

# **Spatial relationships between fishes and amphibians: implications for conservation planning in a Neotropical Hotspot**

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2 **Neotropical Hotspot**

3

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22 **Abstract**

23 *Context* Species distribution patterns are widely used to guide conservation planning and are a  
24 central issue in ecology. The usefulness of spatial autocorrelation analysis has been highlighted in several  
25 ecological applications so far. However, spatial assumptions in ecology are highly scale-dependent, in  
26 which geographical relationships between species diversity and distributions can have different  
27 conservation concerns.

28 *Objecives* An integrative landscape planning was designed to show the spatial distribution patterns  
29 of taxonomic and functional diversity of amphibians and fishes, from multiple species traits regarding  
30 morphology, life history, and behavior.

31 *Methods* We used spatial, morphological and ecological data of amphibians and fishes to  
32 calculated the functional diversity and the spatial autocorrelation of species.

33 *Results* Mapping results show that the higher taxonomic and functional diversity of fishes are  
34 concentrated in the West Atlantic Forest. Considering amphibians, they are located in the East portion of  
35 the biome. Spatial autocorrelation of species indicates the regions of the Serra do Mar and the southern  
36 part of the Central Corridor as the main overlapped species distribution areas between both groups.

37 *Conclusions* New key conservation sites were reported within the Brazilian Atlantic Forest hotspot,  
38 revealing cross-taxon mismatches between terrestrial and freshwater ecosystems. This study offers useful  
39 spatial information integrating suitable habitats of fishes and amphibians to complement existing and  
40 future research based on terrestrial and freshwater conservation. New priorities for biodiversity  
41 conservation in rich-species regions highlight the importance of spatial pattern analysis to support land-  
42 use planning in a macroecological context.

43

44 **Keywords**

45 Taxonomic Diversity . Functional Diversity . Macroecology . Atlantic Forest . Conservation planning

46

47 **Introduction**

48

49 In the face of the global biodiversity crisis, multi-species conservation strategies are essential to achieve  
50 ecological outcomes (Mendenhall et al. 2012; Dinerstein et al. 2020; Jung et al. 2021). The use of spatial  
51 patterns of biodiversity components to support conservation actions has become one of the main research

52 topics in ecology (Rodrigues et al. 2011; Westgate et al. 2014). There is an urgent need for reliable data  
53 on species composition and distribution for conserving biodiversity habitats and reducing biodiversity  
54 losses (Dinerstein et al. 2020; Mokany et al. 2020). However, time and money are running out for  
55 biodiversity strategies, which hampers the development of cost-effective conservation planning (O'Bryan  
56 et al. 2020; Strassburg et al. 2020; Yang et al. 2020). It is also necessary to consider that measuring the  
57 world's huge biodiversity patterns is difficult under the intense human pressure across species' ranges in  
58 natural ecosystems (Williams et al. 2005; O'Bryan et al. 2020). As an alternative, many conservation  
59 plans rely on cross-taxon congruencies to safeguard biodiversity patterns in balance with environmental  
60 emergency management (Hess et al. 2006; Westgate et al. 2014; Yang et al. 2020).

61           There are several elaborated definitions of cross-taxon congruence for conservation planning  
62 (Westgate et al. 2014). According to Heino (2010), it can be defined as the strong correlation of  
63 biodiversity measurements between taxonomic groups across a set of localities. Usually, assemblages of  
64 well-known and mapped species are used to predict less-studied groups' presence (Lawler et al. 2015).  
65 Thus, cross-taxon congruence aims to accelerate the process of delimiting areas for conservation based on  
66 some species' requirements (Fraveau et al. 2006; Weerd and Haes 2010; Rodrigues et al. 2011). It is  
67 known that only cross-taxon congruence is not enough for one species group to be a good predictor for  
68 the distribution of another (Gaston 1996; Padial et al. 2012, Dufлот et al. 2022), but it is an essential  
69 requirement for these relationships to be positive (Hess et al. 2006; Lawler et al. 2015). Although this  
70 approach may introduce some practical limitations, it has been shown useful to investigate ecological and  
71 spatial relationships in aquatic and terrestrial ecosystems (Heino et al. 2005; Heino 2010; Westgate et al.  
72 2014).

73           The Brazilian Atlantic Forest represents a biodiversity hotspot with high species richness, high  
74 levels of endemism, and high rates of habitat loss due to human occupation (Myers et al. 2000; Oyakawa  
75 et al. 2006; Ribeiro et al. 2009). Fragmentation of the Atlantic Forest has promoted the success of  
76 generalists and loss of specialist species leading to taxonomic and functional impoverishment of species  
77 (Sfair et al. 2016; Lourenço-de-Moraes et al. 2020). Within this heterogeneous ecosystem, some areas  
78 stand out as extremely important hotspots (i.e. specific points of high species richness) due to the high  
79 potential for biodiversity corridors (Carnaval et al. 2009; Lourenço-de-Moraes et al. 2019a; Campos et al.  
80 2020).

81            In this paper, the spatial patterns of taxonomic and functional diversity of fishes and amphibians  
82 were assessed to support efficient landscape planning for aquatic and terrestrial ecosystems in the  
83 Brazilian Atlantic Forest. Cross-taxon congruence of taxonomic and functional diversity patterns between  
84 fishes and amphibians were tested as a shortcut for mapping biodiversity components from small spatial  
85 scales. The results may help applied conservation strategies considering each group's functional role (i.e.,  
86 fishes and amphibians) in an integrative way. This study offered an essential contribution to the  
87 conservation of terrestrial and freshwater ecosystems, having crucial implications for ecosystems under  
88 human pressure in different spatial scales.

