

1 **A process to support species conservation planning and climate change readiness in**  
2 **protected areas**

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13 **Abstract** –Global change will cause species range shifts, affecting species interactions. The  
14 conservation implications of species range shifts are widely unknown. Through forming an  
15 ecology-bioinformatics partnership at the National Evolutionary Synthesis Center-Encyclopedia  
16 of Life-Biodiversity Heritage Library Research Sprint, we developed an analytical pipeline to  
17 test whether global trends are forcing shifts of mutually dependent species in different spatial  
18 directions. We calculated potential overlap between dependent species across climate scenarios  
19 within protected areas. We selected the Great Green Macaw (*Ara ambiguus*) and its nesting host  
20 tree the Giant Almendro (*Dipteryx panamensis*) as a proof-of-concept species pair that will be  
21 affected by range shifts. We demonstrate with modeling that the Great Green Macaw will lose  
22 approximately 64.0% of suitable habitat in future scenarios, while the Giant Almendro will lose  
23 59.7% of suitable habitat. Species habitat overlaps across 85.3 % of its currently predicted  
24 distribution and 69.07% of the remaining habitat predicted in future scenarios. After accounting  
25 for spatially explicit protected areas networks, only 20.3% and 40.2 % of remaining habitat  
26 persists within protected areas across climate scenarios for the Almendro and Macaw,  
27 respectively, and 19.9 % of that habitat overlaps between the species. Currently, we are  
28 conducting a literature review to select and expand our list of species for use in the pipeline to  
29 detect trends for climate readiness planning in protected areas networks. The analytical pipeline  
30 will produce habitat suitability maps for multiple climate scenarios based on current  
31 distributions, and these maps will potentially be embedded into the Encyclopedia of Life as free,  
32 downloadable files. This is just one of several broader impact products from the research. This  
33 work demonstrates that modeling the future distribution of species is limited by biotic  
34 interactions and that conservation planning should account for climate change scenarios.

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36 **Keywords:** biodiversity, predictive modeling, species interactions, mutualisms, climate change,  
37 conservation planning

38

## 39 **Introduction**

40 Species and communities are in continuous interaction, with species among trophic levels  
41 driving selective processes and affecting the ability of other species to adapt to climate change.  
42 Creating self-sustaining populations through management action requires an understanding of  
43 ecological settings, including species interactions (Van der Putten, Macel, and Visser, 2010).  
44 Habitat ranges will expand or contract due to changing climates, and we will see new species  
45 assemblages and interactions (Carvalho et al., 2011; Araújo and Guisan, 2006; Raxworthy et al.,  
46 2008; Williams and Jackson 2007). A clear example of this scenario is the warming of ocean  
47 temperatures, which allowed for a range shift of sea urchins in Tasmania. The urchins shifted to  
48 a region without natural predators, causing an estimated net loss of 150 taxa within Tasmanian  
49 macroalgal beds (Ling et al., 2009). Biotic interactions have proven to significantly affect both  
50 the explanatory and predictive power of bioclimatic envelope models not only at local and  
51 regional scales but also at macro scales thus it is critical to include them when modeling potential  
52 effects of climate change in species distributions (Araújo & Luoto, 2007; Araújo & Rozenfeld,  
53 2014). By modeling future climate change scenarios and predicting new species assemblages, we  
54 can determine if current protected areas networks will cover future ranges and the probable  
55 species overlap zones for management (Redford, et al., 2011). This is complex, and may be best  
56 completed for species pairs before incorporating multiple species assemblages. For example, will  
57 the mutualism between the endangered Great Green Macaw (*Ara ambiguus*) and the Almendro  
58 tree (*Dipteryx panamensis*) continue if their ranges counter shift?(Monge et al., 2003), and how  
59 much will these species' ranges differ comparatively throughout present and future scenarios?  
60 (Dunn et al., 2009; Kiers et al., 2010). We predict that global climate change trends are forcing  
61 range shifts of the mutually dependent species Great Green Macaw and the Almendro tree in

62 different spatial directions and outside of protected area networks, which could easily be  
63 calculated after estimating the species ranges with distribution models. However, our primary  
64 interest is academic; how can we easily transfer our findings for one set of species interactions to  
65 other academic researchers and managers?

