

UNIVERSIDADE FEDERAL DE SÃO CARLOS
CENTRO DE CIÊNCIAS BIOLÓGICAS E DA SAÚDE
PROGRAMA DE PÓS-GRADUAÇÃO EM ECOLOGIA E RECURSOS NATURAIS

Flávia Gomes de Mello

How short-term variation influence the relative importance of environmental
and spatial factors associated to anuran dissimilarity composition

São Carlos

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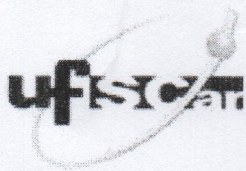
How short-term variation influence the relative importance of environmental
and spatial factors associated to anuran dissimilarity composition

Dissertação apresentada ao Programa de Pós-Graduação em Ecologia e Recursos Naturais da Universidade Federal de São Carlos como parte dos requisitos para obtenção do título de Mestre em Ecologia e Recursos Naturais.

Orientação: Prof^o Dr. Fernando Rodrigues da Silva

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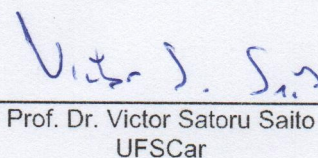
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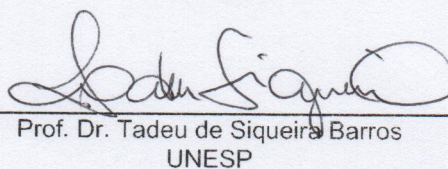
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FORMATAÇÃO:

Este trabalho segue as exigências do Regimento Interno do Programa de Pós-Graduação em Ecologia e Recursos Naturais (PPGERN) da Universidade Federal de São Carlos – UFSCAR (<http://www.ppgern.ufscar.br/>). A dissertação foi redigida no formato de artigo científico para apreciação no periódico *Plos One* ISSN: 1932-6203. Contudo, realizamos algumas alterações em relação as normas descritas pela *Plos One* que julgamos melhorar a apresentação da dissertação. São elas: i) acrescentamos ao artigo um resumo redigido em português; e ii) inserimos as legendas das figuras e tabelas no final do artigo. Nos apêndices é possível encontrar todo o material suplementar.

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Resumo

Compreender os processos que originam os padrões na composição de espécies e a variação na biodiversidade através do espaço tem sido um dos principais tópicos estudados dentro da teoria de metacomunidades. Contudo, a maioria dos trabalhos utilizaram dados “fixos” das comunidades e poucos estudos examinaram a importância de incluir variabilidade temporal nas análises. Neste estudo, nós avaliamos a distribuição da diversidade beta na composição de comunidades de anuros ao longo de três anos e considerando todo o período de estudo em diferentes escalas espaciais na Mata Atlântica brasileira: i) sete comunidades distribuídas na região costeira; ii) sete comunidades distribuídas na região do interior; e iii) todas as comunidades juntas. Nós particionamos a diversidade beta total nos componentes substituição de espécies e aninhamento, e depois, utilizamos a partição de variância para explorar a importância relativa dos fatores espaciais e ambientais relacionados com a variação na distribuição da composição de espécies de anuros ao longo dos anos. A substituição de espécies foi o componente predominante da diversidade beta de anuros. Nós também observamos que os valores médios dos componentes da diversidade beta diminuíram quando a composição de espécies foi analisada considerando o período total de estudo e aumentaram com o aumento da extensão espacial. Além disso, nossos resultados indicam que a composição de espécies de anuros na Mata Atlântica são dinâmicas no tempo e espaço, e os fatores explicando a distribuição dos componentes substituição de espécies e aninhamento são dependentes do ano de amostragem e da extensão espacial. Portanto, estudos de metacomunidades que não consideram mudanças temporais e espaciais devem ser cuidadosos com respeito as generalidades de suas conclusões biológicas.

