninus* | Chalk-browed Mockingbird | reg | 73 | 13 | 1 | LC | LC | gen |  |
| *Myiodynastes solitarius* | Chalk-browed Mockingbird | reg | 46 | 17 | 1 | LC | LC | gen |  |
| *Penelope obscura* | Dusky-legged Guan | def | 960 | 23 | 3 | LC | LC | mod |  |
| *Penelope superciliaris* | Rusty-margined Guan | def | 850 | 20 | 3 | LC | LC | mod |  |
| *Pipile jacutinga* | Black-fronted Piping-Guan | def | 1250 | 24 | 3 | EN | EN | ext |  |
| *Pitangus sulphuratus* | Great Kiskadee | reg | 61 | 16 | 1 | LC | LC | gen |  |
| *Procnias nudicollis* | Bare-throated Bellbird | reg | 174 | 25 | 3 | VU | NT | ext |  |
| *Pteroglossus aracari* | Black-necked Aracari | reg | 232 | 29 | 3 | LC | LC | mod |  |
| *Pteroglossus bailloni* | Saffron Toucanet | reg | 139 | 24 | 3 | NT | NT | mod |  |
| *Pyroderus scutatus* | Red-ruffed Fruitcrow | reg | 357 | 27 | 3 | LC | LC | mod |  |
| *Ramphastos ariel* | Ariel Toucan | reg | 362 | 31 | 3 | VU | LC | ext |  |
| *Ramphastos dicolorus* | Red-breasted Toucan | reg | 400 | 31 | 3 | LC | LC | mod |  |
| *Selenidera maculirostris* | Spot-billed Toucanet | reg | 160 | 25 | 3 | LC | LC | mod |  |
| *Tityra braziliensis* | Black-tailed Tityra | reg | 68 | 19 | 2 | LC | LC | mod |  |
| *Trogon rufus* | Black-throated Trogon | reg | 53 | 18 | 1 | LC | LC | mod |  |
| *Trogon surrucura* | Surucua Trogon | reg | 73 | 18 | 1 | LC | LC | mod |  |
| *Trogon viridis* | White-tailed Trogon | reg | 88 | 20 | 2 | LC | LC | mod |  |
| *Turdus albicollis* | White-necked Thrush | reg | 54 | 11 | 2 | LC | LC | gen |  |
| *Turdus amaurochalinus* | Creamy-bellied Thrush | reg | 63 | 11 | 2 | LC | LC | gen |  |
| *Turdus flavipes* | Yellow-legged Thrush | reg | 60 | 12 | 2 | LC | LC | mod |  |
| *Turdus leucomelas* | Pale-breasted Thrush | reg | 69 | 12 | 2 | LC | LC | gen |  |
| *Turdus rufiventris* | Rufous-bellied Thrush | reg | 70 | 12 | 2 | LC | LC | gen |  |
| *Turdus subalaris* | Eastern Slaty Thrush | reg | 50 | 12 | 2 | LC | LC | mod |  |