89

## 90 **Materials and Methods**

91

92 Study area

93

94 Research design and analysis were conducted in the most threatened biodiversity hotspot on Earth (Myers  
95 et al. 2000) – the Brazilian Atlantic Forest. This biome had an original coverage with about 1.5 million  
96 square kilometers extended in the tropical and subtropical regions (Myers et al. 2000), of which only  
97 12.9% remain in Brazil, Argentina, and Paraguay (Ribeiro et al. 2009). In the Brazilian territory, the  
98 biome comprises the coastal region from the Rio Grande do Sul to the Rio Grande do Norte states (Fig.  
99 1), retaining only around 11% of its original extension reduced to scattered forest remnant areas with a  
100 high diversity of native species (Ribeiro et al. 2009).

101

102 Spatial range, species richness, and functional traits

103

104 Geographical distribution records of fishes and amphibian species were obtained according to three  
105 databases: (1) Global Biodiversity Information Facility – GBIF (<https://www.gbif.org>); (2) Species Link  
106 (<http://www.splink.org.br>) and (3) IUCN Red List database, version 2021.1 (IUCN, 2021). To prepare the  
107 spatial data of the species, the ArcGIS Pro software (ESRI, 2019) was used to build a presence/absence  
108 binary matrices for combining the species distribution databases. Therefore, the studied area was mapped  
109 in a grid system of 0.1 latitude/longitude degrees, creating a network with 10,359 grid cells. The Atlantic

110 Forest area limits considered in this study followed the definitions of the Brazilian Ministry of  
111 Environment (MMA 2018).

112 For analyses, only species data regarding adult individuals of fishes and amphibians within the  
113 Brazilian Atlantic Forest were considered. According to specialized literature for each taxonomic group,  
114 all species distributions of fishes and amphibians were compiled in a dataset (see Supporting  
115 Information). Species nomenclature was standardized following the Catalog of fishes database (Ota et al.  
116 2018; Eschmeyer et al. 2021) and the Amphibians Species of the World database (Frost 2021). Spatial  
117 distribution records that did not give the correct name of the species were not included in the dataset (i.e.,  
118 species with "aff." or "cf.").

119 In total, 649 species of fishes and 453 amphibians (see Table S1); ~90% of species were  
120 gathered in the Brazilian Atlantic Forest (see Table S2). Functional traits of the listed species (only adult  
121 characteristics) were based on specialized literature (see Table S4 and S6). The functional traits were  
122 grouped into morphology, ecology, and behavior categories which are characteristics commonly found in  
123 the literature to represent broadly the ecosystem support services performed by the studied groups (e.g.  
124 Hocking and Babbitt 2014; Villéger et al. 2017; Lourenço-de-Moraes et al. 2019b). For fishes, 10  
125 functional traits were evaluated: (1) total body length; (2) presence of spines; (3) occurrence of parental  
126 care; (4) type of fertilization (internal or external); (5) presence of migration; (6) trophic category  
127 (carnivorous, piscivorous, insectivorous, invertivorous, omnivorous, zooplanktivorous, detritivorous,  
128 herbivorous, algivorous, hematophagus, mucifagus, lepidophagus, and/or oophagus); (7) mouth position  
129 (inferior, subterminal, terminal or superior); (8) position occupied by the species in the water column  
130 (bentopelagic, benthic or pelagic); (9) habitat (lentic, lotic, and both); and (10) period of activity  
131 (nocturnal, diurnal, and both) (see Table S4). The relationship of each trait to ecosystem services can be  
132 seen in Table S3.

133 For amphibians, the following functional traits were used according to Haddad et al. (2013),  
134 Campos et al. (2017), and Lourenço-de-Moraes et al. (2019b, 2020): (1) body size; (2) appendices (apodal  
135 and tetrapod); (3) activity (nocturnal, diurnal, and both); (4) toxicity (toxic, nontoxic, unpalatable, or bad  
136 odor); (5) habitat (forested area, open area, and both); (6) habit (arboreal, phytotelmata, terrestrial,  
137 cryptozoic, fossorial, rheophilic, semi-aquatic, and aquatic); (7) calling site (bamboo grove, swamp or  
138 lake, bromeliad, forest floor, tree canopy, caves or burrows, rock wall, backwater river, stream, river,  
139 shrubs, grasslands and not sing); and (8) reproductive mode (1 to 39 modes; see Haddad and Prado 2005);

140 for more details about species traits and the relationship of each amphibian trait to ecosystem services see  
141 Table S5-6. Additional information on the richness and distribution data for amphibian species was  
142 obtained according to Lourenço-de-Moraes et al. (2019b).

143

144 Ecological niche modeling

145

146 Spatial occurrences of species were transformed in presence/absence matrices, using the "Spatial Join"  
147 ArcGIS toolbox in ArcGIS Pro software (ESRI 2019). Then, vector files based on expert knowledge of  
148 the species' ranges and forest remnant polygons were combined into an overall coverage for species  
149 distribution modeling. Only spatial occurrences of species distribution data intersected on at least one grid  
150 cell were considered (i.e., ~ 10 km<sup>2</sup>). In addition, ecological niche models (ENMs) were used to predict  
151 and map each fish's potential distribution area and amphibian species in the Atlantic Forest.