Palavras-chave: montagem de comunidades, aninhamento, substituição de espécies, diversidade temporal, partição da variância.

1 How short-term variation influence the relative importance of environmental and
2 spatial factors associated to anuran dissimilarity composition

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28 **Abstract**

29 Understanding the processes that create the patterns of species composition and biodiversity
30 variation across the space has been one of the main topics within the theory of metacommunities.
31 However, most studies rely on static snapshots of community data and few studies have examined
32 the importance of including temporal variability. Here, we examined beta diversity distribution of
33 anuran community composition through three years and considering the whole period of study at
34 different spatial extents in the Brazilian Atlantic Forest: i) seven inland communities; ii) seven
35 coastal communities; and iii) communities pooled together. We partitioned total beta diversity into
36 species replacement and nestedness-resultant components then we used variation partitioning to
37 explore the relative importance of environmental and spatial factors explaining the distribution of
38 anuran community changes over the years. Species replacement was the predominant component of
39 anuran beta diversity. We observed that average values of beta diversity components decrease when
40 species composition of whole period of study are pooled together and increase with increasing
41 spatial extent. Furthermore, our results indicate that Brazilian Atlantic Forest anuran community
42 compositions are dynamic in space and time, and the factors explaining the distribution of species
43 replacement and nestedness-resultant are dependent of the sampling year and spatial extent. Thus,
44 metacommunity studies that do not evaluate different spatial and temporal changes should be
45 cautious about the generality of their biological conclusions.

46

47 Keywords: community assembly, nestedness-resultant, species replacement, temporal diversity,
48 variation partitioning

49

50 **Introduction**

51 Understanding the roles of dispersal, and niche-based (i.e. habitat filtering and biotic
52 interactions) and stochastic (i.e. random colonization-extinction) processes in shaping local
53 communities has been the main subject of metacommunity theory [1, 2, 3, 4]. In the last decades,
54 several empirical studies in metacommunity ecology have examined the relative importance of
55 space and environmental factors on the similarity of species composition among local sites relying
56 on static snapshots of community data [5, 6, 7]. The traditional absence of temporal variability on
57 community composition suggests that the structure of metacommunity remains constant through
58 time. However, richness and community composition change over time [8, 9, 10], and effects of
59 temporal variability in metacommunity theory remains little understood. For example, Fernandes et
60 al. (2014) [11] found that seasonal floodplain-fish metacommunity is structured by changes
61 between dispersal limitation and environmental filter through time. In contrast, Baselga et al. (2015)
62 [12] observed that land cover changes in agricultural landscape had little impact on temporal beta
63 diversity of bird assemblages. Considering that environmental and spatial processes are dependent
64 on the time of sampling, metacommunity studies based on single snapshots may differ about the
65 importance of different factors shaping local communities (*e.g.* patterns might be linked to
66 environmental factors at one year, but spatial factors at another year), especially when communities
67 are sampled across different periods.

68 Here, we simultaneously assessed spatial and short-term variation in anuran community
69 dissimilarity in the Brazilian Atlantic Forest. We partitioned total beta diversity into species
70 replacement and nestedness-resultant components [13, 14] through three years and considering the
71 whole period of study at different spatial extents: i) seven inland communities; ii) seven coastal
72 communities; and iii) communities pooled together. Evaluating local community dissimilarities at
73 different spatial extent, can be a tool to detect mechanisms structuring metacommunities that may
74 be interacting at local and/or regional scales [15, 16]. In this case, relationships between
75 environmental and spatial factor with community dissimilarity may be a question of spatial scale

76 and the range of environmental variation examined [17, 18, 19]. For example, patterns of
77 community dissimilarity associated with species interactions would be more likely to be explained
78 at smaller extent, whereas patterns of community dissimilarity associated with dispersal from
79 regional species pool would be more likely to be explained by larger extent [17, 18]. Furthermore,
80 evaluating species replacement and nestedness-resultant components of beta diversity can shed light
81 on the mechanistic underpinnings these patterns [20, 21, 22]. Compositional dissimilarity of two
82 local communities may reflect two antithetic phenomena, species turnover and species loss/gain
83 (Fig 1a) that when ignored might lead to inappropriate conclusions [13]. Therefore, these beta
84 diversity components should be disentangled in order to identify the underlying processes
85 responsible for observed patterns of community dissimilarity.