**Supplementary Table S2: Expected range shift for the main seed dispersers of the palm tree *Euterpe edulis*, as a function climate change, forest loss and dispersal constraints.** Range shifts were estimated as proportional change in the number of cells predicted as suitable. We used a combination of ecological niche models, calibrated with climatic data, to which habitat thresholds and dispersal simulation models were incorporated as additional layers into predictions of species potential distribution. IniDist indicates species current potential distribution (in number of suitable cells). Subsequent values indicate expected % variation in suitable potential distribution, as well as the absolute number of suitable cells, under different future scenarios. Large-bodied indicates that species body mass is > 400g. Forest specialist indicates whether the species occurs only in forest-like habitats (1 = forest specialist) or also occupies open and artificial habitats (0 = not a forest specialist).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species binomial | IniDist | Climate change | | | | | |  | Climate change, forest loss and dispersal constraints | | | | | Large-bodied | Forest-specialist |
|  |  | Mitigation | |  | B.A.U. | |  |  | Mitigation | |  | B.A.U. | |  |  |
|  |  | % | Abs |  | % | Abs |  |  | % | Abs |  | % | Abs |  |  |
| *Aramides cajaneus* | 39097 | 0.02 | 39936 |  | 0.07 | 41925 |  |  | 0.02 | 39936 |  | 0.07 | 41925 | 0 | 0 |
| *Baryphthengus ruficapillus* | 5195 | -0.28 | 3755 |  | -0.51 | 2566 |  |  | -0.71 | 1502 |  | -0.75 | 1309 | 0 | 1 |
| *Carpornis cucullata* | 1387 | 1.06 | 2862 |  | 0.67 | 2316 |  |  | -0.25 | 1034 |  | -0.45 | 768 | 0 | 1 |
| *Carpornis melanocephala* | 797 | -0.25 | 596 |  | -0.53 | 375 |  |  | -0.8 | 156 |  | -0.94 | 51 | 0 | 1 |
| *Celeus flavescens* | 5451 | 0.01 | 5487 |  | 0.38 | 7527 |  |  | 0.01 | 5487 |  | 0.38 | 7527 | 0 | 0 |
| *Crax blumenbachii* | 135 | -0.64 | 27 |  | -0.8 | 49 |  |  | -1 | 0 |  | -1 | 0 | 1 | 1 |
| *Lipaugus ater* | 265 | -0.84 | 43 |  | -1 | 0 |  |  | -1 | 0 |  | -1 | 0 | 0 | 1 |
| *Lipaugus lanioides* | 1649 | -0.02 | 1609 |  | 0.04 | 1707 |  |  | -0.45 | 905 |  | -0.51 | 810 | 0 | 1 |
| *Lipaugus vociferans* | 5993 | -0.55 | 2724 |  | -0.98 | 137 |  |  | -0.94 | 377 |  | -1 | 14 | 0 | 1 |
| *Mimus saturninus* | 22247 | -0.29 | 15896 |  | -0.46 | 12001 |  |  | -0.29 | 15896 |  | -0.46 | 12001 | 0 | 0 |
| *Myiodystes solitarius* | 13247 | -0.29 | 9343 |  | 0.52 | 20168 |  |  | -0.29 | 9343 |  | 0.52 | 20168 | 0 | 0 |
| *Penelope obscura* | 5268 | -0.14 | 4516 |  | -0.51 | 2574 |  |  | -0.72 | 1461 |  | -0.75 | 1292 | 1 | 1 |
| *Penelope superciliaris* | 9689 | -0.17 | 8062 |  | -0.71 | 2845 |  |  | -0.84 | 1587 |  | -0.94 | 618 | 1 | 1 |
| *Pipile jacutinga* | 2224 | -0.55 | 1001 |  | -0.42 | 1297 |  |  | -0.81 | 428 |  | -0.77 | 512 | 1 | 1 |
| *Pitangus sulphuratus* | 41313 | -0.08 | 37976 |  | -0.42 | 23970 |  |  | -0.08 | 37976 |  | -0.42 | 23970 | 0 | 0 |
| *Procnias nudicollis* | 4737 | 0.5 | 7116 |  | 0.66 | 7860 |  |  | -0.64 | 1712 |  | -0.66 | 1608 | 0 | 1 |
| *Pteroglossus aracari* | 4085 | 0.25 | 5104 |  | 0.72 | 7039 |  |  | -0.77 | 936 |  | -0.78 | 914 | 0 | 1 |
| *Pteroglossus bailloni* | 3091 | 0.97 | 6076 |  | 0.54 | 4770 |  |  | -0.46 | 1672 |  | -0.55 | 1394 | 0 | 1 |
| *Pyroderus scutatus* | 8692 | -0.09 | 7887 |  | -0.44 | 4826 |  |  | -0.64 | 3159 |  | -0.72 | 2461 | 0 | 1 |
| *Ramphastos ariel* | 2166 | 0.65 | 3565 |  | 0.3 | 2806 |  |  | -0.27 | 1591 |  | -0.57 | 923 | 0 | 1 |
| *Ramphastos dicolorus* | 5058 | -0.01 | 4990 |  | -0.55 | 2297 |  |  | -0.57 | 2193 |  | -0.62 | 1945 | 0 | 1 |
| *Selenidera maculirostris* | 2209 | 0.11 | 2459 |  | -0.54 | 1026 |  |  | -0.72 | 626 |  | -0.86 | 308 | 0 | 1 |
| *Tityra braziliensis* | 9153 | -0.27 | 6659 |  | -0.54 | 4232 |  |  | -0.74 | 2414 |  | -0.8 | 1830 | 0 | 1 |
| *Trogon rufus* | 6487 | -0.19 | 5247 |  | -0.49 | 3276 |  |  | -0.88 | 803 |  | -0.84 | 1063 | 0 | 1 |
| *Trogon surrucura* | 10175 | -0.26 | 7481 |  | -0.78 | 2270 |  |  | -0.6 | 4077 |  | -0.83 | 1721 | 0 | 1 |
| *Trogon viridis* | 20234 | 0.06 | 21548 |  | -0.38 | 12539 |  |  | -0.23 | 15637 |  | -0.6 | 8065 | 0 | 1 |
| *Turdus albicollis* | 9174 | 0.13 | 10395 |  | -0.03 | 8873 |  |  | 0.13 | 10395 |  | -0.03 | 8873 | 0 | 0 |
| *Turdus amaurochalinus* | 10186 | -0.35 | 6650 |  | -0.61 | 4019 |  |  | -0.35 | 6650 |  | -0.61 | 4019 | 0 | 0 |
| *Turdus flavipes* | 2509 | 0.53 | 3851 |  | 0.37 | 3441 |  |  | -0.3 | 1763 |  | -0.46 | 1346 | 0 | 1 |
| *Turdus leucomelas* | 13895 | -0.33 | 9376 |  | -0.74 | 3665 |  |  | -0.33 | 9376 |  | -0.74 | 3665 | 0 | 0 |
| *Turdus rufiventris* | 12195 | -0.05 | 11550 |  | -0.27 | 8849 |  |  | -0.05 | 11550 |  | -0.27 | 8849 | 0 | 0 |
| *Turdus subalaris* | 6905 | -0.61 | 2667 |  | -0.95 | 351 |  |  | -0.83 | 1190 |  | -0.97 | 185 | 0 | 1 |

**Supplementary Table S3: Accuracy of species distribution models of the frugivorous birds that effectively disperse seeds of the palm *Euterpe edulis*.** Models were calibrated with climatic information across species ranges, using occurrence records. AUC is the area under the receiver operation curve, TSS is the true skills statistic, both are the mean value over 100 replications through the sub-sampling procedure calculated based on the test dataset:

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Species binomial |  | # records |  | AUC |  | TSS |  | Predictors\* | | | | | | |
| *Euterpe edulis* | |  |  |  |  |  |  |  |  |  |  |  |  |  |
| climate+soil | | 575 |  | 0.84 |  | 0.64 |  | BIO8 | BIO13 | BIO19 | BDTICM | ORCDRC | SNDPPT |  |
| climate-only | | 575 |  | 0.83 |  | 0.57 |  | BIO2 | BIO8 | BIO13 | BIO19 |  |  |  |
| *Aramides cajaneus* | | 201 |  | 0.81 |  | 0.61 |  | BIO2 | BIO3 | BIO8 | BIO13 | BIO14 | BIO18 |  |
| *Baryphthengus ruficapillus* | | 407 |  | 0.92 |  | 0.81 |  | BIO2 | BIO4 | BIO6 | BIO13 | BIO18 |  |  |
| *Carpornis cucullata* | | 314 |  | 0.92 |  | 0.8 |  | BIO2 | BIO7 | BIO9 | BIO13 |  |  |  |
| *Carpornis melanocephala* | | 253 |  | 0.84 |  | 0.66 |  | BIO7 | BIO8 | BIO13 | BIO15 |  |  |  |
| *Celeus flavescens* | | 557 |  | 0.91 |  | 0.73 |  | BIO2 | BIO4 | BIO8 | BIO13 | BIO19 |  |  |
| *Crax blumenbachii* | | 42 |  | 0.89 |  | 0.77 |  | BIO3 | BIO13 | BIO14 |  |  |  |  |
| *Lipaugus ater* | | 137 |  | 0.92 |  | 0.8 |  | BIO3 | BIO8 | BIO19 |  |  |  |  |
| *Lipaugus lanioides* | | 238 |  | 0.85 |  | 0.73 |  | BIO2 | BIO4 | BIO8 | BIO13 |  |  | BIO19 |
| *Lipaugus vociferans* | | 387 |  | 0.83 |  | 0.6 |  | BIO2 | BIO4 | BIO8 | BIO13 | BIO14 | BIO18 |  |
| *Mimus saturninus* | | 335 |  | 0.85 |  | 0.71 |  | BIO5 | BIO9 | BIO18 | BIO19 |  |  |  |
| *Myiodystes solitarius* | | 737 |  | 0.8 |  | 0.63 |  | BIO2 | BIO3 | BIO13 | BIO14 |  |  |  |
| *Penelope obscura* | | 573 |  | 0.93 |  | 0.78 |  | BIO3 | BIO9 | BIO18 | BIO19 |  |  |  |
| *Penelope superciliaris* | | 477 |  | 0.83 |  | 0.65 |  | BIO2 | BIO8 | BIO13 | BIO14 | BIO18 | BIO19 |  |
| *Pipile jacutinga* | | 211 |  | 0.92 |  | 0.79 |  | BIO2 | BIO11 | BIO14 | BIO15 | BIO18 |  |  |
| *Pitangus sulphuratus* | | 110 |  | 0.85 |  | 0.61 |  | BIO2 | BIO3 | BIO5 | BIO18 |  |  |  |
| *Procnias nudicollis* | | 517 |  | 0.92 |  | 0.76 |  | BIO2 | BIO4 | BIO8 | BIO15 | BIO18 |  |  |
| *Pteroglossus aracari* | | 408 |  | 0.83 |  | 0.61 |  | BIO2 | BIO12 | BIO18 |  |  |  |  |
| *Pteroglossus bailloni* | | 252 |  | 0.91 |  | 0.73 |  | BIO2 | BIO4 | BIO9 | BIO15 | BIO18 |  |  |
| *Pyroderus scutatus* | | 393 |  | 0.9 |  | 0.72 |  | BIO2 | BIO7 | BIO9 | BIO12 | BIO15 | BIO18 |  |
| *Ramphastos dicolorus* | | 460 |  | 0.94 |  | 0.82 |  | BIO2 | BIO8 | BIO13 | BIO18 | BIO19 |  |  |
| *Ramphastos ariel* | | 203 |  | 0.86 |  | 0.66 |  | BIO2 | BIO4 | BIO9 | BIO12 | BIO15 | BIO18 |  |
| *Selenidera maculirostris* | | 283 |  | 0.91 |  | 0.77 |  | BIO2 | BIO9 | BIO15 | BIO18 |  |  |  |
| *Tityra braziliensis* | | 404 |  | 0.84 |  | 0.62 |  | BIO2 | BIO4 | BIO8 | BIO13 | BIO18 | BIO19 |  |
| *Trogon rufus* | | 299 |  | 0.85 |  | 0.61 |  | BIO2 | BIO8 | BIO13 | BIO15 | BIO18 |  |  |
| *Trogon surrucura* | | 602 |  | 0.89 |  | 0.79 |  | BIO2 | BIO4 | BIO9 | BIO13 |  |  |  |
| *Trogon viridis* | | 485 |  | 0.81 |  | 0.62 |  | BIO2 | BIO4 | BIO8 | BIO13 | BIO18 |  |  |
| *Turdus albicollis* | | 648 |  | 0.88 |  | 0.68 |  | BIO2 | BIO3 | BIO7 | BIO8 | BIO15 | BIO18 |  |
| *Turdus amaurochalinus* | | 1033 |  | 0.86 |  | 0.65 |  | BIO2 | BIO3 | BIO8 | BIO13 | BIO19 |  |  |
| *Turdus flavipes* | | 489 |  | 0.92 |  | 0.76 |  | BIO2 | BIO7 | BIO8 | BIO13 | BIO18 | BIO19 |  |
| *Turdus leucomelas* | | 1063 |  | 0.84 |  | 0.62 |  | BIO2 | BIO4 | BIO8 | BIO13 | BIO14 | BIO18 | BIO19 |
| *Turdus rufiventris* | | 1146 |  | 0.85 |  | 0.66 |  | BIO2 | BIO3 | BIO8 | BIO13 | BIO15 |  |  |
| *Turdus subalaris* | | 112 |  | 0.87 |  | 0.74 |  | BIO2 | BIO4 | BIO9 | BIO18 |  |  |  |

\* Codes for predictors:

Soil

BDTICM = Absolute depth to bedrock

ORCDRC = Soil organic carbon content

SNDPPT = Weight percentage of the sand particles (0.05–2 mm)

Climatic

BIO1 = Annual Mean Temperature

BIO2 = Mean Diurnal Range (Mean of monthly (max temp - min temp))

BIO3 = Isothermality (BIO2/BIO7) (\* 100)

BIO4 = Temperature Seasonality (standard deviation \*100)

BIO5 = Max Temperature of Warmest Month

BIO6 = Min Temperature of Coldest Month

BIO7 = Temperature Annual Range (BIO5-BIO6)

