

1-31-2019

## Back to the Future: Conserving Functional and Phylogenetic Diversity in the Amphibian-Climate Refuges

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### Recommended Citation

Lourenço-de-Moraes, R., Campos, F.S., Ferreira, R.B. et al. *Biodivers Conserv* (2019) 28: 1049.  
<https://doi.org/10.1007/s10531-019-01706-x>

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1 **Back to the future: Conserving functional and phylogenetic diversity in the amphibian-climate refuges.**

2

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21

22 **Abstract** Climate refuges have been used by several species over historical climate change. Ectothermic species  
23 often display good models for climate change studies because they are highly sensitive to temperature. Analysis  
24 of species loss with ecosystem and evolutionary values helps to understand environmental processes and climate  
25 consequences. Here, we associate the functional and phylogenetic diversity of amphibians in the Atlantic Forest  
26 hotspot, using multiple models for the present and future conditions. Through a novel approach, we predict  
27 species' threat status by 2080, following the IUCN's criterion B1. Our results estimate a drastic reduction in  
28 species richness, ecosystem functioning and evolutionary history at low latitudes and altitudes. We show that  
29 species will tend to disperse to the areas with milder temperatures (i.e., high latitudes/altitudes). Some of these  
30 areas are the same climate refuges that have been suggested for the Late Pleistocene. We highlight that 60% of

31 amphibians can become threatened under future conditions. This work advances the knowledge on climate  
32 refuges for amphibian ecology and evolution, supporting complementary tools for conservation strategies.

33

34 **Keywords:** Anthropocene, Climate change, Atlantic Forest, Anura, Gymnophiona

35

#### 36 **Acknowledgements**

37 We thank Thiago F. Rangel for providing access computational to the platform Bioensembles. We are grateful to  
38 the Asociación Española de Ecología Terrestre (AEET) for the research award granted to conduct this research.

39 We thank the Institut de Biologia Evolutiva (CSIC-UPF) for making the use of lab computers available. We  
40 thank the CNPq (140710/2013-2; 152303/2016-2) and the CAPES Foundation (99999.001180/2013-04) for the  
41 financial support in this work. We also thank the Technical and Scientific Committee of the Forest Institute of  
42 São Paulo (COTEC), Environmental Institute of Paraná (IAP), and the Chico Mendes Institute for the logistical  
43 support and the collection licenses (ICMBio/SISBIO:30344; 44755).

44

## 45 **Introduction**

46 Over millions of years, the Earth has undergone several climatic transformations that seem to appear to be  
47 cyclical (Raup and Sepkoski 1982). During these changes, most species had to take refuge in areas with milder  
48 environments and better resource availability (Haffer 1969; Mayr and O'Hara 1986; Bush 1994; Bush and  
49 Oliveira 2006; Carnaval et al. 2009; Bush et al. 2011). However, these cyclical events lead to five massive  
50 extinctions (Raup and Sepkoski 1982; Jablouski 1994; Bambach 2006; Barnorsky et al. 2011).

51 The current Anthropocene Age is directing toward the sixth mass extinction of the biodiversity (Wake and  
52 Vredenburg 2008; Barnosky et al. 2011; Dirzo et al. 2014).

53         Anticipating climate consequences on biogeographic patterns are key to address changes on functional  
54 and phylogenetic diversity relations to organism-mediated ecosystem goods and services (Montoya and Raffaelli  
55 2010; Cardinale et al. 2011; Prather et al. 2012), as well as evolutionary processes (Thuiller et al. 2011; Pio et al.  
56 2014). In this context, studies available about climate change should be evaluated integrating functional and  
57 phylogenetic diversity (Sobral and Cianciaruso 2012; Campos et al. 2017). Functional diversity is the value and  
58 variation of species and their characteristics that influence the functioning of communities (Tilman 2001) and the  
59 phylogenetic diversity is a measure of the diversity of a community that incorporates the phylogenetic  
60 relationships of species (Magurran 2004). Thus, it is possible to associate ecological and evolutionary  
61 approaches into spatial decision-making for conservation. The assumption that closely phylogenetic species have  
62 the same ecosystem roles is still an uncertain issue (Webb et al. 2002). Phylogenetic structure of communities  
63 depends on how the ecological characteristics evolved (Sobral and Cianciaruso 2012). Therefore, ecosystem  
64 functioning and stability are often correlated with changes in evolutionary process, producing several  
65 implications for ecological and human well-being on short-time scales (Alberti 2015).

66         Climate change is one of the main threats to global biodiversity (Thomas et al. 2004; Pereira et al.  
67 2010), continuously promoting variations in physiological and ecological processes that directly affect the  
68 distribution and persistence of species (Stenseth et al. 2002; MacDonald et al. 2004; Huey et al. 2009). Some  
69 studies have addressed how climate change affects individual performances (Huang et al. 2013; Holt and  
70 Jorgensen 2015), demographic dynamics (Lukoscheck et al. 2013; Pomara et al. 2014), and species richness  
71 (Lemes and Loyola 2013; Ferro et al. 2014). Predictive outcomes have included adaptation to novel conditions  
72 (Quintero and Wiens 2013), expansion or retraction of species' extent of occurrence (Ferro et al. 2014; Lemes et  
73 al. 2014), isolation to climate refuges (Puschendorf et al. 2009), and in the worst cases, species extinctions

74 (Thomas et al. 2004). Such climate change effects are the reasons there is a growing consensus that management  
75 decisions for biodiversity conservation must take into account this phenomenon (Araújo and Rahbek 2007).

76 Ecological niche models (ENMs), also referred to as species distribution models (SDMs) (Peterson et  
77 al. 2011; Rangel and Loyola 2012), have been used increasingly to estimate species ranges for future scenarios  
78 of climate change (Peterson et al. 2011). These models can be used to evaluate the current and future hotspots of  
79 functional and phylogenetic diversity (Thuiller et al. 2011; Loyola et al. 2013; Pio et al. 2014), working as  
80 efficient conservation tools (Del Toro et al. 2015). Ectothermic animals are highly susceptible to climate change  
81 (Pounds et al. 2006; Sinervo et al. 2010) due to the due to the interdependence of their behavioral-physiological  
82 functions in relation to the external environment (Ribeiro et al. 2012). More specifically, amphibians are very  
83 sensitive to environmental changes (Lourenço-de-Moraes et al. 2014) due to their metabolic features (Duellman  
84 and Trueb 1994), at high temperatures amphibians lose water to the atmosphere (Wells 2007) and may have  
85 local extinctions (Becker et al. 2007). Therefore, using ENMs may be an effective tool in predicting dispersion  
86 driven by climate change for amphibian species (Pie et al. 2013; Ribeiro et al. 2015), and may help to conserve  
87 these species.

88 The consequences of human activities go further than the loss of species and various studies reported  
89 losses of both evolutionary history and functional diversity at different landscapes (Purvis et al. 2000; Flynn et  
90 al. 2009; Mayfield et al. 2010). The Anthropocene is characterized by drastic climate change (especially warmer  
91 temperature), causing a massive defaunation (Dirzo et al. 2014). Facing this scenario, many species may be  
92 underestimated for their threat status (e.g., Ocampo-Peñuela et al. 2016). Carnaval et al. (2009) found three  
93 points of refuge during the Pleistocene, included areas of altitude in the mountain range of southeastern and  
94 northeastern in Atlantic Forest. Recent studies have suggested that areas of high altitude may be important  
95 refuges for vertebrates during the Anthropocene (Loyola et al. 2013; Lemes et al. 2014; Campos et al. 2017). In  
96 this context, we tested the hypothesis that the high elevation areas are refuges for amphibians and may maintain  
97 their contribution to ecosystem services and evolutionary potential. To address this hypothesis, we analysed the  
98 present and future distribution of taxonomic, functional and phylogenetic diversity of Atlantic Forest amphibian  
99 species. We correlated this diversity with altitude in both periods and analysed the retraction of species in the  
100 direction to higher areas. We also projected the potential species conservation status for 2080 based on the IUCN  
101 criteria.

102

## 103 **Materials and Methods**

### 104 *Study area*

105 We focused our analyses on the Atlantic Forest Biodiversity Hotspot (Myers et al. 2000), which originally  
106 covered around 150 million ha with heterogeneous environmental conditions provided by a wide range of  
107 climatic belts and vegetation formations (Tabarelli et al. 2005; Ribeiro et al. 2009). This biome has an altitudinal  
108 range from sea level to the mountain chains of Serra do Mar and Serra da Mantiqueira (Cavarzere and Silveira  
109 2012). This region has a longitudinal range with different forest compositions due to a diminishing gradient in  
110 rainfall from the coast to the interior, and a latitudinal range extending into tropical and subtropical environments  
111 (Ribeiro et al. 2009) (Fig. 1).