66  
67 Studying species interactions specifically for conservation planning and climate change  
68 readiness will require access to species distribution models. Currently, a suite of programs exist  
69 to estimate future changes in species distributions but the reality is that these programs take a  
70 significant amount of time to implement or the models are behind paywalls (Walsh, Dicks, and  
71 Sutherland, 2014). Indeed, conservation managers worldwide have access to less than 9% of all  
72 conservation science publications (Fuller, Lee and Watson, 2014). To address this need, we  
73 attended a workshop pairing biologists with computer programmers to improve data usage in the  
74 Encyclopedia of Life (EOL). The EOL integrates multiple networks and databases into a single  
75 free user interface under the leadership of the Smithsonian Institution (Parr et al., 2012).  
76 Functionality in EOL is added to increase its ease-of-use, practicality, and content. Content is  
77 curated by biodiversity experts. A priority of EOL is to increase the number of biodiversity  
78 experts who can implement complex computer programs and also provide in-depth knowledge  
79 for specific taxa. Few biodiversity experts have both skill sets, meaning therefore collaborative  
80 projects provide prolific additions to EOL through harvesting multiple databases.

81  
82 In our project, we developed a tool to automate species distribution models, analyze overlap in  
83 up to two species distribution models, and allow current and future spatial data to be made freely  
84 available in EOL. We used a popular species distribution modeling algorithm, Maxent, to create

85 testable predictions to query and demonstrate functionality. We had *a priori* identified the  
86 endangered Great Green Macaw (*Ara ambiguus*) and the Giant Almendro tree (*Dipteryx*  
87 *panamensis*) as appropriate mutualistic species. The tree is the primary nesting and feeding  
88 source for the macaw in Costa Rica, and the macaw disperses the seeds of the tree. We asked  
89 whether land reserved for conservation protection will include one, both, or neither of the  
90 mutually dependent species in the future. The pipeline was used to estimate the species' habitat  
91 overlap now and in the future. We expected that most habitat currently overlaps. Our main  
92 concern was with future overlap and future conservation management areas; are current  
93 protected areas adequate to sustain this bird-tree relationship? Herein, we describe a proof-of-  
94 concept tool to automate and make freely available species distribution models. We evaluate our  
95 tool by predicting that these species will overlap in current predictive models and they will  
96 overlap less across climate regimes and also shift their overlap outside of protected areas.

97

## 98 **Methods**

99 We wrote a script that automates species distribution models harvested from online databases.  
100 We based the development of this script on the premise of full automation, with the entire  
101 pipeline executed on a single command. The pipeline can be implemented to produce species  
102 distribution models for species in large database servers, specifically the Encyclopedia of Life.

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104 *Tool:* All the code and the data to perform this analysis is stored in the GitHub repository  
105 'EOLBHL' (Otegui, 2014).

106

107 *Study system:* We completed a literature review to select a mutualistic species familiar to the  
108 public. We selected the Great Green Macaw (See *Ara ambiguus* at EOL: <  
109 <http://eol.org/pages/311764/overview>>) and the Giant Almendro tree (See *Dipteryx panamensis*  
110 at EOL: < <http://eol.org/pages/11245372/overview>>). Almendro trees and fruits support more  
111 than 90% of nests and 85% of the birds' diets (Powell et al., 1999; Chassot et al., 2002), although  
112 subspecies report alternate breeding and feeding roosts tree species (Berg et al., 2007).

113 Consequent recovery plans for this species identified species persistence as contingent on its co-  
114 occurrence with Almendro trees (Arndt, et al., 2000). To identify conservation priority areas, one  
115 study used remote imagery to estimate that 2 trees/ha occur across 140,178 ha of land in northern  
116 Costa Rica, and ~67, 000 ha of this land is suitable habitat for the Great Green Macaw (Chun,  
117 2008). Approximately 76% of habitat suitable for the Great Green Macaw overlaps with regions  
118 determined to contain >50 % intact forest cover. Most of these areas were in biological reserves.  
119 In this study, we identify habitat within protected areas throughout the Americas.