BIO8 = Mean Temperature of Wettest Quarter

BIO9 = Mean Temperature of Driest Quarter

BIO10 = Mean Temperature of Warmest Quarter

BIO11 = Mean Temperature of Coldest Quarter

BIO12 = Annual Precipitation

BIO13 = Precipitation of Wettest Month

BIO14 = Precipitation of Driest Month

BIO15 = Precipitation Seasonality (Coefficient of Variation)

BIO16 = Precipitation of Wettest Quarter

BIO17 = Precipitation of Driest Quarter

BIO18 = Precipitation of Warmest Quarter

BIO19 = Precipitation of Coldest Quarter

**Supplementary Table S4:**  **Ingested seed size and strength of selection for the frugivorous bird that act as main seed dispersers of the jussara palm *Euterpe edulis*.** The direction of selection refers to the *Pf* - *Zt* term of the formula *Zt*+*1*= *Zt* + *h2* (*Pf* - *Zt*), in which *Zt* is the expected maximum seed size at generation t, *h2* is the mean heritability of seed size, *Pf* is the maximum seed size each frugivore species can swallow, and *h2* (*P* - *Zt*) is the response to selection at generation *t*.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Species | Direction of selection | Maximum ingested seed size | |  | Ingested seed size (mm) | |
|  | *Pf* - *Zt* |  | *Pf* (mm) |  | Mean | Standard deviation |
| *Aramides cajaneus* | 0.00 |  | 12.94 |  | 11.34 | 0.67 |
| *Baryphthengus ruficapillus* | 0.00 |  | 13.12 |  | 11.62 | 0.72 |
| *Carpornis cucullata* | 0.00 |  | 13.49 |  | 11.10 | 0.72 |
| *Carpornis melanocephala* | 0.00 |  | 13.49 |  | 11.10 | 0.72 |
| *Celeus flavescens* | 0.00 |  | 13.26 |  | 11.76 | 0.72 |
| *Crax blumenbachii* | -0.20 |  | 12.67 |  | 11.06 | 0.72 |
| *Lipaugus ater* | 0.00 |  | 13.53 |  | 11.09 | 0.72 |
| *Lipaugus lanioides* | 0.00 |  | 13.53 |  | 11.09 | 0.72 |
| *Lipaugus vociferans* | 0.00 |  | 13.53 |  | 11.09 | 0.72 |
| *Mimus saturninus* | -0.63 |  | 12.19 |  | 11.11 | 0.72 |
| *Myiodynastes solitarius* | 0.00 |  | 13.4 |  | 11.11 | 0.72 |
| *Penelope obscura* | -0.21 |  | 12.66 |  | 11.06 | 0.72 |
| *Penelope superciliaris* | 0.00 |  | 13.88 |  | 11.36 | 0.72 |
| *Pipile jacutinga* | -0.21 |  | 12.66 |  | 11.06 | 0.72 |
| *Pitangus sulphuratus* | 0.00 |  | 13.4 |  | 11.11 | 0.72 |
| *Procnias nudicollis* | -0.27 |  | 12.6 |  | 10.98 | 0.72 |
| *Pteroglossus aracari* | 0.00 |  | 13.34 |  | 11.87 | 0.48 |
| *Pteroglossus bailloni* | 0.00 |  | 13.14 |  | 12.26 | 0.50 |
| *Pyroderus scutatus* | 0.00 |  | 13.52 |  | 11.10 | 0.72 |
| *Ramphastos ariel* | 0.00 |  | 13.2 |  | 11.54 | 1.07 |
| *Ramphastos dicolorus* | 0.00 |  | 13.51 |  | 11.85 | 0.69 |
| *Selenidera maculirostris* | 0.00 |  | 13.32 |  | 11.88 | 0.59 |
| *Tityra braziliensis* | 0.00 |  | 13.4 |  | 11.11 | 0.72 |
| *Trogon rufus* | 0.00 |  | 13.08 |  | 11.58 | 0.72 |
| *Trogon surrucura* | 0.00 |  | 13.08 |  | 11.58 | 0.72 |
| *Trogon viridis* | 0.00 |  | 13.08 |  | 11.58 | 0.72 |
| *Turdus albicollis* | -0.80 |  | 12 |  | 10.93 | 0.73 |
| *Turdus amaurochalinus* | -0.79 |  | 12.01 |  | 11.09 | 0.72 |
| *Turdus flavipes* | -0.80 |  | 11.99 |  | 11.09 | 0.72 |
| *Turdus leucomelas* | -0.80 |  | 11.99 |  | 11.09 | 0.72 |
| *Turdus rufiventris* | -0.80 |  | 11.99 |  | 11.09 | 0.72 |
| *Turdus subalaris* | -0.78 |  | 12.02 |  | 11.09 | 0.72 |

Supplementary codes

Data collection and cleaning

Occurrence data for frugivores of the palm *Euterpe edulis* was obtained from virtual databases, in addition to those from the ATLANTIC datasets, and then checked for errors, duplicates and inconcistencies.

**library**(spocc)**library**(rvertnet)**library**(plyr) *# list of species names*frug <- **as.character**(**read.csv**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/Ocorrencias/Frugivoros/frug.csv"), h=F)  *# Get occurrences*bi1 <- **occ**(query = frug, from = **c**("gbif", "bison", "inat", "ebird", "ecoengine", "vertnet"), has\_coords = T) bi1.fix <- **fixnames**(bi1, how = "query") bi2 <- **occ2df**(bi1.fix)  *##### Clean occurrences  
# NAs*bi3 <- bi3[**-which**(**is.na**(bi3)), ] *# Convert la/long to numeric*bi3**$**lon <- **as.numeric**(bi3**$**lon)bi3**$**lat <- **as.numeric**(bi3**$**lat) *# Coordinate based cleaning***library**("scrubr") *# Remove impossible, incomplete and unlikely coordinates*dp <- bi3 **%>%** **coord\_impossible**() **%>%** **coord\_incomplete**() **%>%** **coord\_unlikely**()  *# Deduplicate*dp1 <- **duplicated**(dp)sp <- dp[**-**dp1, ]

Ecological niche modelling

Here, we will model the ecological niche of frugivore birds of the *Euterpe edulis* palm. To do so, we apply an ensemble procedure on models fitted to climate data and the occurrence records collected previously.