112

### 113 *Spatial species data*

114 We obtained spatial data of amphibian species through six steps: 1. We built a dataset with all the  
115 species distributed in the Atlantic Forest according to Haddad et al. (2013); 2. We included the species  
116 occurrences records available through the Global Biodiversity Information Facility (GBIF: <http://www.gbif.org>);  
117 3. We added maps of geographical ranges for each species from the IUCN Red List of Threatened Species  
118 (IUCN 2017); 4. We filtered out species that only occur in forested environments overlapping the spatial species  
119 data by the Atlantic Forest remnant map (SOS Mata Atlântica and INPE 2015), excluding all urban areas from  
120 the species distribution data; 5. We conducted complementary fieldwork in the major Atlantic Forest remnants of  
121 Brazil to supplement the dataset with observed functional traits, such as body size, reproductive mode, habitat,  
122 activity, poison patterns, habit and calling site (see Supplementary material Appendix 1, Fig. A1); and 6. We  
123 modelled the potential present and future distribution of species using ecological niche modelling.

124 We used the “Spatial Join” ArcGIS toolbox to transform species' spatial occurrences in matrices,  
125 matching rows from the join features to the target features based on their relative spatial locations. Then, we  
126 combined vector files based on expert knowledge of the species' ranges and forest remnant polygons into an  
127 overall coverage for species distribution modelling. We only considered spatial occurrences by those species  
128 where the distribution data intersected at least a grid cell (i.e. ~ 10 km<sup>2</sup>). We used forest remnant data to meet  
129 the habitat patch requirements based on visual interpretation at a scale of 1:50,000, delimiting more than 260,000  
130 forest remnants with a minimum mapping area of 0.3 km<sup>2</sup>. Therefore, we considered a species present in a cell if  
131 its spatial range intersected more than 0.3 km<sup>2</sup>. We also used the “Count Overlapping Polygons” ArcGIS

132 toolbox to obtain the species richness at the spatial resolution assessed, removing all duplicate records from the  
133 analyses (i.e. repeated records of a species at a single locality).

134

135 *Ecological niche modelling, species richness and turnover*

136 We used ArcGIS 10 software (ESRI 2010) to build presence/absence matrices from the species  
137 distribution data by superimposing a grid system with cells of 0.1 latitude/longitude degrees, creating a network  
138 with 10,359 grid cells. In total, we assessed the geographical ranges of 453 amphibian species (five  
139 Gymnophionas and 448 Anurans) covered by our grid system. We only considered a grid cell occupied by those  
140 species where the centre of the grid cell intersected with the species ranges. We also used the “Count  
141 Overlapping Polygons” ArcGIS toolbox to obtain species richness at the spatial resolution assessed, removing all  
142 duplicate records from the analyses (i.e. repeated records of a species at a single locality).

143 Considering that species occurrence patterns are determined at large-scales by responses of organisms  
144 to different environmental conditions (reflecting the Grinnellian component of the ecological niche, *sensu*  
145 Soberón 2007), we used ecological niche models (ENMs) to predict the distribution area of amphibian species in  
146 the Atlantic Forest. For this, we used the species occurrence matrix and the layers of climatic-environmental  
147 variables, resulting in a suitability matrix, which we used to model and map the potential distribution of each  
148 species evaluated.

149 We used the following bioclimatic variables in the modelling process: 1. annual mean temperature; 2.  
150 annual temperature range; 3. precipitation of the wettest month; 4. precipitation of the driest month; and 5.  
151 precipitation of the warmest quarter. We obtained these variables for the present and future (mean of simulations  
152 for 2080-2100) from CMIP5 – Coupled Models Intercomparison Project Phase 5 ([http://cmip-  
153 pcmdi.llnl.gov/cmip5/](http://cmip-pcmdi.llnl.gov/cmip5/); and also at <http://ecoclimate.org>, see Lima-Ribeiro 2015), and downscaled to the  
154 resolution of 0.1 degrees. We also used altitude as predictor of richness and dispersion from the dataset available  
155 at WorldClim Global Climate Data ([www.worldclim.org](http://www.worldclim.org)). We assumed altitude will remain constant through  
156 time, these permit to perform future predictions. For the future, we used the greenhouse gas concentration  
157 trajectory corresponded to the Representative Concentration Pathway (RCP) 4.5, which represents a moderated  
158 emission scenario within an optimistic context. This moderate scenario (RCP4.5) incorporates historical  
159 emissions pathways and land cover information to meet potential climate policies (Thomson et al. 2011). We  
160 choose this scenario believing to present better information than extreme scenarios (pessimistic RCP 8.5 or  
161 optimistic RCP 3). In the context, we used simulations provided by four Atmosphere-Ocean General Circulation

162 Models (AOGCMs): CCSM, CNRM, MIROC and MRI, which were obtained from CMIP5 (Coupled Model  
163 Intercomparison Project – Phase 5) for the consensus model. Original data resolution varied from 1° to 2.8° (in  
164 longitude and latitude) and both present and future climate variables were re-scaled to fit our grid resolution.

165 We performed four conceptually and statistically different ENMs based on presence data (i.e. only  
166 occurrences are known, absences are unknown) using the algorithms: 1. Bioclim (BIO, Busby 1991) based on  
167 bioclimatic envelope logic; 2. Gower Distance and Euclidean Distance (GD, EUD, Carpenter et al. 1993) based  
168 on environmental distance approach; 3. Maximum Entropy (ME, Phillips et al. 2006) and random forest (RF,  
169 Breiman 2001) based on machine learning technique; and 4. Ecological Niche Factor Analysis (ENFA, Hirzel et  
170 al. 2002) based on multivariate analysis, and Genetic Algorithm for Rule set Production (GARP, Stockwell and  
171 Noble 1992). Given the particularities of each model, they provided different predictions, generating  
172 uncertainties about which model is more appropriate to represent the geographical distribution of species (Diniz-  
173 Filho et al. 2009). To overcome this uncertainty and minimize errors, we employed the ensemble forecasting  
174 approach, which offers a consensus of multiple models (Araújo and New 2006). The main idea of ensemble  
175 forecasting is that different sources of errors will affect each niche model in different ways and, by obtaining a  
176 consensus result of these models, errors will tend to cancel each other out and produce a more trustworthy and  
177 conservative solution (Diniz-Filho et al. 2010). Assuming that the richness consensus model (CONS) reduces  
178 uncertainty and error associated with alternative ENMs, we interpreted only the range sizes from the CONS  
179 model.

180 We randomly partitioned presence and absence (pseudo-absence in the case of Maxent) data of each  
181 species into 75% for calibration (or training) and 25% for evaluation (or test); repeating this process 10 times by  
182 cross-validation for all models. For each ENM, we converted the continuous predictions of suitability into a  
183 binary vector of 1/0 (presence and absence in each cell), finding the threshold that maximizes sensitivity and  
184 specificity values in the receiver operating characteristic (ROC). The ROC curve is generated by plotting the  
185 fraction of true positives vs. the fraction of false positives at various threshold settings. The distribution areas  
186 were estimated obtaining 280 predictions (7 models x 10 randomizations x 4 AOGCMs) for each species and  
187 time-period of climatic conditions (i.e. present and future). This allowed us to generate a frequency of  
188 projections in the ensemble. Then, we generated the frequency of projections weighted by the total sum of  
189 squares (TSS) statistics for the present and future (the best models according to this metric have more weight in  
190 our consensus projections). The TSS range from -1 to +1, where values equal to +1 is a perfect prediction and  
191 values equal to or less than zero is a prediction no better than random (Allouche et al. 2006; Eskildsen et al.



2013). We considered the species present only in cells where at least 50% of models retained in the ensemble point out the species as present. In our analyses, we obtained the CONS for each AOGCM and time period (present and 2080). Thus, we obtained the final maps of richness for present, future and turnover through the average of values projected by CONS for each grid cell – considering the different GCMs. We ran all models using the computational platform Bioensembles (Diniz-Filho et al. 2009), and mapped results using the software SAM v.4.0 (Rangel et al. 2010). To determine the species patterns of amphibians of the Atlantic Forest, we employed the modelling strategy at the community level of “predict first, assemble later” (*sensu* Overton et al. 2002), where the ranges of individual species are modelled one at a time as a function of environmental predictors and then overlapped to obtain the species richness.

We calculated species turnover between present and future species distributions in each cell according to formula  $100 * ((G+L)/(S+G))$ . (Thuiller 2005), where “G” refers to the number of species gained, “L” the number of species lost and “S” the species richness (contemporary) found in the cell.

#### *Functional and Phylogenetic Diversity*

We used the following functional traits according to Haddad et al. (2013), and supplemented with data from our fieldwork: 1. body size; 2. appendices (apodal and tetrapod); 3. activity (nocturnal, diurnal, and both); 4. toxicity (toxic, nontoxic, unpalatable, or bad odour); 5. habitat (forested area, open area, and both); 6. habit (arboreal, phytotelmate, terrestrial, cryptozoic, fossorial, rheophilic, semi-aquatic, and aquatic); 7. calling site (bamboo grove, swamp or lake, bromeliad, forest floor, tree canopy, caves or burrows, rock wall, backwater river, stream, river, shrubs, grasslands and not sings); and 8. reproductive mode (1 to 39 modes; see Haddad and Prado 2005; see Supplementary Material Appendix 1, Table A1 for traits details). Each functional trait contributes to ecosystem supporting services through direct and indirect changes on the ecosystem functions and their processes (Hocking and Babbitt 2014). For further details of specific functions and ecosystem supporting services of each one of the functional traits assessed, see Supplementary Material Appendix 1, Table A2.