152 For ecological niche models (ENMs), we apply the species occurrence matrix and the layers of  
153 climatic-environmental variables, resulting in a suitability matrix. We used the following bioclimatic  
154 variables in the modeling process: (1) annual mean temperature; (2) annual temperature range; (3)  
155 precipitation of the wettest month; (4) precipitation of the driest month; and (5) precipitation of the  
156 warmest quarter. We obtained these variables from CMIP5—Coupled Models Intercomparison Project  
157 Phase 5 (<http://cmip-pcmdi.llnl.gov/cmip5/>; and at <http://ecoclimate.org>, see Lima-Ribeiro et al. 2015),  
158 and downscaled to the resolution of 0.1 degrees. We used simulations provided by four Atmosphere-  
159 Ocean General Circulation Models (AOGCMs): CCSM (Community Climate System Model), CNRM  
160 (Centre National de Recherches Météorologiques), MIROC (Model for Interdisciplinary Research on  
161 Climate), and MRI (Meteorological Research Institute), which were obtained from CMIP5 (Coupled  
162 Model Intercomparison Project—Phase 6) for the consensus model. Original data resolution varied from  
163 0.9° to 2.8° (in longitude and latitude) and the climate variables were re-scaled to fit our grid resolution.  
164 We also used altitude as a predictor of richness and dispersion for fishes and amphibians, and numbers of  
165 rivers for fishes from the dataset available at WorldClim Global Climate Data  
166 (<http://www.worldclim.org>).

167 We performed four conceptually and statistically different ENMs based on presence data (i.e.,  
168 only occurrences are known, absences are unknown) using the algorithms: (1) Bioclim (BIO, Busby  
169 1991) based on bioclimatic envelope logic; (2) Gower Distance and Euclidean Distance (GD, EUD,

170 Carpenter et al. 1993) based on environmental distance approach; (3) Maximum Entropy (ME, Phillips et  
171 al. 2006) and Random Forest (RF, Breiman 2001) based on machine learning technique; and (4)  
172 Ecological Niche Factor Analysis (ENFA, Hirzel et al. 2002) based on multivariate analysis, and Genetic  
173 Algorithm for Ruleset Production (GARP, Stockwell and Noble 1992). Given each model's  
174 particularities, they provided different predictions, generating uncertainties about which model is more  
175 appropriate to represent the geographical distribution of species (Diniz-Filho et al. 2009). To overcome  
176 this uncertainty and minimize errors, we employed the ensemble forecasting approach, which offers a  
177 consensus of multiple models (Araújo and New 2006). The main idea of ensemble forecasting is that  
178 different sources of errors will affect each niche model in different ways and, by obtaining a consensus  
179 result of these models, errors will tend to cancel each other out and produce a more trustworthy and  
180 conservative solution (Diniz-Filho et al. 2010). Assuming that the species richness consensus model  
181 (CONS) reduces uncertainty and error associated with alternative ENMs, we interpreted only the CONS  
182 model's range sizes.

183         We randomly partitioned the presence and absence data of each species into 75% for calibration  
184 (or training) and 25% for evaluation (or test); repeating this process 10 times by cross-validation for all  
185 models. For each ENM, we converted the continuous predictions of suitability into a binary vector of 1/0  
186 (presence/absence in each cell), finding the threshold that maximizes sensitivity and specificity values in  
187 the receiver operating characteristic (ROC). The ROC curve is generated by plotting the fraction of true  
188 positives versus the fraction of false positives at various threshold settings. The distribution areas were  
189 estimated obtaining 280 predictions (7 models  $\times$  10 randomizations  $\times$  4 AOGCMs) for each species. This  
190 allowed us to generate a frequency of projections in the ensemble. Then, we generated the frequency of  
191 projections weighted by true skill statistics (TSS) (the best models according to this metric have more  
192 weight in our consensus projections). The TSS range from  $-1$  to  $+1$ , where values equal to  $+1$  is a perfect  
193 prediction and values equal to or less than zero is a prediction no better than random (Allouche et al.  
194 2006; Eskildsen et al. 2013). We considered the species present only in cells where at least 50% of  
195 models retained in the ensemble point out the species as the present. In our analyses, we obtained the  
196 CONS for each AOGCM. Thus, we obtained the final maps of species richness through the average of  
197 values projected by CONS for each grid cell—considering the different GCMs.

198         All models were performed using the computational platform Bioensembles (Diniz-Filho et al.  
199 2009) and mapped results using the software SAM v.4.0 (Rangel et al. 2010). To determine the species



200 richness patterns of fishes and amphibians of the Atlantic Forest, the modeling strategy at the community  
201 level of "predict first, assemble later" were employed (Overton et al. 2002), where the ranges of  
202 individual species are modeled one at a time as a function of environmental predictors and then  
203 overlapped to obtain the species richness. This approach is called stacked of Species Distribution Models  
204 – SDMs (Dubuis et al. 2011; Hof et al. 2012; Mata et al. 2017).

205

206 Data analyses

207

208 After the establishment of Taxonomic Diversity (TD), the Functional Diversity (FD) from the generated  
209 functional traits database for fish and amphibians were estimated according to the FD index (Petchey and  
210 Gaston, 2006). The FD index measures the extent of complementarity between species characteristics  
211 values (Petchey and Gaston 2006), relating directly to the ecological niche concept (Cianciaruso et al.  
212 2009). The protocol proposed by Petchey and Gaston (2006) was followed to calculate functional  
213 diversity (FD): (1) construction of a species-trait matrix; (2) conversion of the species-trait matrix into a  
214 distance matrix; (3) clustering distance matrix into a dendrogram (UPGMA); and (4) calculating  
215 functional diversity by summing dendrogram branch lengths of species community. Besides, the FD  
216 considers the dependence of distances between species in the n-dimensional space (Petchey and Gaston  
217 2006). The method proposed by Pavoine et al. (2009) was used to create the distance matrices through the  
218 distance of Gower (1971). The Gower distance was selected due to being the most recommended distance  
219 for simultaneously assessing continuous and categorical variables (Gower 1971).