**library**(sdm)**library**(raster)**library**(usdm)**library**(rgdal)**library**(rgeos) *# Table to save results*resu <- **matrix**(nrow = **length**(frug), ncol = 9)**colnames**(resu) <- **c**("sp\_name","records","AUC","COR","Deviance","TSS","iniDist" ,"finalDist","rangeShift")**for** (i **in** 1**:** **length**(frug)) { t <- **as.character**(frug[i])sp <- sp1[sp1**$**sp**==**t, **c**('longitude','latitude')]sp**$**species <- 1**coordinates**(sp) <- **~** longitude **+** latitude *#---- remove collinear variables*spx <- **extract**(pres, sp) *# pres is climate information for the present*spx <- spx[**-which**(**is.na**(spx)),]v1 <- **vifcor**(spx, th=0.6) *# identify collinear variables with corr>0.6 that should be excluded*bio <- **exclude**(pres,v1) *# exclude the correlated variables that were identified in v1  
  
  
# sdmModel data*d <- **sdmData**(species**~**., train=sp, predictors= bio, bg=**list**(n=10000,method='gRandom',remove=TRUE)) *# Fitting SDMs*m <- **sdm**(species **~** . , d, methods=**c**("rf", "maxlike", "brt", "bioclim"),  replication=**c**("sub"), test.p=25, n=100, parallelSettings = **list**(ncore=10, method='parallel'))

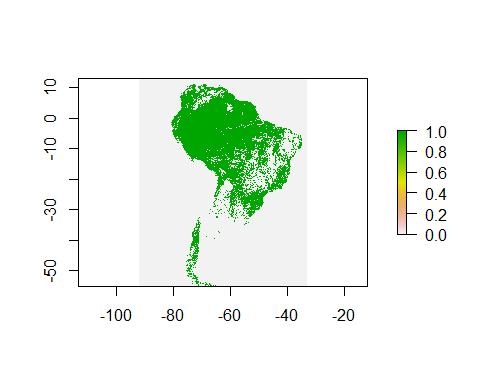
*# Ensembling*en <- **ensemble**(m, pres,  setting=**list**(method='weighted',stat='TSS'), parallelSettings = **list**(ncore=10, method='parallel')) *# Evaluation*e <- **getEvaluation**(m) *# Save which variables were used and evaluation results for all species*evals[i, "frug"] <- **gsub**(" ", "\_", t)evals[i, "records"] <- **nrow**(**as.data.frame**(d))**-**10000evals[i, "AUC"] <- **round**(**mean**(e**$**AUC), 2)evals[i, "COR"] <- **round**(**mean**(e**$**COR), 2)evals[i, "Deviance"] <- **round**(**mean**(e**$**Deviance),2)evals[i, "TSS"] <- **round**(**mean**(e**$**TSS),2) *# Find binarization threshold*df <- **data.frame**(**as.data.frame**(d),**coordinates**(d)) *# presence points and predictors associated*pr <- **extract**(en, df[,**c**('longitude','latitude')]) *# estimates of habitat suitability from presence points*ev <- **evaluates**(df**$**species, pr) *# evaluate prediction (observed vs expected)*th <- ev**@**threshold\_based**$**threshold[[2]] *# threshold that maximizes sensitiv + specificity  
  
# Binary prediction present-day*pa <- en pa[] <- **ifelse**(pa[] **>=** th, 1, 0) *# convert from continuous to binary  
  
# Projection on future climates*

enf <- **ensemble**(m, biof, setting=**list**(method='weighted',stat='TSS'), parallelSettings = **list**(ncore=10, method='parallel')) *# biof is climate information for the future  
  
  
# Binary projection future*paf <- enfpaf[] <- **ifelse**(paf[] **>=** th, 1, 0)}

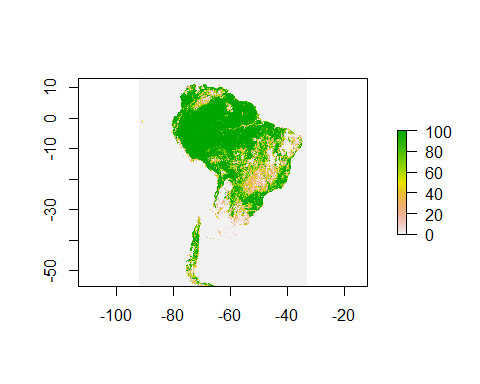
Forest cover thresholds

Then, we simulate defaunation based on minimum habitat size. First, we create a raster grid of 10km² with percent forest cover.

*# raster of tree cover in the future***library**(raster)tree <- **raster**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Defor/tree\_South\_fut.tif") tree[tree**==**2] <- 0 *# keep only cells of "trees"***plot**(tree)



ref <- **aggregate**(tree, fact=10, fun=sum) *# set resolution of a "landscape" (10km²) and sum the number of tree cover cells***plot**(ref)



Now, we will apply different thresholds of forest cover, depending on species vulnerability to forest loss. Three functional groups are defined: - extreme forest specialists - moderate forest specialists - generalists

For the extreme forest specialists, suitable climate regions with less than 50% forest cover are considered unable to support viable populations.