We followed the protocol proposed by Petchey and Gaston (2006) to calculate functional diversity (FD): 1. construction of a species-trait matrix; 2. conversion of species-trait matrix into a distance matrix; 3. clustering distance matrix into a dendrogram (UPGMA); and 4. calculating functional diversity by summing dendrogram branch lengths of species community. To create the distance matrices, we used the method Gower distance proposed by Pavoine et al. (2009).

We used the phylogenetic diversity index (Faith 1992) to quantify the phylogenetic diversity (PD),

222 which comprises the sum of the branches lengths of the phylogenetic tree of all species assessed and is often  
223 used in the assessment of phylogenetic diversity of con-current species (e.g., Rodrigues and Gaston 2002; Safi et  
224 al. 2011; Trindade-Filho et al. 2012). The PD index has appropriate ways of accounting for relatedness between  
225 taxa and evolutionary history in a conservation context (Pio et al. 2011).

226 We based the phylogenetic distance through 207 species nucleotide sequences obtained from GenBank  
227 (Benson et al. 2013) and provided by the National Center for Biotechnology Information (NCBI) (See  
228 Supplementary Material Appendix 1, Table A3). Following the protocol proposed by Pyron and Wiens (2011) in  
229 an extant amphibian phylogeny, we used 12 genes to produce a novel estimate phylogeny for the Atlantic Forest  
230 amphibians (i.e. 11,906 bp for each species), though three mitochondrial genes were included: cytochrome b (cyt-  
231 b), and the large and small sub-units of the mitochondrial ribosome genes (12S/16S); and nine nuclear genes: C-  
232 X-C chemokine receptor type 4 (CXCR4), histone 3a (H3A), sodium–calcium exchanger (NCX1), pro-  
233 opiomelanocortin (POMC), recombination-activating gene 1 (RAG1), rhodopsin (RHOD), seventh-in-absentia  
234 (SIA), solute-carrier family 8 (SLC8A3), and tyrosinase (TYR). For the length-variable regions, we performed  
235 multiple pairwise comparisons by the online version of MAFFT v.6.8 and the G-INS-i algorithm (Kato and Toh  
236 2008). After, we put together alignments of all genes in the same alignment using the software SequenceMatrix  
237 1.7.7 (Vaidya et al. 2011) to concatenate the supermatrix previously produced.

238 We analysed the phylogenetic relationships with Bayesian analyses in software BEAST 1.8 (Drummond  
239 and Rambaut 2007). We generated the phylogeny based on the combined data matrix using a HKY model of  
240 sequence evolution for one partition for all genes, under a Yule speciation process as the tree prior and an  
241 uncorrelated relaxed clock. After removal of the burn-in, we run the Yule process for 100 million generations,  
242 ensuring that the number of generations after convergence were sufficient assessed with Tracer v1.6 (Drummond  
243 and Rambaut 2007), combining the results with the use of Logcombiner 1.8 and Treeanotator 1.8 (Drummond  
244 and Rambaut 2007). We considered the nodes strongly supported if they received probability (pp) support values  
245  $\geq 0.95$ . Thus, we reconstructed a new phylogenetic tree using the Mesquite software version 3.0 (Maddison and  
246 Maddison 2015).

247 To verify whether functional diversity (FD) and phylogenetic diversity (PD) was influenced by species  
248 richness (Devictor et al. 2010), we used independent swap null models (Gotelli and Entsminger 2001), according  
249 to the protocol proposed by Swenson (2014). The values provided by such models are more sensitive to  
250 preserving both site diversity and species frequency of occurrence while randomizing the pairs of species/sites,  
251 which ensure that patterns of trait assembly do not simply reflect differential occurrence of particular species

252 (Ackerly et al. 2006; Swenson 2014) for present and future times. The null model is totally independent of the  
253 species richness of an assemblage (Swenson 2014), which provides expected values at different species richness  
254 levels (Mouchet et al. 2010). Hence, we tested if the functional and phylogenetic diversity were higher, equal or  
255 lower than expected by chance for each grid cell (random or non-random pattern), assuming a random  
256 distribution in which every species could occupy any grid cell in the biome. For each pruning event (present and  
257 future), we computed 1,000 replicates of random remaining PD and FD, allowing us to obtain a *P*-value of  
258 predicted PD and FD as compared to the distribution of the random replicates. All analyses were performed  
259 using the packages “ade4”, “picante”, “FD” and “vegan” through the R software (R Development Core Team  
260 2017).

261

### 262 *Species Richness, and Functional and Phylogenetic Diversity vs. Topography and Spatial References*

263 We used correlation matrices to compare the topographic patterns and spatial references (altitude and  
264 latitude) to the values obtained by the richness consensus model for CONS, Turnover, FD and PD in each grid  
265 cell for present and future time (2080). Thus, we correlated the values obtained for CONS, FD and PD with  
266 altitude, and the turnover values with altitude and latitude using simple linear regression models.

267 We used correlation matrices to compare the topographic patterns and bioclimatic variables (altitude vs  
268 bioclimatic variables) to the values in each grid cell for present and future conditions. Using multiple linear  
269 regression models for the correlation matrices, we compared the following bioclimatic variables: 1. annual mean  
270 temperature; 2. annual temperature range; 3. precipitation of the wettest month; 4. precipitation of the driest  
271 month; and 5. precipitation of the warmest quarter.

272

### 273 *Threat status of species facing climate change*

274 From the individual range sizes (i.e. number of occupied cells) of each species in present and future, we  
275 estimated the threat status of amphibian species by 2080, fitting the species' extent of occurrence under the  
276 IUCN's criterion B1 (IUCN, 2015). We considered the following threat categories: 1. Extinct (EX) = 0 km<sup>2</sup>, 2.  
277 Critically Endangered (CR) = occurrence < 100 km<sup>2</sup>; 3. Endangered (EN) = occurrence < 5,000 km<sup>2</sup>; 4.  
278 Vulnerable (VU) = occurrence < 20,000 km<sup>2</sup>; and 5. Nonthreatened (NT) = occurrence > 20,000 km<sup>2</sup>.

279 We also evaluated the percentage of range loss for the future. We considered the following categories:  
280 1. species with total loss 100%; 2. species whose loss is estimated at 80% for the projected time interval; 3. the  
281 species whose loss is estimated at 50% for the projected time interval; 4. the species whose loss is estimated at

282 30% for the projected time interval; and 5. the species whose loss is estimated at below 30% for the projected  
283 time interval.

284 .

## 285 **Results**

286 The results from the total sum of squares (TSS) for most species presented average and standard deviation of  
287  $0.61 \pm 0.11$ , indicating relatively high fit model. The overlap of individual species ranges generated by the  
288 CONS model suggested that the highest species richness values were restricted almost entirely to the eastern-  
289 central portion of the Atlantic Forest in the present times (Fig. 2, 3 and 4). Species richness pattern showed no  
290 significant relationships with the altitude ( $r^2 = 0.000$ ,  $P = 0.182$ , Fig. 4c). The future predictions produced by  
291 CONS from different AOGCMs pointed out the losses of climatically suitable areas in this region by 2080, with  
292 the species richness directed to the east-central portion of the Atlantic Forest. In this case, species richness  
293 increased toward higher altitude ( $r^2 = 0.132$ ,  $P < 0.001$  Fig. 3d). In general, CCSM and MRI showed two distinct  
294 species-rich areas and CNRM and MIROC produced more homogeneous results, with the latter being more  
295 restrictive (Fig. 2a-d). By combining the results of the AOGCMs in a full ensemble model, we found that in the  
296 future the species richness peaks are likely to be restricted to a reduced portion of the central-eastern region of  
297 the biome in locations closer to the mountain regions of the Atlantic Forest (Fig. 3).

298 Temporal turnover was high after the results of AOGCMs were combined in a full ensemble model.  
299 Changes in species composition are predicted to be greater on the western edge and on the northeastern edge of  
300 the biome. Higher turnover rates were found at lower latitudes ( $r^2 = 0.308$ ,  $P < 0.001$ ) and lower altitudes ( $r^2 =$   
301  $0.307$ ,  $P < 0.001$ ) (see Fig. 4a-c).

302 Our results showed high Functional Diversity (FD) in the regions of the eastern Atlantic Forest with the  
303 highest rates in the east-central region rising to the northeast in the present time (Fig. 5a, c). In 2080, these  
304 values will decrease from 17.30 to 15.53 at its maximum value (Fig. 5b), and will have a significant higher loss  
305 in areas of lower altitudes (Fig. 5b, d). High rates of FD were found mainly in the south of Bahia to the south of  
306 São Paulo states. High values of FD were correlated with high altitude for both the present ( $r^2 = 0.004$ ,  $P <$   
307  $0.001$ , Fig. 5c) and future ( $r^2 = 0.101$ ,  $P < 0.001$ , Fig. 5d).