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121 *Species locality data:* In our first step we dynamically accessed species' occurrence data from  
122 the GBIF occurrence application programming interface and performed quality control of GBIF  
123 data (<<http://www.gbif.org/developer/occurrence>>). We found 900 records for *Ara ambiguus*  
124 and 95 records for *Dipteryx panamensis*. We removed incomplete or duplicate records, and  
125 confirmed whether species had 20 or more verified points with georeferencing accuracy greater  
126 than 900 square meters (Hernandez et al., 2006; Phillips, S., and M. Dudík. 2008). We found 775  
127 locality points for *Ara ambiguus* that fit our criteria and we added those to the Macaw model. We  
128 used 68 *Dipteryx panamensis* locality points that fit our quality control criteria and added those  
129 to the Almendro model.

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*Protected areas layers:* We used spatial data from the World Database on Protected Areas (WDPA) at (<http://protectedplanet.net/>). For this project, we selected only protected areas from the Americas for the spatial overlap of protected areas and habitat suitability of the Great Green Macaw and the Almendro tree.

*Environmental data layers:* We used abiotic data from WorldClim ([www.worldclim.org](http://www.worldclim.org)) for species distribution models (Hijmans et al., 2005). Climatic and elevation data was downloaded from the WorldClim data set at 2.5 degree resolution, which is approximately a 4.5 by 4.5 km grid at the equator. For future climate scenarios, we used the Community Climate System Model 4.0 with the representative concentration pathway of 2.6 W/m , the most conservative estimate from the IPCC AR5 (<http://www.ipcc.ch/report/ar5/>). For both present and future systems, we used each of the annually derived bioclimatic values (11 variables).

*Species Distribution Models:* The species distribution algorithm Maxent is a density estimator (Phillips et al., 2006). Using known presence points, the relative proportion of occurrence is estimated across large areas. The available habitat for an organism, given its current distribution, is calculated using static environmental predictor variables. The availability of fairly small (400 + square km) environmental data cells from WorldClim for past, present, and future climate scenarios has proliferated the use of this algorithm in generating predictive maps for species used in conservation management and biodiversity research (Peterson et al., 2011). We integrated our python pipeline with the R modeling environment using the rPy2 package (<https://pypi.python.org/pypi/rpy2/2.2.6>). This allowed us to run Maxent models directly

153 through Python, without having to ask for user input or having to run two different scripts in two  
154 different languages. Maxent scenarios were generated for current and future climate scenarios in  
155 the R package 'dismo' (Hijmans et al., 2013). We assessed model performance using: 1) A  
156 conservative threshold of 0.9 for the test area under the receiver operating characteristic curve  
157 (ROC AUC) where closer to 1 is optimal (Elith et al., 2006), and 2) A p-value <0.05 for the eight  
158 internal training and test binomial test performed by Maxent (two each for minimum presence,  
159 10 percentile presence, equal sensitivity and specificity, maximum sensitivity plus specificity).  
160 We used the logistic output of Maxent using the default prevalence value of 0.5 which indicates  
161 the probability of presence at ordinary occurrence points, i.e. 50% chance of the species being  
162 present in suitable areas (Elith, et al., 2011). The output files of Maxent are not presence-absence  
163 maps (0-1 values) but rather maps of continuous data showing the probability distribution that a  
164 species occurs at a location. This represents the environmental similarity of that pixel with the  
165 pixels where the species is known to occur. Therefore to calculate overlap among species and  
166 within protected areas networks, we applied a threshold of probable occurrence. We coded each  
167 grid cell with a > 60% probability as a presence cell (1) and <60% probability as an absence cell  
168 (0).