220 Independent swap null models (Gotelli and Entsminger 2001) were used to verify whether FD  
221 was influenced by TD (Devictor et al. 2010), according to the protocol proposed by Swenson (2014). The  
222 null model is independent of the species richness of an assemblage. In this way, it ensures that the  
223 patterns of assembly of characteristics do not simply reflect particular species' differential occurrence  
224 (Swenson 2014). Thus, every ~10 km<sup>2</sup> of the grid cells was tested to verify whether the values attributed  
225 to functional diversity were higher, equal, or lower than expected in a randomized and non-random  
226 distribution, assuming a random distribution in which every species could occupy any grid cell in the  
227 biome (for further details, see Swenson 2014). For analysis, were computed 1,000 replicates of FD,  
228 obtaining a p-value of predicted FD as compared to the distribution of the random replicates. All analyses  
229 were performed using the packages "ade4" (Dray and Dufour 2007), "picante" (Kembel et al. 2010), "FD"

230 (Laliberté and Legendre 2010), and "vegan" (Oksanen et al. 2018) through software R (R Core Team  
231 2020).

232 We then used simple linear regression models (testing normality through the Shapiro-Wilk test)  
233 to evaluate TD (CONS) and FD correlations in each grid cell. Correlation matrices were used to compare  
234 the topographic patterns and spatial references (altitude and latitude) to the values obtained by the  
235 richness consensus model for TD and FD in each grid cell. Thus, we correlated the values obtained for  
236 TD and FD with altitude and latitude using simple linear regression models. We also calculated the values  
237 overlap of TD and FD between groups in each cell. For this, we considered only areas with values  $\geq 50\%$   
238 of the total value obtained for each index (i.e., TD and FD). From these areas containing the highest  
239 values, we build overlap maps between TD and FD. Thus, we avoided the possibility of obtaining  
240 statistical significance that could emerge from high congruence in the order of areas with low TD and FD  
241 values (Fattorini et al. 2012). We performed all analyses on the R program using the "vegan" package (R  
242 Core Team 2020).

243

## 244 **Results**

245

246 With the maximum mapped values of 295 fish species (TD) and 36.6 FD index per grid in the 10,359  
247 cells evaluated. The highest indices of TD and FD of fish occurred in the western Atlantic Forest (Fig. 2a,  
248 c). This region corresponds to the areas that make up the Paraná River basin. High values of TD and FD  
249 were observed in the eastern of the Atlantic Forest, in the Serra do Mar region. This area is composed of a  
250 small part of the Paraná River basin, the southeastern and eastern Atlantic basins. In addition, the linear  
251 regression analysis of the data showed a high correlation between the TD and FD index of fish species ( $R^2$   
252 = 0.98;  $P < 0.001$ ) (Fig. 2b). This means that the regions that contain a high species richness also harbor a  
253 greater diversity of ecosystem functions.

254 For amphibians, the maximum values were 155 species (TD) and 17.8 FD index per grid in the  
255 10,359 cells evaluated. The highest concentrations of these indices are to the eastern of the biome (Fig.  
256 2d, f), mainly in the Serra do Mar, Atlantic Forest Central Corridor, and Endemism Area of Pernambuco  
257 (altitude areas). Amphibian TD and FD values are also highly correlated ( $R^2 = 0.95$ ;  $P < 0.001$ ) (Fig. 2e).

258 In general, mapping the assemblages' relationships, important spatial mismatches, and low  
259 congruencies were revealed among the biodiversity components. The results showed no correlation

260 between TD of fish and amphibians ( $R^2 = 0.006$ ;  $P < 0.001$ ), as well as for FD ( $R^2 = 0.003$ ;  $P < 0.001$  –  
261 Fig. 3). On the cross-taxon congruence of points  $\geq 50\%$  of the total value, fishes and amphibians also  
262 presented low spatial overlap in TD (0.19%) and FD (2.58%) (Fig. 4). Overlapping areas between TD) and  
263 and FD of fishes and amphibians correspond mainly to the regions of the Serra do Mar and southern  
264 portion of the Central Corridor of the Atlantic Forest, and the Pernambuco Endemism Centre. Further,  
265 when considered only the areas of TD and FD indexes  $\geq 50\%$  of the total value, it was observed a lower  
266 correlation for TD ( $R^2 = 0.69$ ;  $P < 0.001$ ) and for FD ( $R^2 = 0.95$ ;  $P < 0.001$ ).

267

## 268 **Discussion**

269

270 The cross-taxon congruence patterns highlight three main areas of interest ('hotpoints') aquatic and  
271 terrestrial conservation within the Brazilian Atlantic Forest (see Fig. 4). Besides, Serra do Mar and  
272 Central Corridor also refuge the only regions in the biome that displays high congruence between the  
273 taxonomic and functional diversity of fishes and amphibians. Considering only fishes, the most important  
274 hotpoint is located in the west of the biome, in the Paraná River basin – Upper Paraná River Floodplain.  
275 This is the last stretch of the Paraná River that is free of dams and received some species of fishes after a  
276 set of waterfalls that acted as natural geographic barriers to be submerged by Itaipu Reservoir in 1983  
277 (Agostinho and Julio 2002; Agostinho et al. 2015). Some invasions of species have changed the trophic  
278 relationships (Benedito-Cecilio and Agostinho 1999; Alves et al. 2017) due to the recent impact of the  
279 Itaipu Reservoir. Thus, it is highly recommended the use of cross-taxon congruence between these groups  
280 to define conservation strategies and biomonitoring studies in the Brazilian Atlantic Forest.