308 The highest values of Phylogenetic Diversity (PD) in the present time are distributed in the east-central  
309 region, mainly in the region of Serra do Mar rising to the Central Corridor and in a small part of Pernambuco (in  
310 high altitude areas) (Fig. 6a, c). For 2080, these values will decrease from 5.65 to 5.44 at its maximum value  
311 (Fig. 6b), which will dramatically decrease in the south and north of Bahia, increasing towards the south of the

312 Serra do Mar mountain chain. Higher-altitude regions will be replaced by significant values in the future ( $P <$   
313  $0.001$ , Fig. 6d). Built null models for FD and PD in present and future times showed different values than  
314 expected by chance ( $P < 0.001$ ), indicating a non-random pattern of FD and PD. FD and PD were highly  
315 correlated (present  $r^2 = 0.91$ ,  $P < 0.001$ ; future  $r^2 = 0.94$ ,  $P < 0.001$ ), based on comparison of the CONS consensus  
316 model (present FD –  $r^2 = 0.87$ ,  $P < 0.001$ , PD –  $r^2 = 0.89$ ,  $P < 0.001$ ; future FD –  $r^2 = 0.86$ ,  $P < 0.001$ , PD –  $r^2 =$   
317  $0.84$ ,  $P < 0.001$ ). Therefore, the loss of species richness in the future may be accompanied by the loss of FD and  
318 PD (Fig. 7).

319 The bioclimatic variable correlation with altitude was correlated (present  $r^2 = 0.60$ ,  $P < 0.001$ ; future  $r^2 =$   
320  $0.60$ ,  $P < 0.001$ ), but the only bioclimatic variable with positively relation was the precipitation of the wettest  
321 month (Table 1). The change of bioclimatic variables in high altitude areas can be lower in the future than in the  
322 low altitude areas. It may leave the higher altitudes more favourable to amphibians in the future.

323 The prediction of massive habitat suitability losses under climate change will negatively affect most  
324 (60%) amphibians of the Atlantic Forest and most will be subjected to some level of threat by 2080 (Fig. 8).  
325 According to our estimations under the IUCN's criterion B1, 40% ( $n = 181$  spp.) of the species will be not  
326 threatened. However, 15% ( $n = 62$  spp.) of the species will experience less than 30% reduction from the original  
327 distribution area by considering the projections for a moderate carbon emission scenario. Our results also  
328 indicated that 21.6 % ( $n = 97$  spp.) of the species are expected to be extinct from the biome by 2080. The  
329 summary of the impacts of future climatic alterations on each individual species is given in Supplementary  
330 Material Appendix 1, Table A4. Our results showed that the functional traits can have losses of 30% on average.  
331 The trait habit was that most show reduction and species with the subtrait phytotelmata cannot occur (Fig. 9).

332

### 333 Discussion

334 Our data showed a dramatic reduction of species range (CONS, PD and FD) for 2080. High rates of turnover in  
335 the lower latitudes and lower rates in the high altitudes strengthen the mountains of Atlantic Forest as climatic  
336 refuges (Randin et al. 2009; Araújo et al. 2011). The persistence of the species in their original ranges depend on  
337 their degree of physiological and phenotypic plasticity, antipredator mechanisms, reproductive mode, and  
338 evolutionary adaptation to environmental change (Holt 1990; Visser 2008; Toledo et al. 2012; Urban et al. 2014;  
339 Ferreira et al. 2016; Lourenço-de-Moraes et al. 2016, 2018). As result, some species have increased their ranges,  
340 but with low range in the future. For instance, opportunistic species adapted to warmer and drier environments  
341 had a spatial range expansion (e.g., *Rhinella crucifer*, *Dendropsophus branneri*, *Leptodactylus troglodytes* and

342 *Siphonops annulatus*). Species that live in high altitudes and high latitudes had their ranges little affected, due to  
343 the low temperature increase and high rainfall in these localities. *Brachycephalus brunneus*, a species that due to  
344 its morphology and great dependence on abiotic factors (i.e., temperature and rainfall – 1,300 m a.s.l.; Ribeiro et  
345 al. 2005), had low range changes in our model, which enable it to remain in the future. However, species of this  
346 same genus that occur in the north portion of the Atlantic Forest, such as *B. pulex* (Napoli et al. 2011), also can  
347 become extinct according to the same model.

348 Our results showed that FD and PD have high correlation among themselves and a non-random pattern  
349 of species composition for both present and future times. This pattern suggests that environmental factors may  
350 act as a filter that does not allow the co-existence of similar species (Diamond 1975; Weiher and Keddy 1999).  
351 In addition, historical factors provided biogeographic barriers acting to determine the regional bank of some  
352 species assemblages (Ricklefs and Schluter 1993). We revealed three major areas of FD and PD for the present  
353 time, which are located in the mountains of the Serra do Mar, the Central Corridor of the Atlantic Forest and the  
354 high altitude areas of Pernambuco state. Carnaval et al. (2009) pointed out three climatic refuges for amphibians  
355 during the Pleistocene: 1. Southern Bahia state (located in the Central Corridor of the Atlantic Forest); 2.  
356 Pernambuco state; 3. East-north region of São Paulo (i.e., Serra do Mar). We showed higher rates of PD and FD  
357 in these areas, supporting Carnaval et al. (2009) hypothesis. Our results also suggested climatic refuges in the  
358 Espírito Santo state, the Serra da Mantiqueira region that corresponds to the South of Minas Gerais state, and the  
359 South of Serra do Mar that corresponds to the east of Paraná state. In the future (i.e., 2080), these same areas will  
360 continue as climatic refuges, mainly in higher altitudes. Our model showed that species may have suitable  
361 habitat in higher latitudes and altitudes (see Fig. 3 and 4). Species with access to mountainous regions may  
362 migrate to higher altitude areas, which have lower temperatures (Colwell et al. 2008), and in the case of the  
363 Atlantic Forest, should retain greater humidity due to better-preserved forests cover (Ribeiro et al. 2009). Our  
364 data showed that altitude areas are positively correlated with increased rainfall mainly in the drier months. In  
365 addition, we suggested that areas of higher altitude will have lower temperature under climate change, making  
366 these areas suitable for species survival. Therefore, high altitude areas can be associated to amphibian-friendly  
367 climatic variables using forecast scenarios.

368 Loyola et al. (2013) indicated high values of PD for amphibians in the Atlantic Forest in both the  
369 present and future (i.e., 2080). Our findings contradict these values, indicating low PD values and significant  
370 correlations may result in the loss of richness consensus model (CONS) for the future. However, our results  
371 corroborate the data obtained by Thuiller et al. (2011), which showed that the loss of species richness may be

372 accompanied by the loss of PD. Furthermore, we also found that the loss of species richness in the future will  
373 result in the loss of FD.

374           The historical loss and their relationships do not reflect the actual proportion of loss in relation to the  
375 conservation of species. FD reflected better the loss of ecological functions and evolutionary perspectives,  
376 because similar species from similar phylogenetic clades may not coexist due to possible competitive exclusion  
377 (Arnau et al. 2016). However, closely phylogenetic species may have different roles on the ecosystem  
378 functioning (Webb et al. 2002; Gomez et al. 2010). In these cases, the loss of phylogenetically similar species  
379 may coexist and may have greater losses in processes and ecosystem services (Webb et al. 2002). By framing  
380 evolutionary ecology into conservation science, we revealed that phylogenetic metrics can be relevant tools for  
381 functional landscape planning for threatened amphibian species.

382           According to our results, 60% of the studied species will be threatened or extinct by 2080. It is highly  
383 concerning that 92% of the species of our study are not included in any threatened status by the Brazilian Red  
384 list (Supplementary material Appendix 1, Table A4). Moreover, amphibian species from Atlantic Forest  
385 protected areas are more threatened by extinction than in other Brazilian protected networks (Campos et al.  
386 2016). The Atlantic Forest was destroyed severely and fragmented, resulting in only 9-12% of its original  
387 formation remaining (Ribeiro et al. 2009). The current distributions of species provided by IUCN do not undergo  
388 any type of biological filter (e.g., urban and rural areas). The proximity of the protected areas to urban  
389 environmental, also negatively affect the local species richness (Lourenço-de-Moraes et al. 2018). Because of  
390 this, the analysed data can lead to overestimations, and the results for the future may be even more alarming.

391           Many biotic and abiotic factors can influence the richness and composition of species in an ecosystem  
392 (Diamond 1975). Amphibians are particularly sensitive to environmental changes, and depending on the species,  
393 dispersion may be difficult because of its specializations and diminutive size (Crump 2010; Early and Sax 2011;  
394 Lourenço-de-Moraes et al. 2012, 2014). The main reason behind our choice by the consensus modelling  
395 approach was to look for a straightforward combination of environmental predictors that best explains the  
396 presence-only species distribution across forest remnants. Given that temperature and humidity are the main  
397 climate components that directly affect the biology of amphibians (Carey and Alexander 2003), we selected  
398 these variables along altitudinal gradients to provide a reasonably good representation of the species present in  
399 the forest remnants.