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170 *Data analysis:* The following calculations were completed in R using a modified version of the  
171 '*ModelComparion.R*' script in the EOLBHL repository (Otegui, 2014). We calculated the  
172 overlapping number of 4.5 km<sup>2</sup> grid cells from the resulting present and future Maxent map  
173 models for each species. We calculated the percent overlap habitat suitability between species'  
174 current and future ranges and co-occurrence within protected areas. To compare range estimates  
175 from Chun (2008), we clipped the data to an outline of Costa Rica stored at

176 (<[http://thematicmapping.org/downloads/world\\_borders.php](http://thematicmapping.org/downloads/world_borders.php)>). We used QGIS 2.2.0 (QGIS,  
177 2014) to convert the raster maps into vectors, and we calculated the area of present and future  
178 habitat suitability within protected networks of Costa Rica.

179

## 180 **Results**

181 *Great Green Macaw*: The Macaw model met the performance requirements (ROC AUC=0.987,  
182 p-value <0.05 for the eight internal training and test binomial). Our models revealed 5406 grid  
183 cells with suitable habitat in current scenarios, but only 2603 grid cells in 2050 scenarios (Fig.  
184 1). The total habitat that occurred within protected areas networks in the Americas was 1468  
185 cells in the present scenarios, but future scenarios predict only 518 grid cells will remain in  
186 protected areas networks in the Americas. Of these cells, 20.3 % persist across scenarios  
187 meaning that after 64 % of suitable habitat within protected areas is lost by 2050, a fraction of  
188 that land occurs in the same place, consequently parrots need to move to take advantage of  
189 protected suitable areas in the future ( Fig. 1).

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191 *Giant Almendro*: The Almendro model met the performance requirements (ROC AUC=0.991, p-  
192 value <0.05 for the eight internal training and test binomial). Our models revealed 6339 grid  
193 cells with suitable habitat in current scenarios, but only 1798 grid cells in 2050 scenarios (Fig.  
194 2). The total habitat that occurred within protected areas networks in the Americas was 1532  
195 cells in the present scenarios, but future scenarios predict 616 grid cells will remain in protected  
196 areas networks in the Americas. The biology of this tree is such that it is unlikely to easily  
197 disperse to new areas. After 59.7% of habitat within protected areas networks is lost, 40.2% of  
198 that remaining habitat persists across scenarios (Fig. 1).



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*Species overlap:* Our models revealed that the Great Green Macaw and Giant Almendro share 85.3 % suitable habitat worldwide in current climate conditions. Currently, 28.4 % of co-occurring suitable habitat happens within protected areas. In the future, 69.07 % of grid cells overlap among the species and 19.9 % of co-occurring suitable habitat happens within protected areas.

**Discussion**

We predicted that global climate changes will force range shifts of mutually dependent species in different spatial directions, and outside of protected networks. We found that for at least one mutualistic species pair, ranges do shift when taking into account future climate scenarios. While Almendro currently have a greater range of suitable habitat (2,789,100 ha) than Macaws (2,378,640 ha), Almendro lose more future habitat (791,100 ha) than Great Green Macaw (1,145,300 ha). We hope to compare our model results with that of other mutualistic species pairs and determine if we get similar or dissimilar results among species with differing dispersal abilities as a useful step in understanding the general predictability of future species assemblages. For now, we can compare our study with the previous work we described to reveal the utility of our tool in characterizing current conservation networks. Regarding habitat remaining in the future, 40.2 % of persistent habitat for the Almendro will remain within protected areas, but much less habitat remains for Great Green Macaws (20.3%). The Chun (2008) model for Macaw/Almendro habitat suitability described an area that comprised 2.7% of Costa Rica where 48 % (67,271 ha) of habitat was suitable for macaws. According to this model, 76 % of suitable habitat for macaws occurred in protected forests. We found that, in Costa Rica,

222 64.6% of 450,500 ha of future suitable habitat for the Macaw occurs in protected areas (Fig. 3).  
223 Our model used a standardized algorithm to estimate Macaw habitat suitability and was based on  
224 a simple understanding of one biotic interaction for the species, whereas the previous study used  
225 specialized remotely sensed data with a more specialized algorithm. Regardless, our models  
226 revealed similar results: most, but not all suitable habitat occurs in protected areas. The impetus  
227 to expand protected areas networks via corridors or land acquisition could benefit the species,  
228 even now.