**library**(rgeos) *# ------ Extreme forest specialists (threatened habitat specialists)  
# Species assessed as Critically Endangered (CR), Endangered (EN), or Vulnerable (VU) are referred to as "threatened" species  
# remove predicted presences from landscapes with less than 50% tree cover*iu <- **read.csv**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Planilhas/Lista\_sp.csv", h=T) *# List with information on IUCN status*th <- **c**("CR", "EN", "VU")th\_sp <- iu[iu**$**IUCN **%in%** th, ] *# select only threatened by IUCN*sp <- **as.character**(th\_sp**$**Species) *# these species will be removed from landscapes with less than 50% tree cover*tableS1 <- **data.frame**(**cbind**(sp, **rep**("Extreme forest specialist", **length**(sp)))) *# To incorporate this information on the Table S1***colnames**(tableS1) <- **c**("Species", "Classification")sp <- **gsub**(" ", "\_", sp) *# Landscapes with less than 50% tree cover - do not provide habitat for extreme habitat specialists*land50 <- refland50[land50 **<** 50] <- 0land50[land50 **>=**50 ] <- 1land50 <- **rasterToPolygons**(land50, n=16, na.rm=TRUE, dissolve=T) *# create mask with only landscapes of more than 50% forest cover***library**(maptools)**writeSpatialShape**(land50, "C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Defor/land50.shp")land50 <- **readOGR**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Defor/land50.shp") *# Now remove threatened species from outside these areas***setwd**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Mapas")**dir**() **for** (i **in** 1**:** **length**(sp)) {  list1 <- **list.files**(pattern=**paste0**(sp[i], "\_PA\_"))  **for** (j **in** 1**:** **length**(list1)){  a <- **raster**(list1[j]) b <- (**mask**(a, land50)) **writeRaster**(b, **paste0**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Mapas\_Defaun/", list1[j]), format = "GTiff", overwrite = T) } }

Same same procedure is applied to moderate forest specialists, but to a 30% forest cover threshold.

*# ------- Moderate forest specialists (not threatened)  
# remove predicted presences from landscapes with less than 30% tree cover*no\_th <- **c**("LC", "NT")no\_th\_sp <- iu[iu**$**IUCN **%in%** no\_th, ] *# select only non-threatened*sp\_sp <- no\_th\_sp[no\_th\_sp**$**Specialists**==**1, ] *# select only specialists non-threatened*sp\_sp <- **as.character**(sp\_sp**$**Species) *# these species will be removed from landscapes with less than 50% tree cover*tableS1.1 <- **data.frame**(**cbind**(sp\_sp, **rep**("Moderate forest specialist", **length**(sp\_sp)))) *# To incorporate this information on the Table S1***colnames**(tableS1.1) <- **c**("Species", "Classification")sp\_sp <- **gsub**(" ", "\_", sp\_sp) *# Landscapes with more than 30% tree cover - still may provide habitat for habitat specialists*land30 <- refland30[land30 **<** 30] <- 0land30[land30 **>=**30 ] <- 1**plot**(land30)land30 <- **rasterToPolygons**(land30, n=16, na.rm=TRUE, dissolve=T) *# create mask with only landscapes of more than 50% forest cover***writeSpatialShape**(land30, "C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Defor/land30.shp")**plot**(land30)land30 <- **readOGR**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Defor/land30.shp") *# Now remove specialist species from outside these areas***setwd**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Mapas")**dir**()**for** (i **in** 1**:** **length**(sp\_sp)) {   list1 <- **list.files**(pattern=**paste0**(sp\_sp[i], "\_PA\_"))  **for** (j **in** 1**:** **length**(list1)){   a <- **raster**(list1[j]) b <- (**mask**(a, land30)) **writeRaster**(b, **paste0**("C:/Users/lilia/OneDrive/Pos-doc/PNPD/Cap1/UFO/Mapas\_Defaun/", list1[j]), format = "GTiff", overwrite = T) }}

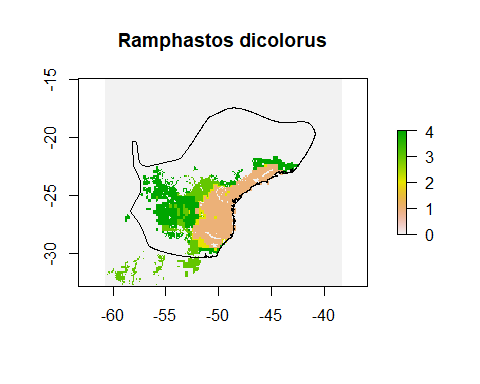
Dispersal-restricted potential distribution of frugivores

In addition to climate suitability and forest cover thresholds, we also simulate occupancy of potential suitable future areas under dispersal constraints posed by landscape fragmentation. The absence of trees was considered - a strong barrier to extreme forest specialists - a weak barrier to moderate forest specialists - not a barrier to generalists

**library**(raster)**library**(rgdal)**library**(MigClim)**library**(sp)barrier <- tree *# raster with future forest cover projections*resu <- NULL *# Table to store results  
  