400           The use of various algorithms to reach a better consensus model have been demonstrated as an effective  
401 strategy to reach outcomes closer to reality, and it is one of the keys to understanding how communities can

402 respond to climate change (Araújo and New 2006; Marmion et al. 2009). Therefore, our consensus model  
 403 showed useful results to plan conservation actions in relation to spatial and temporal patterns in ecology and  
 404 evolution. We introduced a new conservation framework that has sought to understand the functioning of  
 405 ecosystems from the amphibian-climate refuges in an age of extinction.

406 Studies in the Atlantic Forest have been warning about the need to invest in protected areas at high  
 407 altitudes (Lemes et al. 2013; Loyola et al. 2013), mainly in the areas of Serra do Mar and south of Bahia  
 408 (Carnaval et al. 2009; Campos et al. 2017; Campos and Lourenço-de-Moraes 2017). Considering the dramatic  
 409 evolutionary and ecological loss showed in this study, we suggest four large areas as priority for conservation in  
 410 the Atlantic Forest: the Serra do Mar, the Serra da Mantiqueira, the Central Corridor and areas of high altitude in  
 411 the Pernambuco state.

412 Amphibians are very sensitive to climate change mainly due to their metabolic characteristics. Dispersal  
 413 across disturbed areas may be unfeasible for most species. The management of the already conserved areas,  
 414 inserted in the points of climatic refuges, as well as areas of connections to these refuges is indispensable for the  
 415 conservation of the amphibians. Knowing the first climatic refuges facilitates the decision making to conserve  
 416 the amphibians during the climatic changes avoiding mass extinctions.

417

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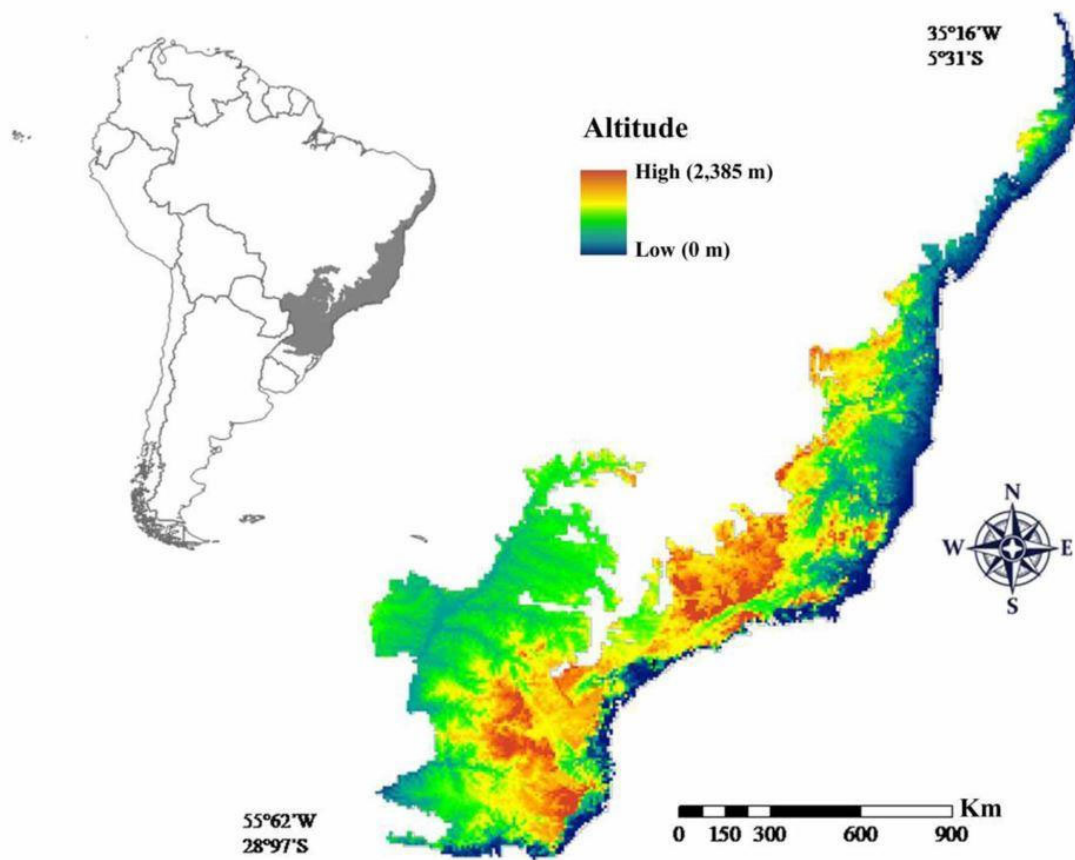
704 **Caption to Tables and Figures**

705 Table 1. Multiple linear regressions on altitude vs bioclimatic variables to present and future.

|                                     | Stimted Std.      | Error             | t value        | <i>P</i>       |
|-------------------------------------|-------------------|-------------------|----------------|----------------|
|                                     | Present/Future    | Present/Future    | Present/Future | Present/Future |
| (Intercept)                         | 3821.527/4566.084 | 85.25597/82.31261 | 44.82/55.47    | <0.001         |
| Annual Mean<br>Temperature          | -152.191/-168.309 | 2.35075/2.33988   | -64.74/-71.93  | <0.001         |
| Temperature<br>Annual Range         | -16.7108/-7.51973 | 0.90175/0.72161   | -18.53/-10.42  | <0.001         |
| Precipitation of<br>Wettest Month   | 2.52711/2.32013   | 0.11515/0.09978   | 21.95/23.25    | <0.001         |
| Precipitation of<br>Driest Month    | -7.93307/-12.0148 | 0.28229/0.22446   | -28.10/-53.53  | <0.001         |
| Precipitation of<br>Warmest Quarter | -0.42978/-0.51133 | 0.03805/0.03226   | -11.29/-15.85  | <0.001         |
| R-squared                           |                   | 0.60/0.59         |                | <0.001         |
| F-statistic                         |                   | 3122/3091         |                |                |

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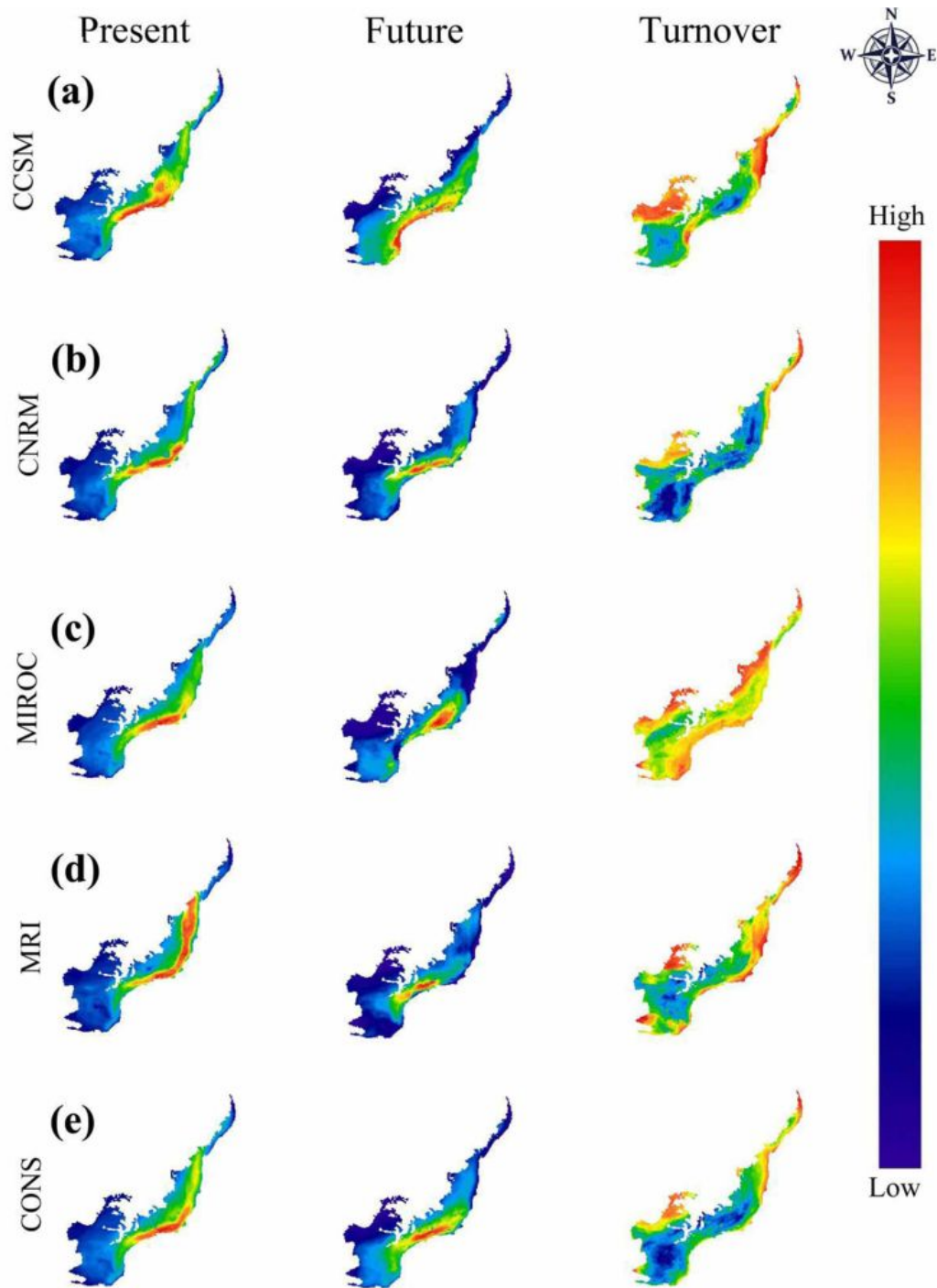
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709 **Fig. 1.** Map of the study area of Brazilian Atlantic Forest hotspot.