86 Brazilian Atlantic Forest, a global biodiversity hotspot [23], originally covered c. 1.3 million
87 km², of which 16% remain not degraded by human activities [24]. This biome harbors as many as
88 600 amphibian species, of which c. 88% are endemic [25]. The great richness and endemism of
89 amphibians in this region are usually attributed to the strong climatic gradients and topographic
90 heterogeneity, and high turnover of amphibian species in space [21, 22], making it an ideal location
91 to assess the role of environmental and spatial factors on community dissimilarity at different
92 spatial extent. Based on this scenario, we asked if environmental and spatial factors correlated to
93 distribution of species replacement and nestedness-resultant components are similar over time or
94 dependent on the sampling year. Our first objective was to evaluate whether species replacement
95 and nestedness-resultant values are congruent through three years and considering the whole period
96 of study at different spatial extents (Fig 1b). Our second objective was to understand if ecological
97 processes such as environmental sorting and dispersal limitation are congruent through three years
98 and considering the whole period of study at different spatial extents (Fig 1c). Thus, if the ability of
99 correlative and mechanistic models to predict community dissimilarity change depending on the
100 year of sampling, the theoretical and applied results of metacommunity studies would be limited to

101 specific year. We hope that this approach will help us to better understand the interaction of spatial
102 and temporal dynamics on the processes structuring community assembly.

103

104 **Material and Methods**

105 **Study area and sampling**

106 We used a short-term dataset with anuran incidence data from 14 protected areas in the
107 Brazilian Atlantic Forest (Fig 2). The sampling was carried out using standardized methods from
108 December to February for three consecutive years (2014 to 2017), totaling 27 days in each
109 protected area. This period is the time of the year when most of annual rainfall occurs and most
110 anuran species are active. Six reproductive habitats were sampled in each area: two ponds, two
111 streams and two transects inside forest fragments. Surveys were carried out on streams and transects
112 inside forest fragments considering always the same extension of 100 m in all areas. Three sampling
113 methods were used to determine the anuran species composition in each reproductive habitat: i)
114 Survey at breeding site [26] - combining a visual and auditory search in the breeding habitats
115 between 19:00 hours and 24:00 hours; ii) survey of larvae with dipnetting - a long and wire hand net
116 (3 mm² mesh size) was used along the margins of ponds and streams, sampling the available
117 microhabitats from 12.00 hours to 18.00 hours; and (iii) visual encounter [27] – two people walked
118 slowly for 30 minutes in trails inside the forest fragment, streams and around ponds looking at
119 microhabitats for individuals hidden under trunks, bromeliads, stones, branches, and leaf litter. The
120 combination of sampling methods increases the efficiency of recording anuran species in
121 communities [28].

122 There is general agreement that the regional species pool and the spatial extent are
123 fundamental issues influencing the processes involved in metacommunity assembly [4]. Thus, we
124 limited the areas sampled in this study at different spatial extent (Fig 2) and regional species pool
125 based on the biogeographic regions of anurans in the Brazilian Atlantic Forest [29]. These authors
126 split anuran species composition into four regions that are broadly congruent with the vegetation

127 formations of the Atlantic Forest: (1) Region 1, located in Atlantic Forest inland areas, composed by
128 semideciduous forest and some areas of transition to the Cerrado; (2) Region 2 comprises mostly
129 the ombrophilous forest, located in the coastal Atlantic Forest in southeastern Brazil; (3) Region 3 is
130 mostly congruent with the Araucaria forest in southern Brazil; and (4) Region 4 encompasses the
131 northeastern Brazilian semideciduous and ombrophilous forests. Our study area comprises the most
132 southeastern region of the country, encompassing the Region 1 and 2 according to the work of
133 Vasconcelos et al (2014).