# Extreme habitat specialists  
# Barrier type = "strong"***for** (i **in** 1**:** **length**(ext)) {   **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar")  a <- **list.files**(pattern = **paste0**(ext[i]))  iniDist <- **raster**(**paste0**("D:/Leddiv/lilian/Cap1/Mapas\_Defaun/", ext[i], "\_pres\_PA.tif"))    barr <- **crop**(barrier, **extent**(iniDist)) *# species-specific extent of barrier cell* barr <- **as.data.frame**(barr, xy=F) barr[**is.na**(barr)] <- 0  iniDist <- **as.data.frame**(iniDist, xy=T) iniDist[**is.na**(iniDist)] <- 0   *# rcp45* **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar") b <- **stack**(a) b45 <- raster**::subset**(b, **grep**("rcp45", **names**(b), value=T)) b45**@**crs <- barrier**@**crs  hsMap <- **as.data.frame**(b45) *# get coordinates*  hsMap[**is.na**(hsMap)] <- 0 *# all NAs converted to 0*   *### Dispersal*   **MigClim.migrate**(iniDist = iniDist,  hsMap = hsMap,  rcThreshold = 1, *#artificial threshold, binarization was made during SDM* envChgSteps = **ncol**(hsMap), dispSteps = **ncol**(hsMap),  barrier = barr, barrierType = "strong", *# Barrier is strong to extreme habitat specialists* replicateNb=3,  testMode=FALSE,  fullOutput=T, keepTempFiles=FALSE)  **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/MigClimTest") *#Saving all species results in a single spreadsheet* results <- **read.table**("MigClimTest\_summary.txt", h=T, stringsAsFactors = FALSE) results[1,"simulName"] <- **paste0** ( ext[i],"\_rcp45") resu <- **rbind** (resu, results)  *# Reclassify raster* *# 0 : unsuitable;* *# 1 : climate refugia* *# 2 =< x =<29999 : colonized* *# x < 0 : locally extinc*  distr.sp <- **raster**("MigClimTest\_raster.asc") *#plot(distr.sp)*  m <- **c**(2, 29999, 2, *#Reclassify positives* 29999, 30000, 3) rclmat <- **matrix**(m, ncol=3, byrow=TRUE) rc <- **reclassify**(distr.sp, rclmat)  s <- **calc**(rc, fun=**function**(x){ *#Reclassify negatives* x[x **<** 0] <- 4  **return**(x)} )  **writeRaster**(s, **paste0**("D:/Leddiv/lilian/Cap1/Anthrop\_maps/", ext[i],"\_rcp45", ".tif"), format="GTiff", overwrite=T)

Note that the final map has 4 categories 0 : always unsuitable 1 : climate refugia - always suitable 2 : potential colonization (became suitable and is accessible) 3 : dispersal limitation (became suitable but is unaccessible) 4 : non-analog climate (became unsuitable)

## OGR data source with driver: ESRI Shapefile ## Source: "C:\Users\lilia\Downloads\data\_0.shp", layer: "data\_0"## with 1 features## It has 15 fields## Integer64 fields read as strings: PRESENCE ORIGIN SEASONAL YEAR



The same is applied to moderate habitat specialists, but the absence of tree is a weak barrier to them

*### Moderate habitat specialists  
# Barrier type = "weak"***for** (i **in** 1**:** **length**(no\_ext)) {   **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar")  a <- **list.files**(pattern = **paste0**(no\_ext[i]))  iniDist <- **raster**(**paste0**("D:/Leddiv/lilian/Cap1/Mapas\_Defaun/", no\_ext[i], "\_pres\_PA.tif"))   barr <- **crop**(barrier, **extent**(iniDist)) barr <- **as.data.frame**(barr, xy=F) barr[**is.na**(barr)] <- 0  iniDist <- **as.data.frame**(iniDist, xy=T) iniDist[**is.na**(iniDist)] <- 0  **nrow**(barr) **==** **nrow**(iniDist)  *# rcp45* **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/") b <- **stack**(a) b45 <- raster**::subset**(b, **grep**("rcp45", **names**(b), value=T)) b45**@**crs <- barrier**@**crs  hsMap <- **as.data.frame**(b45) *# do not get coordinates*  **nrow**(hsMap) **==** **nrow**(iniDist)  hsMap[**is.na**(hsMap)] <- 0 *# all NAs converted to 0*  **nrow**(hsMap) **==** **nrow**(iniDist) **nrow**(barr) **==** **nrow**(iniDist) *# TRUE Number of rows must match*   *### Dispersal*  **MigClim.migrate**(iniDist = iniDist,  hsMap = hsMap,  rcThreshold = 1, *#artificial threshold, binarization was made during SDM* envChgSteps = **ncol**(hsMap), dispSteps = **ncol**(hsMap),  barrier = barr, barrierType = "weak", *# Barrier is weak to moderate habitat specialists* replicateNb=3,  testMode=FALSE,  fullOutput=T, keepTempFiles=FALSE)  **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/MigClimTest") *#Saving all species results in a single spreadsheet* results <- **read.table**("MigClimTest\_summary.txt", h=T, stringsAsFactors = FALSE) results[1,"simulName"] <- **paste0** ( no\_ext[i],"\_rcp45") resu <- **rbind** (resu, results)  distr.sp <- **raster**("MigClimTest\_raster.asc")  m <- **c**(2, 29999, 2, *#Reclassify positives* 29999, 30000, 3) rclmat <- **matrix**(m, ncol=3, byrow=TRUE) rc <- **reclassify**(distr.sp, rclmat)  s <- **calc**(rc, fun=**function**(x){ *#Reclassify negatives* x[x **<** 0] <- 4  **return**(x)} )  **writeRaster**(s, **paste0**("D:/Leddiv/lilian/Cap1/Anthrop\_maps/", no\_ext[i],"\_rcp45", ".tif"), format="GTiff", overwrite=T)}

Yet for habitat generalists, the absence of trees is not considered a barrier.