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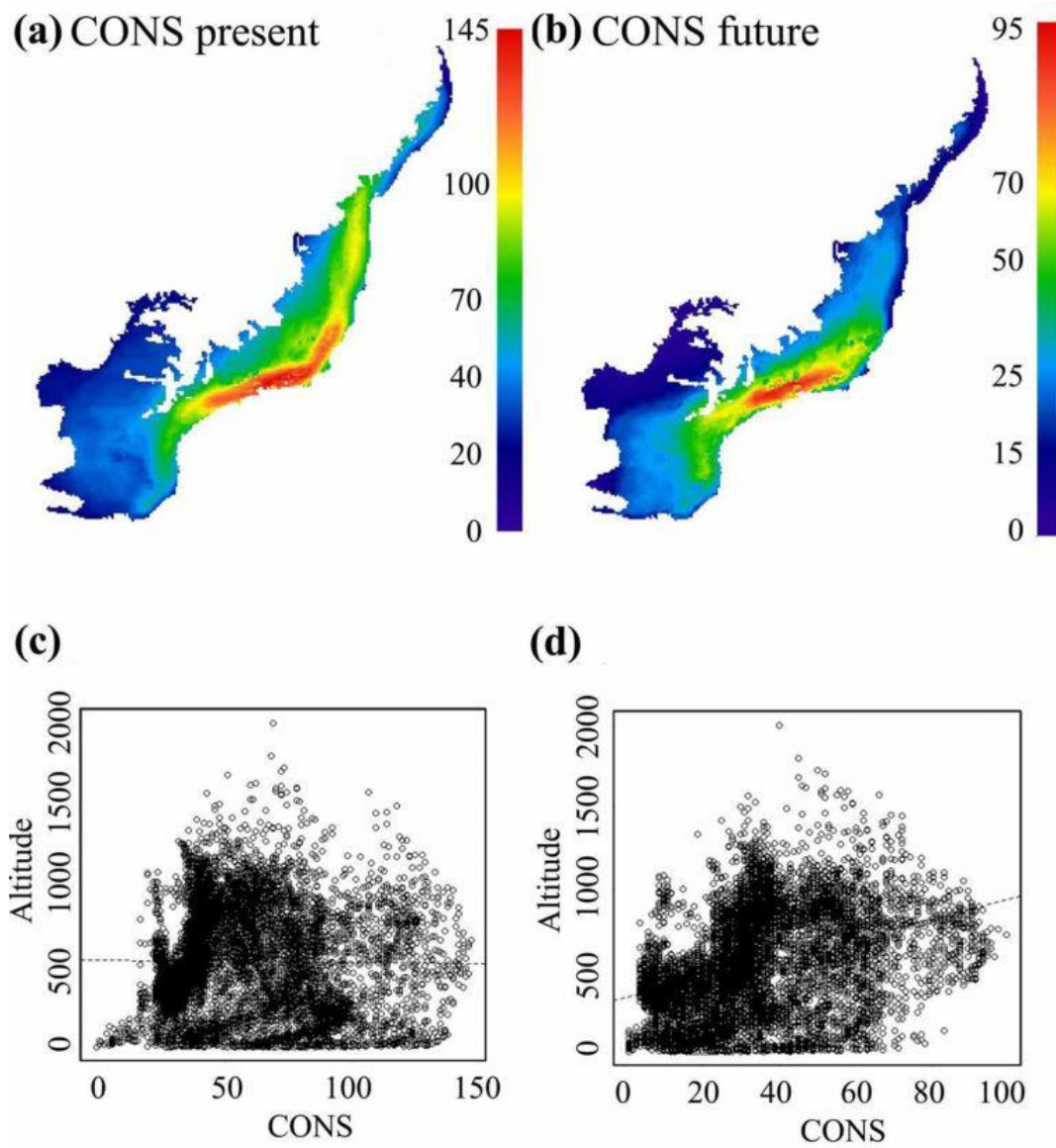
711

712 **Fig. 2.** Species richness and turnover derived from different Global Circulation Models (a) CCSM, CNRM (b),

713 MIROC (c), MRI (d) and Richness Consensual Model-CONS (e) for amphibian species in the present time and

714 for 2080.

715



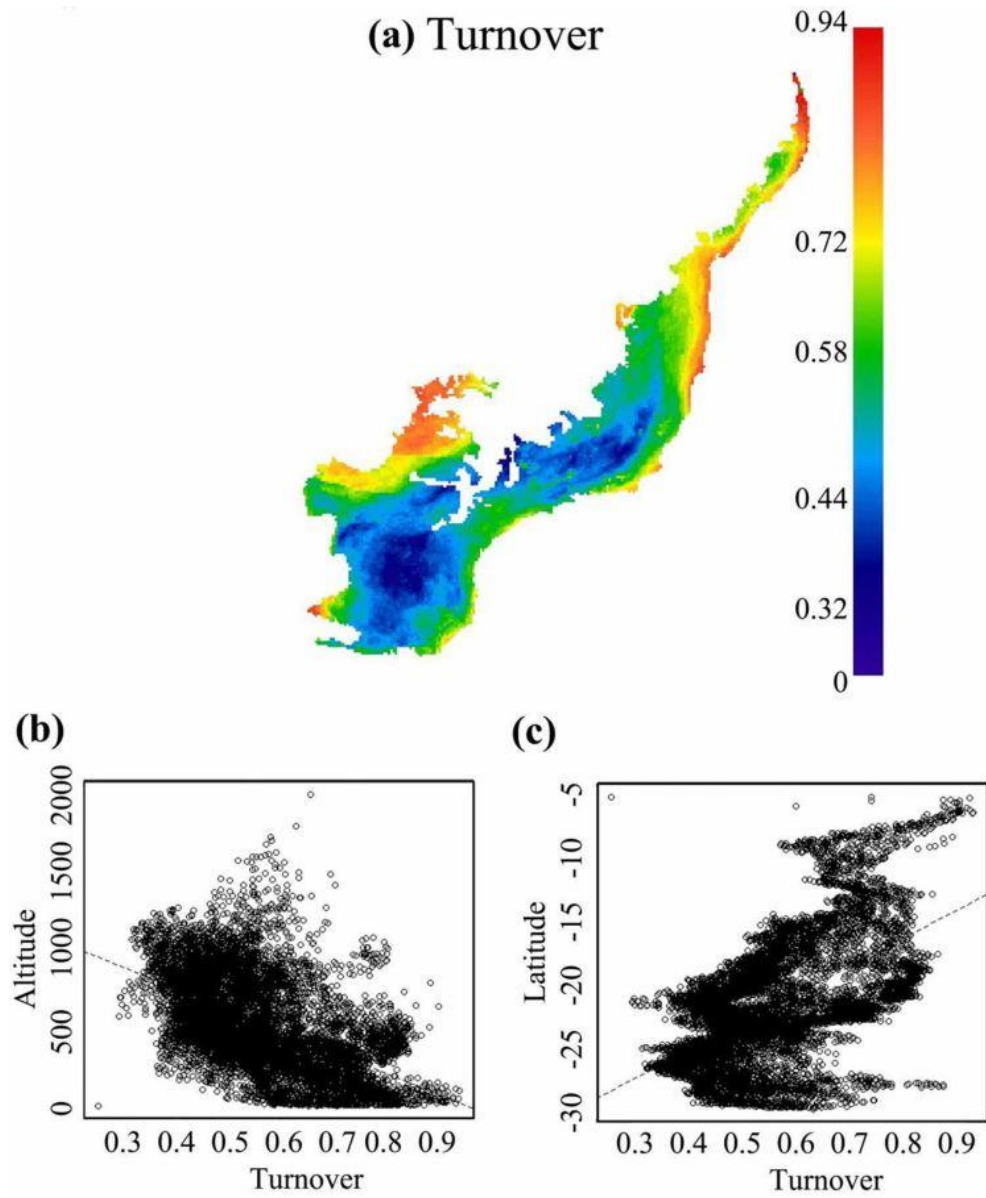
716

717 **Fig. 3.** Species richness derived from consensus model map for present time (a) and for 2080 (b). Relation

718 between amphibian species richness consensual model (CONS) and altitude (in meters) for present time (c) and

719 for 2080 (d).