134

135 **Environmental variables**

136 We gathered monthly precipitation data (December, January and February) for each site
137 over the three sampled years (Table 1). For this, we used accumulated monthly precipitation
138 available in the online governmental platform of the Centro Integrado de Informações
139 Agrometeorológicas (<http://www.ciiagro.sp.gov.br/>). When data were not available, we used the
140 precipitation values from the location closest to the protected area considering a maximum radius of
141 35 km. For statistical analysis, we considered, for each year separately, the sum of precipitation
142 over the three months (Table 2). In contrast, when the data were analyzed together, we used the
143 mean of precipitation over the three years (Table 2). We used Google Earth to obtain maximum
144 (MAEL) and minimum (MIEL) elevation for each protected area. Then, we calculated the
145 elevational range (difference between MAEL and MIEL) (Table 2).

146

147 **Community dissimilarity**

148 We calculate beta diversity between inland and coastal communities separately and after
149 all communities together. We analyze the results of each year and then check the congruence of the
150 results over the years. We used the additive partitioning approach proposed by Baselga (2010, 2012)
151 [13, 14], in which the Sorensen dissimilarity (β_{sor}) index is decomposed into two additive

152 components: (1) the species replacement component (β_{sim}), which measures the proportion of
153 unique species in two sites pooled together if both sites are equally rich; and (2) the nestedness-
154 resultant component (β_{sne}), which measures how dissimilar the sites are due to a nested pattern.

155 We performed Linear mixed effect models to assess the distributions of β_{sor} , β_{sim} and β_{sne}
156 values separately through time using pairwise distances as repeated measures. All analyzes were
157 performed using software R 3.4.3. [30] using 'betapart' [31] and 'nmlle' [32] packages.

158

159 **Relative importance of environmental and spatial factors**

160 We used distance-based Moran's Eigenvector Maps (dbMEMs) [33, 34] to describe
161 spatial structures. The eigenvectors of dbMEM are determined from a truncated geodesic distance
162 matrix calculated using the longest distance connecting two sites in a minimum spanning tree as a
163 threshold. Then, we used a forward selection procedure with double stopping criteria [35] to only
164 select environmental variables and dbMEMs that significantly explained the variance in the species
165 composition matrix [36] considering inland and coastal sites and the sites pooled together
166 separately.

167 We assess the relative importance of environmental and spatial factors (dbMEMs) using
168 variation partitioning [37]. This approach partitions the total percentage of variation into unique and
169 shared contributions of the sets of predictors. The total variation in the pairwise beta diversity
170 components was divided into four fractions: i) the variation explained purely by space; ii) the
171 variation explained purely by environmental variables; iii) the shared variation explained by
172 environmental and space; and iv) unexplained variation (residual). We performed partial
173 redundancy analysis with 999 Monte Carlo permutations to test significance of variation explained
174 purely by environmental and spatial factors [35].

175 All analyzes were performed using software R 3.4.3. [30] using 'vegan' [38] and
176 'adespatial' [39] packages.

177 **Results**

178 **Community dissimilarity**

179 We found that independently of sampling year or spatial extent, β_{sim} was the predominant
 180 component of the beta diversity (Fig 3). Furthermore, average values of dissimilarity species
 181 composition were different considering inland sites ($F_{\beta_{\text{sor}3,60}} = 10.18, p < 0.001; F_{\beta_{\text{sim}3,60}} = 5.23, p =$
 182 $0.002; F_{\beta_{\text{sne}3,60}} = 4.11, p = 0.01$; Fig 3B), coastal sites ($F_{\beta_{\text{sor}3,60}} = 36.39, p < 0.001; F_{\beta_{\text{sim}3,60}} = 37.73, p$
 183 $< 0.001; F_{\beta_{\text{sne}3,60}} = 1.34, p = 0.26$; Fig 3B) and sites pooled together ($F_{\beta_{\text{sor}3,270}} = 34.37, p < 0.001;$
 184 $F_{\beta_{\text{sim}3,270}} = 36.05, p < 0.001; F_{\beta_{\text{sne}3,270}} = 9.49, p < 0.001$; Fig 3C). We also found that independent of
 185 the spatial extent, values of dissimilarity species composition considering years pooled together are
 186 lower than values of dissimilarity species composition from separated years (Fig 3).