281 Most of the Atlantic Forest ecosystems display a highly heterogeneous TD and FD distribution  
282 between fishes and amphibians. For fish, the main hotspots are located in the west of the biome, along  
283 the Paraná River basin. This basin is among the world's five largest water systems (Rosa 1983; Agostinho  
284 et al. 1995). Several studies point to the importance of this region as a high biodiversity source (Bini et al.  
285 2001; Baumgartner et al. 2003; Agostinho et al. 2007; Graça and Pavanelli 2007). In the last decades, the  
286 full extension of the basin in the Brazilian territory has been impacted by the construction of dams to  
287 produce hydroelectric power (Rosa 1983; Agostinho et al. 1995; Stevaux et al. 2009). Considering only  
288 the Upper Paraná River, for instance, there are at least 150 dams built along its course (Stevaux et al.  
289 2009).

290           The impoundment of rivers creates a strong perturbation of fluvial dynamics (Stevaux et al.  
291 2009). Among these disturbances is the alteration of flood magnitude (Souza Filho 2009), the turbidity  
292 reduction by retention of suspended load (Grimshaw and Lewin 1980), bank erosion (Rocha et al 2013),  
293 and reduction in bed form sizes (Dos Santos et al 2017). These alterations can induce significant changes  
294 in all biodiversity (Stevaux et al. 2009). However, this area still stands out as the region with the highest  
295 species richness and fish ecosystem services. Thus, the whole of the Paraná River basin must be  
296 recognized as a focus on the conservation of freshwater fish in this biome.

297           On the other hand, the high priority regions for amphibians are located in east Brazil, comprising  
298 the Serra do Mar, the Serra da Mantiqueira, the Central Corridor of the Atlantic Forest, and the Endemism  
299 Area of Pernambuco (altitude areas) (Carnaval and Moritz 2008; Carnaval et al. 2009; Campos et al.  
300 2017; Lourenço-de-Moraes et al. 2019a, b; Campos et al. 2020). These important Atlantic Forest  
301 remnants have also suffered many environmental impacts from human pressures (Ribeiro et al. 2009;  
302 Rezende et al. 2018). The main factors responsible for amphibian biodiversity declines are habitat loss  
303 and fragmentation, global warming, and diseases (Young et al. 2001; Pounds et al. 2006; Ferreira et al.  
304 2016). Nevertheless, these regions remain well preserved and are still characterized by their high  
305 biodiversity, with many endemic species (Aguiar et al. 2003; Lourenço-de-Moraes et al. 2019b). For  
306 amphibians, this happens because their habitat-specialist patterns in the Atlantic Forest are favored by the  
307 richness of habitats and microhabitats (Figueiredo et al. 2019), and biogeographic barriers which cause a  
308 high degree of isolation among populations (Lourenço-de-Moraes et al. 2020).

309           Among assemblages, the low degree of congruence indicates that selecting one taxon as an  
310 indicator for conservation planning of the other would lead to significant loss of species and ecosystem  
311 functions (Lawler and White 2008; Lawler et al. 2015). Considering that the selection of protected areas  
312 is often based on cross-taxon congruence among different groups (Campos et al. 2014), this strategy  
313 should be cautiously applied in conservation plans. This is because our study showed a negative result  
314 and the lack of settled down standards to this methodology appliance. Results gathered over time indicate  
315 that the patterns found are dependent on the context of the study, ranging widely with the grain, the extent  
316 and the region of analysis (Hess et al. 2006).

317           The only region where fishes and amphibians feature high cross-taxon congruence values ( $\geq$   
318 50%) between TD and FD is the Serra do Mar and the southern part of the Central Corridor. Thus, despite  
319 the smaller number of fish species compared to the Paraná River basin, these areas can also be

320 characterized as ecosystem services hotspots, bringing opportunities to integrate conservation strategies  
321 of terrestrial and aquatic biodiversity. Furthermore, considering that there is still much to be studied in the  
322 region (Menezes et al. 2007), the number of species that occur in these areas of the Atlantic Forest may be  
323 much larger than the one already gathered. The great concentration of biodiversity that characterizes the  
324 Serra do Mar as a zone of high conservation value is because this region harbor most of the forest  
325 remnants of the entire biome (Oyakawa et al. 2006; Ribeiro et al. 2009). The preserved forests are  
326 essential for maintaining not only amphibians' communities but also fish communities. This is because  
327 fish also depend on forest integrity for protection and food (Oyakawa et al. 2006; Menezes et al. 2007).  
328 The Serra do Mar's high preservation index is due to the slope and poor productive soils, which make it  
329 unsuitable for agricultural practices (Aguiar et al. 2003; Oyakawa et al. 2006). Therefore, despite being  
330 located between the two largest metropolitan centers in Brazil, Serra do Mar remains well preserved  
331 (Aguiar et al. 2003), containing most of the forest fragments in the entire Atlantic Forest (Ribeiro et al.  
332 2009).

333           Highly correlated relationships were gathered between TD and FD within each assemblage.  
334 These results match what is usually expected for each group separately. Considering that the greater the  
335 number of species, the greater the probability of different biological characteristics, FD is expected to  
336 increase with TD (Tilman et al. 1997; Balvanera et al. 2006; Cadotte et al. 2011). This high degree of  
337 congruence among diversity measures inside each group indicates a high impact of the composition on  
338 the ecosystem processes (Tilman et al. 1997; Naeem and Wright 2003). This is because species'  
339 functional characteristics determine the contributions that a group will have in ecosystem processes,  
340 affecting their ecological performance (Cadotte et al. 2011). In this way, actions aimed at the  
341 conservation of the most species-rich areas will also protect high ecosystem values.