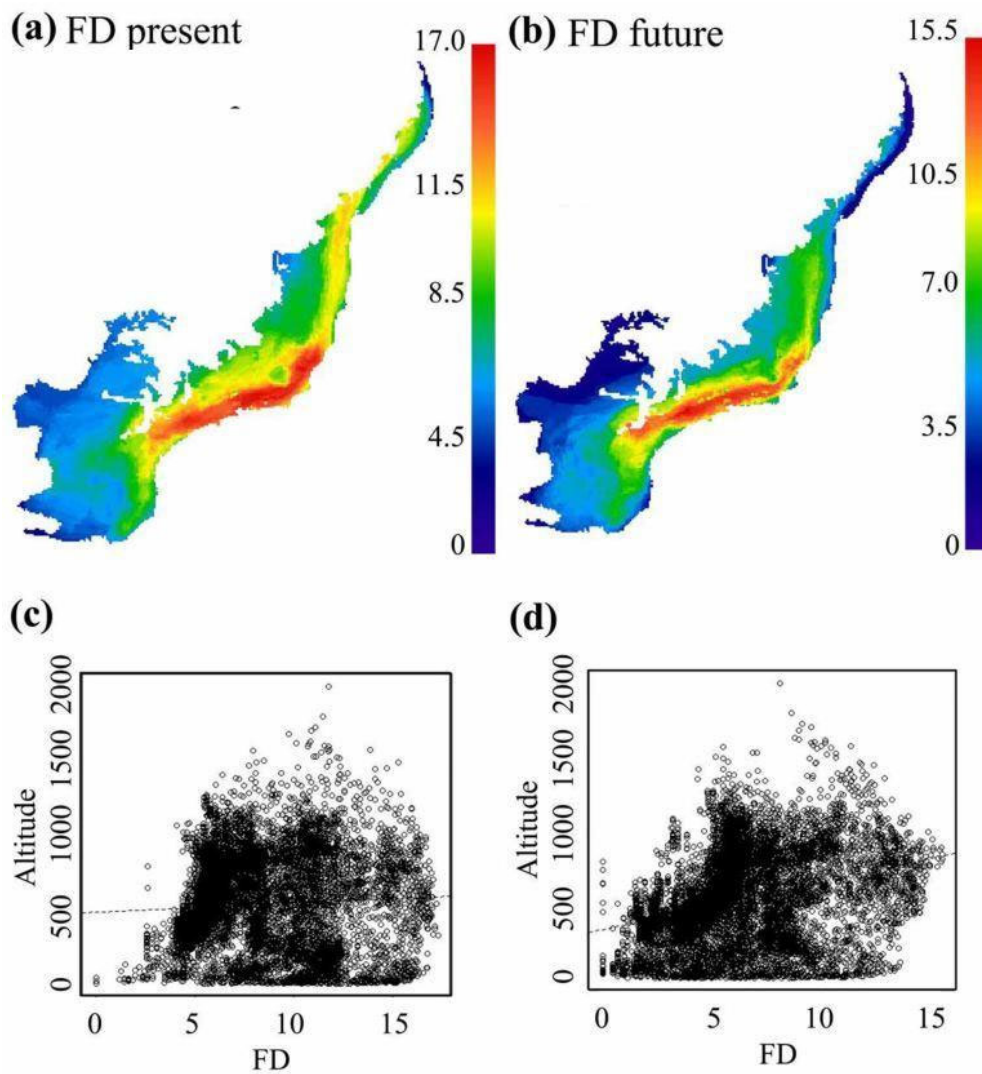
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722 **Fig. 4.** Turnover derived from consensus model map (a). Relation between turnover consensus model with  
723 altitude (in meters) (b), and latitude (c) for amphibian species.

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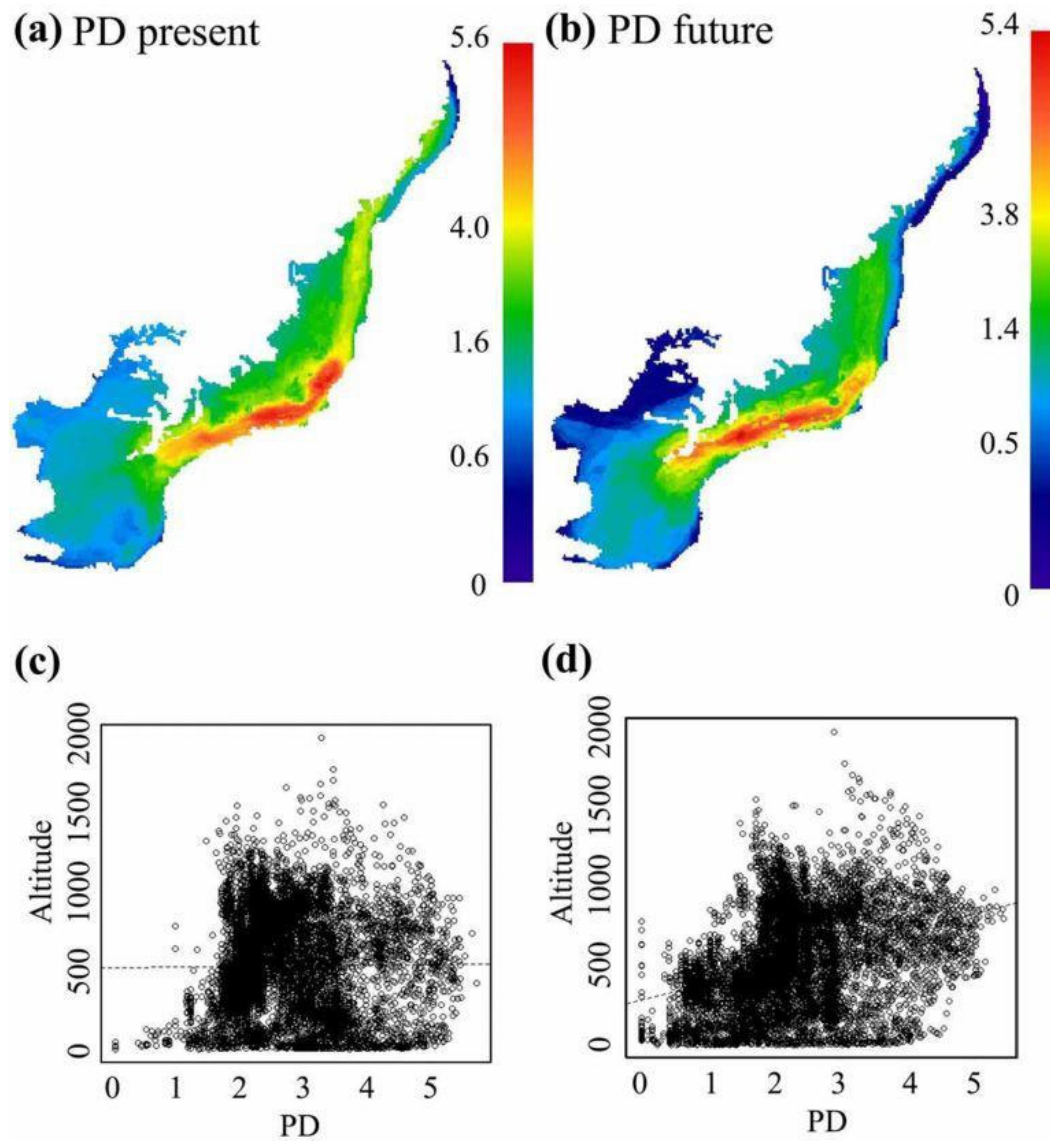
726 **Fig. 5.** Spatial distribution of Functional diversity (FD) derived from amphibian species richness consensus

727 model map for present time (a) and for 2080 (b). Relation between Functional diversity (FD) consensus model

728 and altitude (in meters) for present time (c) and for 2080 (d).