229  
230 Species distribution models do not account for limited dispersal capabilities of Almendro trees or  
231 Great Green Macaws. We consider this a strength rather than weakness of our methodology;  
232 rates for dispersal are unknown or could only be poorly estimated for both species. Only 758  
233 species in EOL Traitbank have a mode of dispersal ('dispersal vector') and 144 species are listed  
234 with a dispersal age in the Traitbank (Parr et al., 2014). When the tool runs for the more than 1  
235 million taxa in EOL, it will be impossible to estimate probable dispersal bounds. Thus, we  
236 selected worldwide abiotic environmental coverage for the Maxent models. We choose this scale  
237 due to the number of species in the EOL and the potential applications of this work (Sidlauskas  
238 et al., 2009). In the case of range expansions and contractions, arbitrarily selecting areal range  
239 bounds for the maps may result in under-predicting the actual dispersal ability of an organism.  
240 Of course, species specific conservation action with regard to species distribution scenarios need  
241 to be used with caution and wisdom—maps are an abstraction of reality.

242  
243 If so desired, managers and scientists can clip the spatial rasters to their own specifications. In  
244 the same vein, some conservation advocates suggest that restoration set-points are inadequate

245 and arbitrary. A proposal for Pleistocene re-wilding suggests introducing megafauna to North  
246 America to restore wild places (Donlan et al., 2006). The species distribution maps could be  
247 downloaded from EOL and used to identify zones with the most habitat similarity outside of  
248 species' current ranges if they are used as restoration and biocontrol agents. In another  
249 application, invasive species can be more effectively identified and fought if areas that naturally  
250 conform to their native range are displayed in the spatial maps resulting from our pipeline  
251 (Jiménez-Valverde et al., 2011). We have described reasons why we modeled habitat suitability  
252 worldwide. An unfortunate shortcoming of this decision is a tendency for diagnostic test results  
253 to indicate greater accuracy of the models than is actually inherent to those models (Lobo, et al.,  
254 2008; Peterson, Papes and Soberón, 2008). However, even a brief idea of potential regions where  
255 species may be introduced and survive can provide powerful baseline insight into species  
256 biology to benefit and inform conservation sciences.

257  
258 In the future, protected areas network should include climate change readiness planning for  
259 mutualistic species that may need direct climate change assistance. We determined that current  
260 protection does not adequately protect the overlapping range of Almendro trees and Great Green  
261 Macaws because much suitable habitat in future scenarios falls outside of current protected areas  
262 networks. Moreover, our models over-predicted the future range of Macaws by upwards of half,  
263 if it must co-occur with Almendro trees. Targeted protected area expansion outside of current  
264 protected areas that conforms to probable dispersal routes of focal species towards more suitable  
265 habitat would create dispersal corridors into the protected areas of the future. In addition,  
266 planting Almendro trees in protected areas suitable for the future distribution could contribute to  
267 the climate readiness and persistence of Great Green Macaws.

268

269 *Future Directions:* The goals of this research include creating a workflow to collate, model, and  
270 analyze multiple species distributions. We used support from the NESCent-EOL-BHL Research  
271 Sprint and a well-known online species database, EOL, to create a proof-of-concept tool to  
272 evaluate habitat suitability models within protected areas. By publishing these analyses online,  
273 we can remove a technological barrier for conservation managers interested in conservation  
274 planning among changing climates scenarios.

275

### 276 **Highlights**

- 277 1. We created a pipeline for species distribution mapping.
- 278 2. Our technical product is available freely, including command line code and example data.
- 279 3. We demonstrated the utility of increasing access to spatial models for climate readiness and  
280 conservation planning.
- 281 4. We found that Great Green Macaws will lose overlapping habitat with its main host tree, the  
282 Giant Almendro. We suggest strategies for this species' conservation.