342           Conservation scientists have been continuously searching for the best methods for identifying  
343 patterns that can be successfully applied in conservation strategies (Myers 2000; Williams et al. 2005).  
344 However, when it comes to spatial relationships, isolated positive or negative results should not be used  
345 as a basis for generalization (Rodrigues and Brooks 2007; Trindade-Filho and Loyola 2011). One of the  
346 biggest challenges for using this approach is that often the strength of correlations can vary among  
347 different locations according to independent environmental factors, with the scale used in the study, with  
348 historical and biogeographical events and methodological shortcomings (Sanders 2002; Hess et al. 2006;  
349 Wolters et al. 2006; Araújo et al. 2008; Lourenço-de-Moraes et al. 2020). This high variability can

350 potentially undermine the usefulness of this approach in conservation actions (Trindade-Filho and Loyola  
351 2011). Considering this variation, it could gather different conclusions if only part of the Atlantic Forest  
352 territory were selected for the present assessment (e.g. in the Serra do Mar). This choice would result in  
353 different landscape management recommendations about the cross-taxon congruence patterns evaluated.

354         It is worth mentioning that fishes and amphibians perform varied and significant ecosystem  
355 services (e.g. energy flow regulation, nutrient cycling, and soil bioturbation; see Whiles et al. 2006;  
356 Hocking and Babbitt 2014). In addition to performing other functions directly related to the maintenance  
357 of human well-being, such as the provision of food resources, medicines, and disease control (Whiles et  
358 al. 2006; Hocking and Babbitt 2014). Thus, considering the role of these species in community  
359 functioning, their disappearance may have potentially systemic implications (Hocking and Babbitt 2014),  
360 leading to loss of terrestrial, freshwater ecosystem services and changes in flow between these ecosystems  
361 (Holmlund and Hammer 1999; Whiles et al. 2006). These losses threaten not only human health but also  
362 their livelihoods (Egoh et al. 2009).

363         In conclusion, before the need to contain increased biodiversity loss, spatial relationships have  
364 been widely considered in conservation strategies (Campos et al. 2014, 2017; Lourenço-de-Moraes et al.  
365 2021). However, the number of researches that show the inconsistency of generalizing the results beyond  
366 their original place of study is increasing (Hess et al. 2006; Trindade-Filho and Loyola 2011). It is  
367 important to note that not all groups are good predictors of biodiversity, and even good predictors may be  
368 efficient for some groups and inefficient for others. In fact, this would lead to a loss of relevant  
369 information on ecosystem functioning and structure. Moreover, this study highlights the positive  
370 relationship between biodiversity and ecosystem functioning. Thus, it is expected that functions  
371 performed by different species are compromised as biodiversity loss occurs. Therefore, taken together,  
372 our results cast doubt on the use of cross-taxon congruence in a different ecosystem and from local to  
373 macro scales.

374

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380

381 **Authors' contributions** ACC, RLM and EB: conceived the ideas of the study; ACC, RLM and FSC:  
382 wrote the manuscript with important contributions for the other authors; ACC and RLM: designed  
383 methodology; ACC and RLM collected the data; ACC and RLM: analyzed the data; ACC, RLM, and  
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389

390 **Data availability (data transparency)** The datasets generated during and/or analysed during the  
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392

393 **Conflict of interest** The authors declare that they have no competing interest.

394

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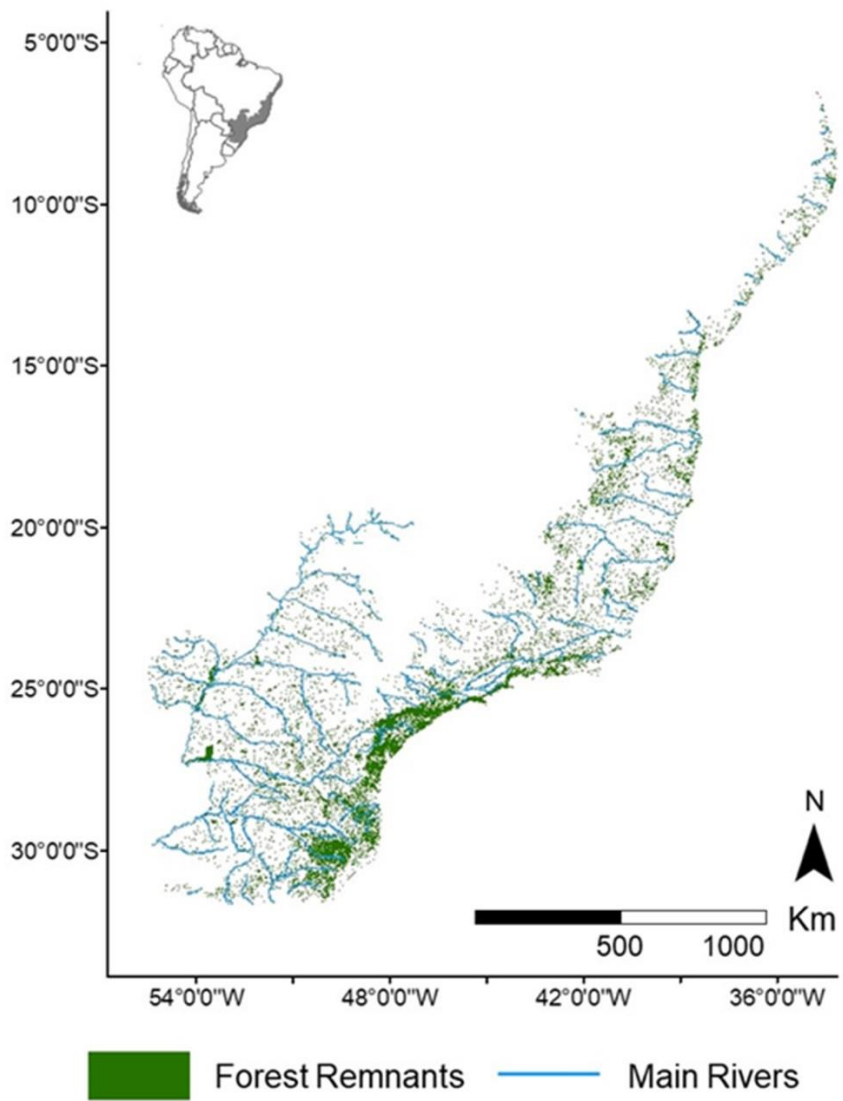