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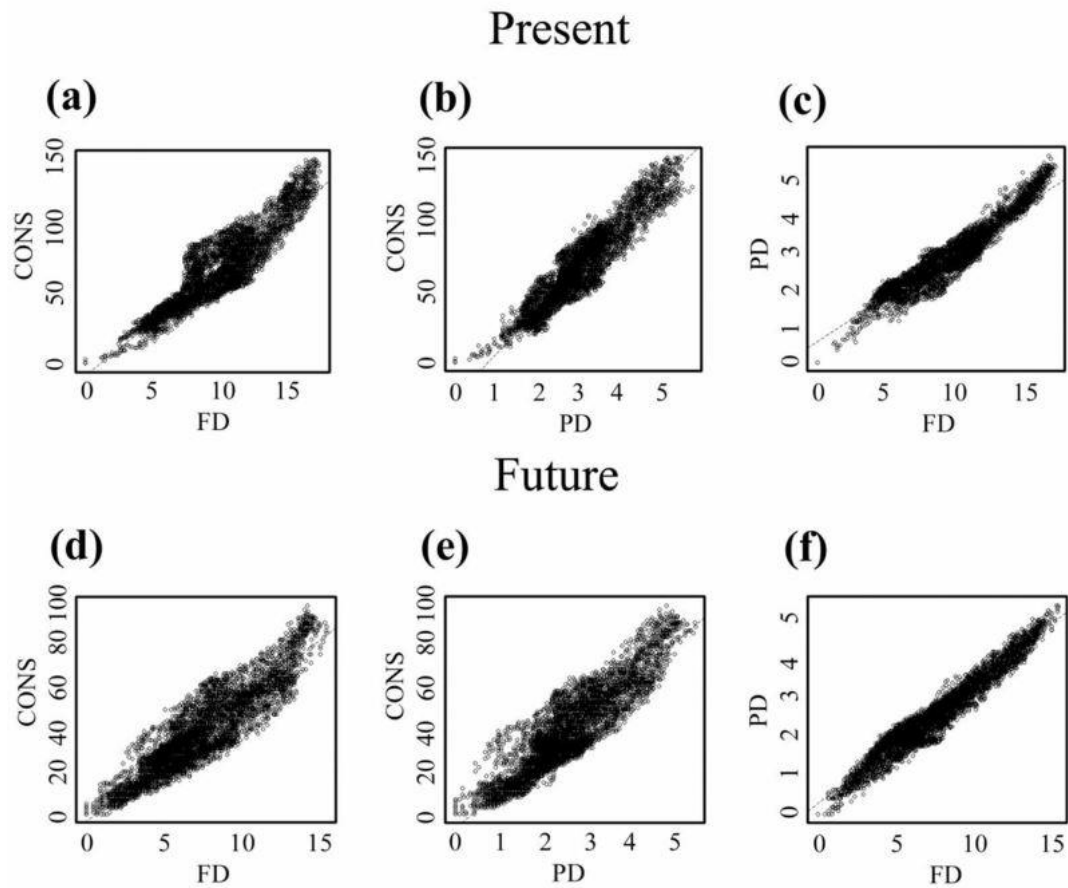
731 **Fig. 6.** Spatial distribution of Phylogenetic diversity (PD) derived from amphibian species richness consensus

732 model map for present time (a) and for 2080 (b). Relation between Phylogenetic diversity (PD) consensus model

733 and altitude (in meters) for present time (c) and for 2080 (d).

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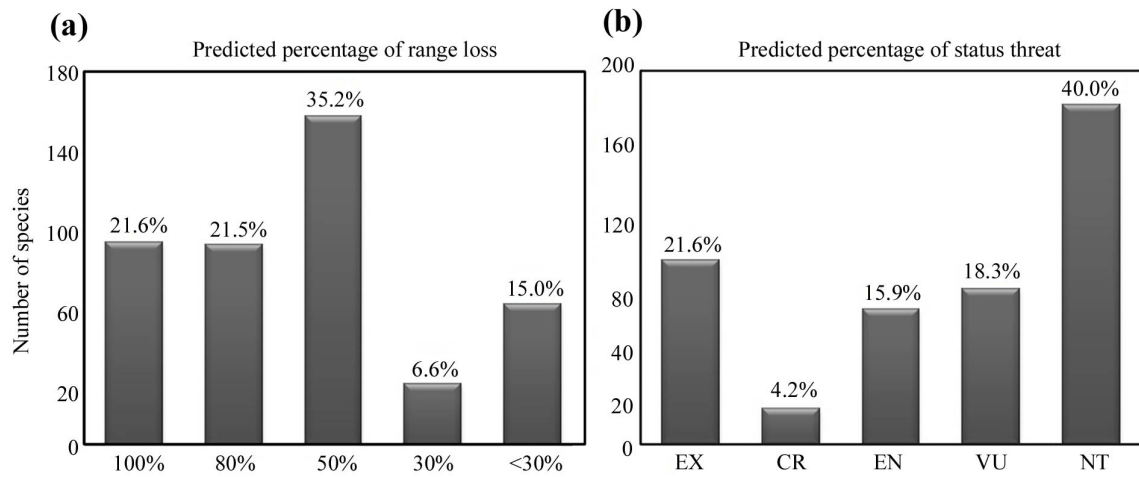
736

737 **Fig. 7.** Relationships between species richness consensual model (CONS), Functional diversity (FD),  
 738 Phylogenetic diversity (PD) of amphibians in the Brazilian Atlantic Forest. Present time: CONS vs FD (a),  
 739 CONS vs PD (b) and FD vs. PD (c); Future time: CONS vs FD (d), CONS vs PD (e) and FD vs PD (f).

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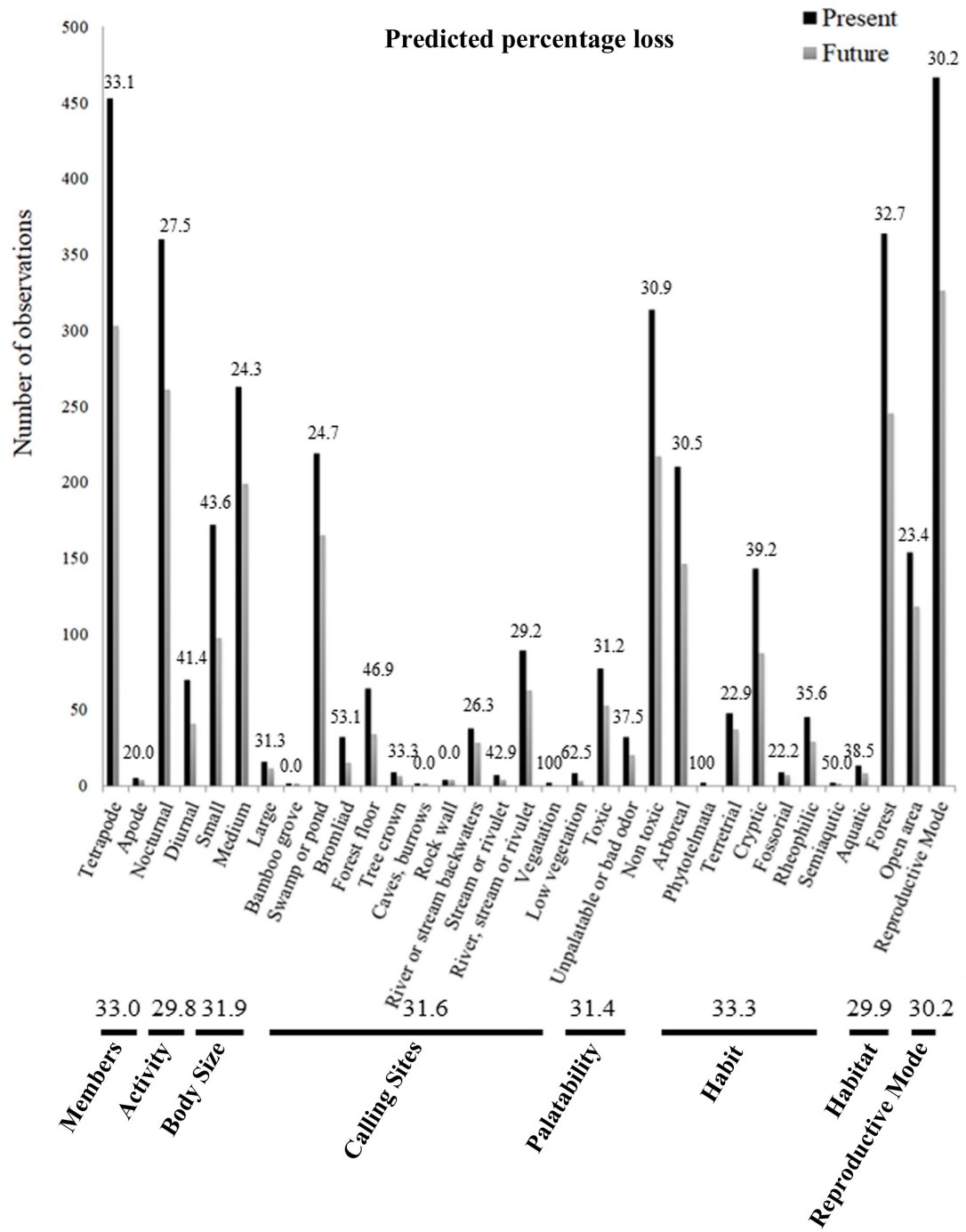
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744 **Fig. 8.** Status of threat projection to 2080 in the face of climate change for amphibians of Atlantic Forest hotspot.

745 In the top of bars is the percentage of species number. (a) percentage of lost species range; (b) status of species:

746 Extinct (EX) 0 km<sup>2</sup>, Critically Endangered (CR) <100 km<sup>2</sup>, Endangered (EN) <5,000 km<sup>2</sup>, Vulnerable (VU) <747 20,000 km<sup>2</sup>, and Nonthreatened (NT) > 20,000 km<sup>2</sup>.

748



749

750 **Fig. 9.** Predicted percentage loss of functional traits and subtraits to 2080 in the face of climate change for  
 751 amphibians of Atlantic Forest hotspot.