283

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289

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294

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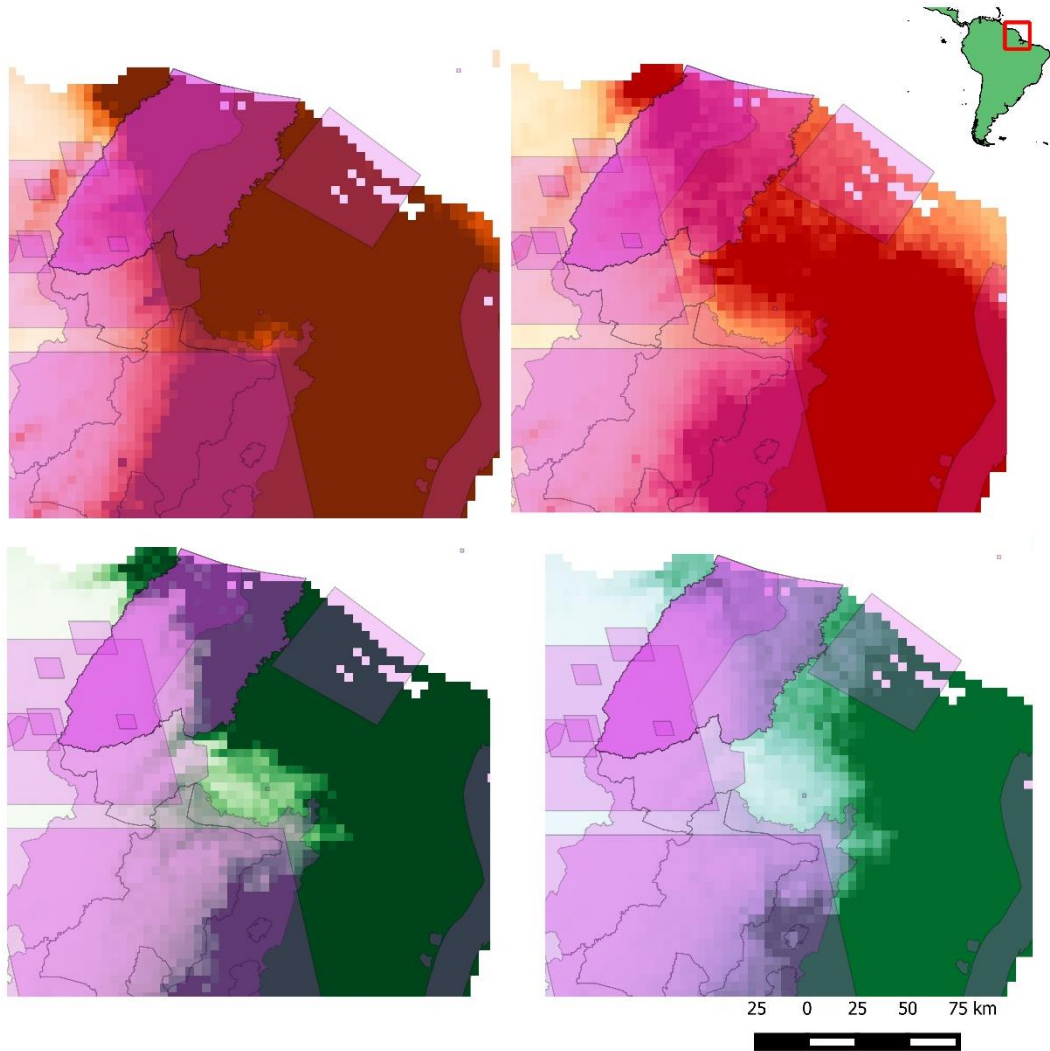
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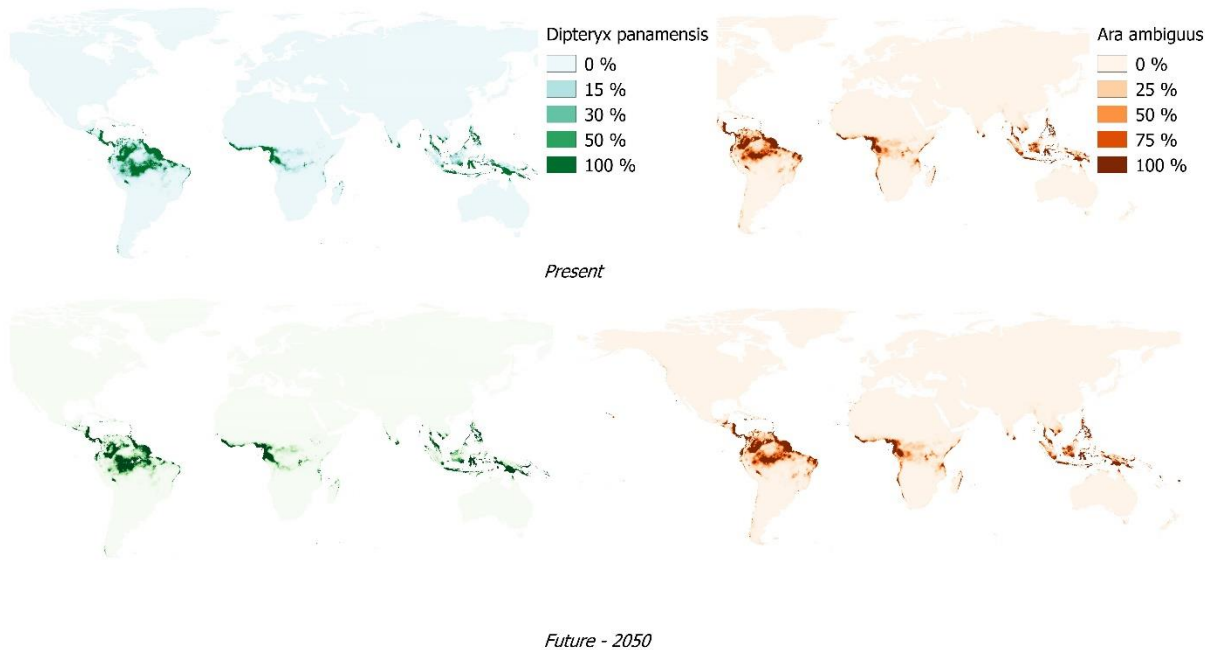