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672

673 **Supporting Information**

674 Additional supporting information may be found online in the Supporting Information section.

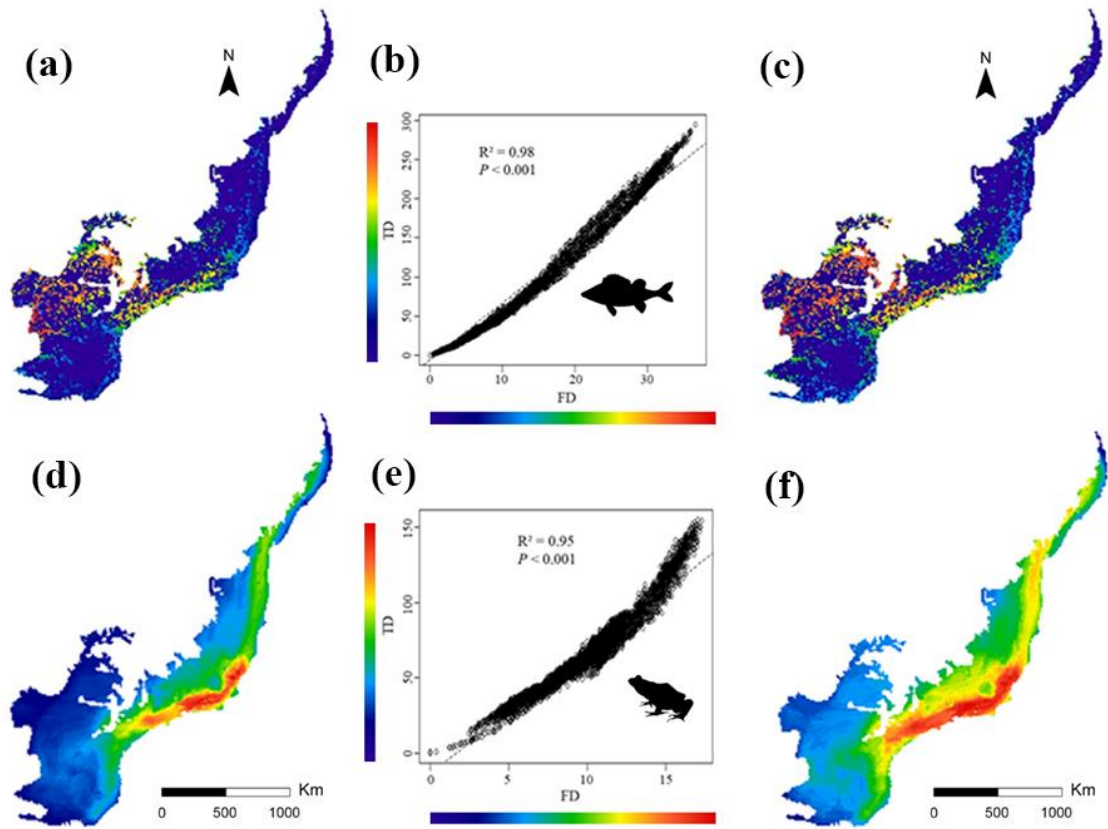


675

676 **Fig. 1** Spatial distribution of the Brazilian Atlantic Forest, according to their forest remnants and main

677 rivers.

678



679

680 **Fig. 2** Spatial distribution of (a) TD, linear correlation between taxonomic (TD) and functional (FD)