*### Habitat generalists  
# Barrier file = empty*no.barr <- barrierno.barr[no.barr**==**1] <- 0 *# Transformed all barrier into non-barrier***for** (i **in** 1**:** **length**(ge)) {   **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/")  a <- **list.files**(pattern = **paste0**(ge[i])) iniDist <- **raster**(**paste0**("D:/Leddiv/lilian/Cap1/Mapas\_Defaun/", ge[i], "\_pres\_PA.tif"))  barr <- **crop**(no.barr, **extent**(iniDist))  iniDist <- **as.data.frame**(iniDist, xy=T) iniDist[**is.na**(iniDist)] <- 0  barr <- **as.data.frame**(barr, xy=F) barr[**is.na**(barr)] <- 0  *# rcp45* **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/") b <- **stack**(a) b45 <- raster**::subset**(b, **grep**("rcp45", **names**(b), value=T))  hsMap <- **as.data.frame**(b45) *# do not get coordinates* **nrow**(hsMap) **==** **nrow**(iniDist) hsMap[**is.na**(hsMap)] <- 0 *# all NAs converted to 0*   *### Dispersal*  **MigClim.migrate**(iniDist = iniDist,  hsMap = hsMap,  rcThreshold = 1, *#artificial threshold, binarization was made during SDM* envChgSteps = **ncol**(hsMap), dispSteps = **ncol**(hsMap),  barrier = barr, *#Barrier file is empty, but required to run simulations* replicateNb=3,  testMode=FALSE,  fullOutput=T, keepTempFiles=FALSE)  **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/MigClimTest")  *#Saving all species results in a single spreadsheet* results <- **read.table**("MigClimTest\_summary.txt", h=T, stringsAsFactors = FALSE) results[1,"simulName"] <- **paste0** ( ge[i],"\_rcp45") resu <- **rbind** (resu, results)  distr.sp <- **raster**("MigClimTest\_raster.asc") m <- **c**(2, 29999, 2, *#Reclassify positives* 29999, 30000, 3) rclmat <- **matrix**(m, ncol=3, byrow=TRUE) rc <- **reclassify**(distr.sp, rclmat)  s <- **calc**(rc, fun=**function**(x){ *#Reclassify negatives* x[x **<** 0] <- 4  **return**(x)} )  **writeRaster**(s, **paste0**("D:/Leddiv/lilian/Cap1/Anthrop\_maps/", ge[i],"\_rcp45", ".tif"), format="GTiff", overwrite=T)  }

**Palm seed dispersal scenarios**

To incorporate the effect of seed dispersers on colonization of analog climates of the palm tree *Euterpe edulis*, we created two dispersal scenarios - passive - frugivore-based dispersal

To do so, we first assume that co-occurrence precedes the biotic interaction, by projecting pairwise shared environmental correlations into geographical space.

We will provide an example for extreme forest specialists, but steps were repeated for the whole species subset.

**for** (i **in** 1**:** **length**(ext)) {   **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar")  a <- **list.files**(pattern = **paste0**(ext[i]))  iniDist <- **raster**(**paste0**("D:/Leddiv/lilian/Cap1/Mapas\_Defaun/", ext[i], "\_pres\_PA.tif")) *#initial distribution frugivore* iniPalm <- **raster**("D:/Leddiv/lilian/Cap1/Mapas\_Defaun/Euterpe\_edulis\_pres\_PA.tif") *#initial distribution palm tree*  *# Shared environmental correlates* iniMatch <- **sum** (iniDist, iniPalm) *#co-occurrence - iniMatch* iniMatch[iniMatch**!=**2] <- 0 iniMatch[iniMatch**==**2] <- 1  *# Barrier defined according to frugivore's perspective* barr <- **crop**(barrier, **extent**(iniMatch)) *#barrier* barr <- **as.data.frame**(barr, xy=F) barr[**is.na**(barr)] <- 0  iniDist <- iniMatch  iniDist <- **as.data.frame**(iniDist, xy=T) iniDist[**is.na**(iniDist)] <- 0  *# rcp45* **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar")  *# Frugs* b <- **stack**(a) b45 <- raster**::subset**(b, **grep**("rcp45", **names**(b), value=T))  *# Palm* p45 <- **list.files**(pattern =**c**("Euterpe\_edulis")) p45 <- **stack**(p45) p45 <- raster**::subset**(p45, **grep**("rcp45", **names**(p45), value=T)) p45 <- raster**::subset**(p45, **grep**("\_PA\_", **names**(p45), value=T))   b45 <-**stack**(b45, p45)  *# hsMap Match* indices <- **seq**(1**:**8) b45<- **stackApply**(b45, indices, fun = sum) *#plot(b45)*  b45[b45**!=**2000] <- 0 b45[b45**==**2000] <- 1000 *# habitat suitability maps should include values from 0 to 1000, acording to MigClim's requirements* **plot**(b45)  b45**@**crs <- barrier**@**crs  hsMap <- **as.data.frame**(b45) *# do get coordinates*  hsMap[**is.na**(hsMap)] <- 0 *# all NAs converted to 0*   *### Dispersal* **MigClim.migrate**(iniDist = iniDist,  hsMap = hsMap,  rcThreshold = 1, *#artificial threshold, conversion was made during SDM* envChgSteps = **ncol**(hsMap), dispSteps = **ncol**(hsMap),  barrier = barr, barrierType = "strong", *# Barrier is strong to extreme habitat specialists* replicateNb=3,  testMode=FALSE,  fullOutput=T, keepTempFiles=FALSE)  **setwd**("D:/Leddiv/lilian/Cap1/Disp\_bar/MigClimTest") *#Saving all species results in a single spreadsheet* results <- **read.table**("MigClimTest\_summary.txt", h=T, stringsAsFactors = FALSE) results[1,"simulName"] <- **paste0** ("Euterpe\_", ext[i],"\_rcp45") resu <- **rbind** (resu, results)  *# Reclassify raster* *# 0 : unsuitable;* *# 1 : climate refugia* *# 2 =< x =<29999 : colonized* *# x < 0 : locally extinc*  distr.sp <- **raster**("MigClimTest\_raster.asc") *#plot(distr.sp)*  m <- **c**(2, 29999, 2, *#Reclassify positives* 29999, 30000, 3) rclmat <- **matrix**(m, ncol=3, byrow=TRUE) rc <- **reclassify**(distr.sp, rclmat)  s <- **calc**(rc, fun=**function**(x){ *#Reclassify negatives* x[x **<** 0] <- 4  **return**(x)} )  **plot**(s)  **writeRaster**(s, **paste0**("D:/Leddiv/lilian/Cap1/Anthrop\_maps/Euterpe/", "Euterpe\_", ext[i],"\_rcp45", ".tif"), format="GTiff", overwrite=T)}