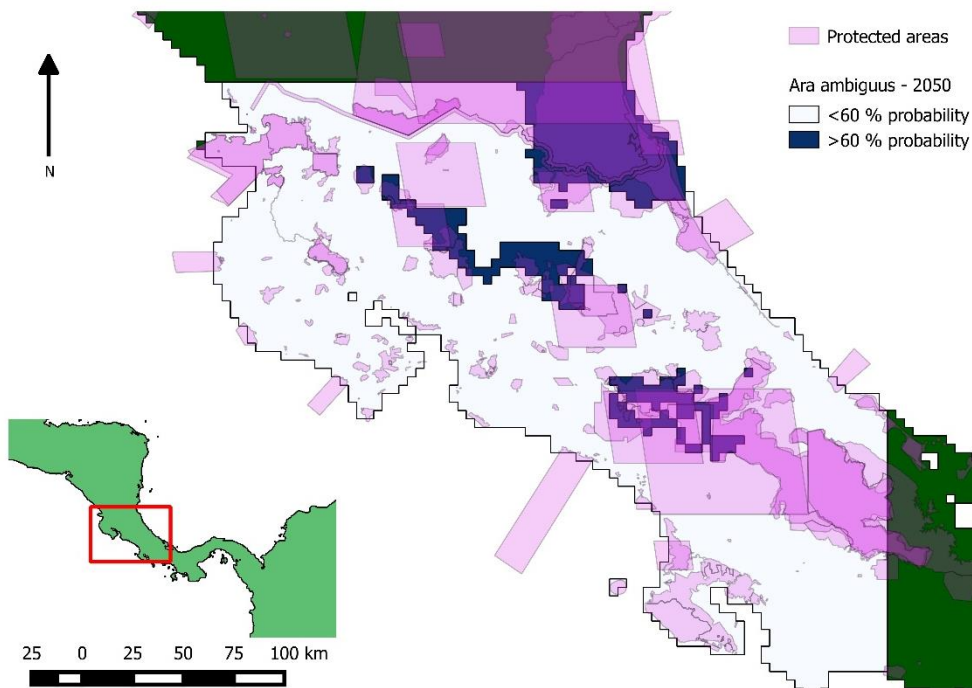
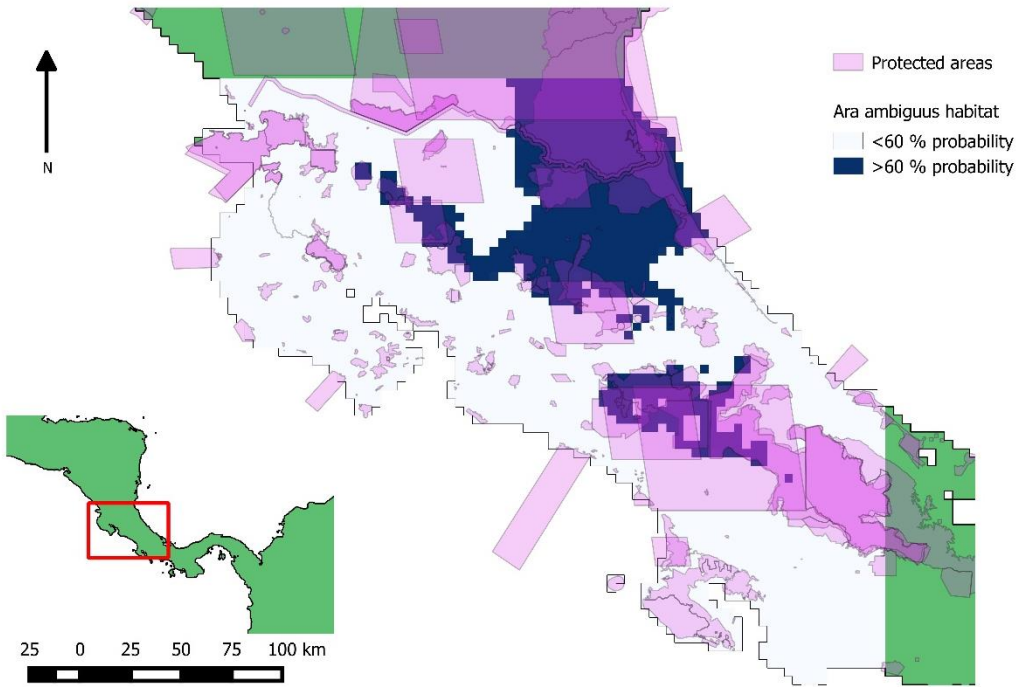
394

395 **Figure 1.** Loss of habitat across present (L) and future (R) climate scenarios will affect  
396 protected areas of the Great Green Macaw (top) and the Almendro tree (bottom). Habitat  
397 suitability colored as in Fig.2. Protected areas are filled in purple.

398  
399

400 **Figure 2.** Worldwide spatial models for two species, the Great Green Macaw (L: *Ara ambiguus*)  
401 and the Giant Almendro (R: *Dipteryx panamensis*), resulting from the spatial map pipeline in  
402 each climate scenario. Maps colored according to probability that a species could occur in a 2.5  
403 arc-minute grid cell. Model specifications included in text.  
404





407 **Figure 3.** Current species distribution maps for the Great Green Macaw generated in the pipeline  
 408 indicate more than 60 % of suitable habitat is protected in Costa Rica (top). Our study finds that  
 409 only 20.3% of suitable habitat persists inside of current protected areas by 2050, assuming no  
 410 human intervention (bottom).