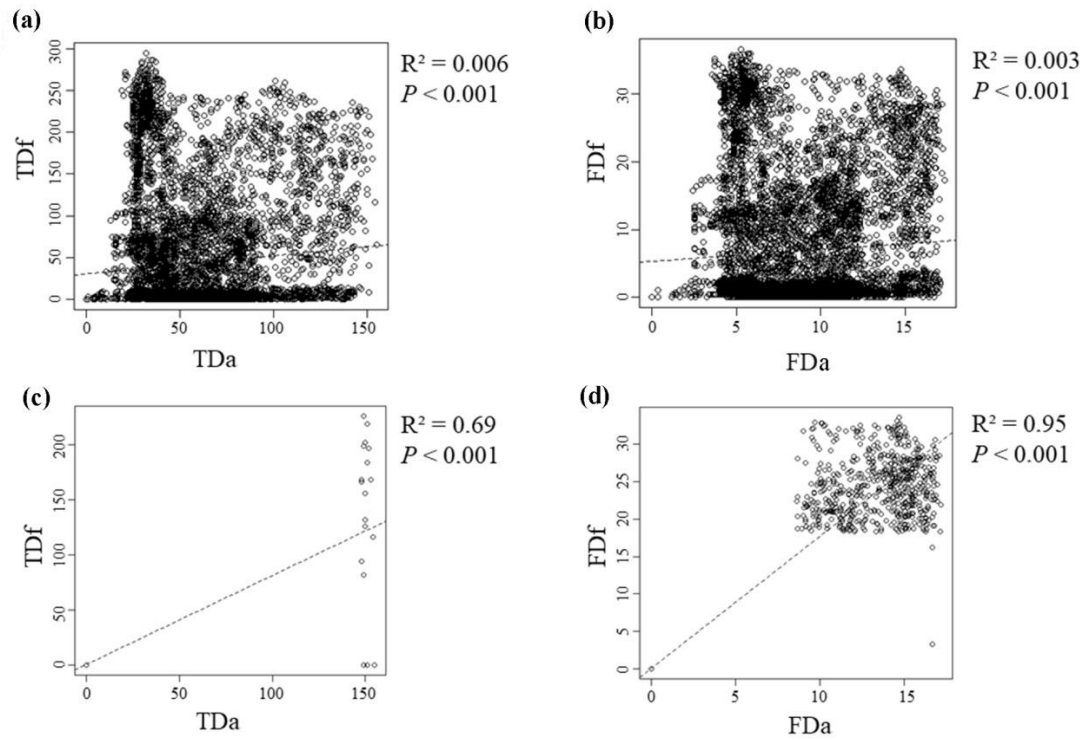
681 diversity of fishes (b), and FD of fishes in the Brazilian Atlantic Forest (c); spatial distribution of (d) TD,

682 linear correlation between TD and FD of amphibians (e), and FD of amphibians in the Brazilian Atlantic

683 Forest (f).

684

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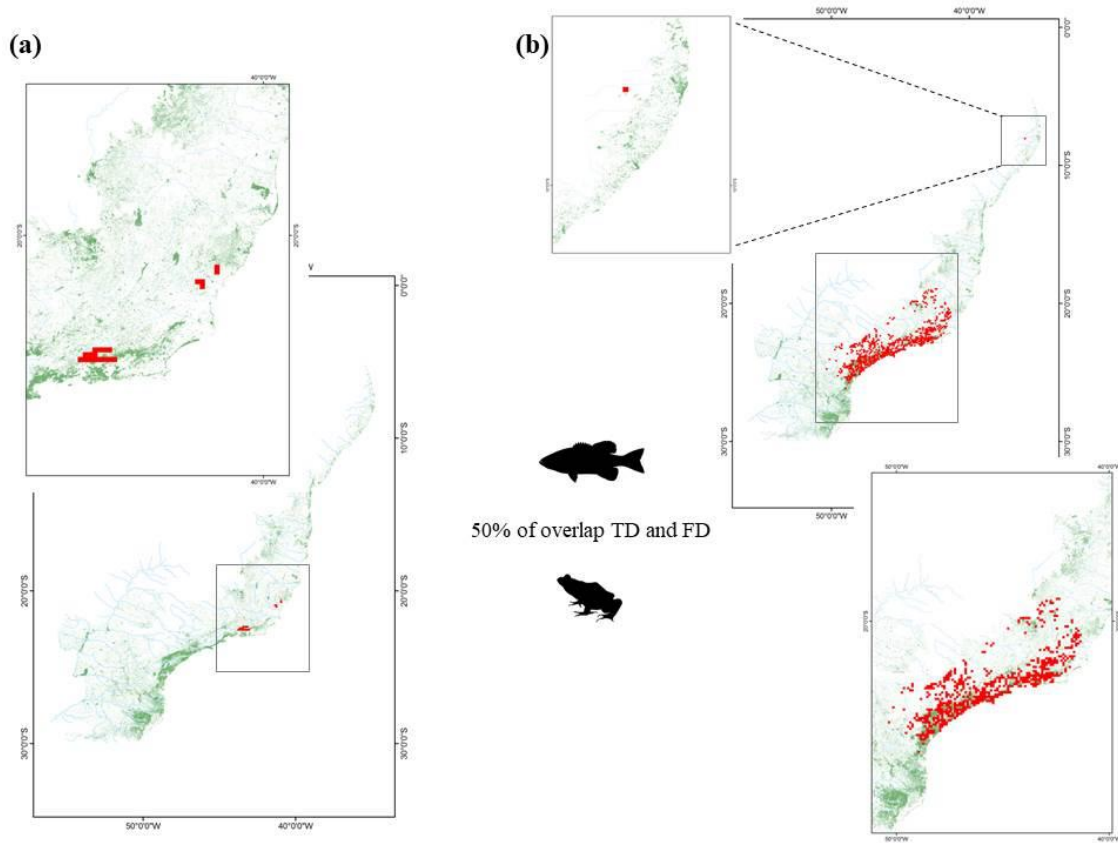
686

687 **Fig. 3** Linear correlation of taxonomic and functional diversity of fishes (TDF/FDF) and amphibians

688 (TDa/FDa). The analyses of (a) and (b) contain 100% of the values obtained, and (c) and (d) only contain

689 values of TD and FD  $\geq 50\%$  of the total value.

690



691

692 **Fig. 4** Overlapping areas in red between taxonomic diversity (TD) and functional diversity (FD) of fishes  
 693 and amphibians ( $\geq 50\%$  of the total) in the Brazilian Atlantic Forest. (a) TD (0.19%) and (b) FD (2.58%).