187

188 **Relative importance of environmental and spatial factors**

189 The strength of relative importance of the environmental and spatial factors through time
 190 was depended on the sampling year and spatial extent (Fig 4). For inland sites,
 191 the total dissimilarity (β_{sor}) between communities was explained by environmental variables and
 192 space only in the second year (Fig 4A). During the first year species replacement (β_{sim}) was not
 193 associated with environmental factors, but in the other years, there were association with these
 194 factors (Fig 4B). Still for the inland communities, the nestedness component (β_{sne}) was explained
 195 by the environment and space only in the first year sampled (Fig 4C). However, when we analyze
 196 the data of the three years together we do not observe a power of explanation of both environmental
 197 and spatial factors (Fig. 4A-C).

198 For coastal communities in general, environmental variables had little or no explanatory
 199 power for each year separately and from the years together (Fig 4D-F). The spatial factors not
 200 explained the dissimilarity between communities in the second year, but instead explained from
 201 0.24 to 0.43 of the variation on species replacement for the other years and years pooled together

202 (Fig 4D-F). When we consider the communities pooled together, we notice a decrease in the
203 explanation power of the environmental variables and an increase in the power of explanation of the
204 space on the beta diversity. In this case we still observe a variation in the force of explanation of the
205 space between the years (Fig 4G-I). Furthermore, we found that increasing the spatial extent the
206 values of residual for β_{sor} and β_{sim} decrease (Fig 4G-H). In addition, the nestedness component
207 (β_{sne}) was explained by the environment and space only in the first and second years (Fig 4I).

208

209 **Discussion**

210 We observed a temporal and spatial variation independently of the beta diversity component.
211 The correlation of environmental and spatial variables with dissimilarity distributions was
212 dependent on the year sampled. According to Dornelas et al. (2012) [40], among the main factors to
213 which temporal changes in biodiversity can be attributed are systemic changes (reflection of a non-
214 stationary system where there are long-term changes in ecological directions), which may be
215 anthropogenic or natural processes. Although many studies focus on temporal variation in
216 biological communities caused by anthropogenic disturbances [8], these variations also occur
217 frequently in natural environments due for example to colonization of new spaces, adaptive
218 radiations and annihilation of a community [40]. However, each time observation can arise from the
219 combination of deterministic and stochastic effects, and the processes involved in these changes
220 depend on the components of biodiversity being studied and on the spatial and temporal extent of
221 the data [40].

222 Although many works performed with vertebrate and temporal beta diversity have found
223 important results, most of them used a long-term scale [41, 12]. Here we use a short-term scale,
224 since amphibians in addition to having a shorter life cycle compared to birds or mammals for
225 example, are easily affected by periodic climatic conditions, extinguishing or propitiating the
226 increase of certain species or populations in the localities. Environmental variability occurs over
227 time because of environmental fluctuations, and these changes may cause temporary microhabitats

228 and thus contribute to a difference in species composition of the community in different periods [42,
229 43]. Here, for the inland communities, the environmental variables had greater explanatory power
230 explaining beta diversity distribution than in the second and third year of sampling that were drier
231 years for some communities compared to the first year sampled (Table 1). For coastal communities
232 that are in the wettest portion of the biome, we observed no influence of the environmental
233 variables explaining the dissimilarity between them for the first and third year of sampling, which
234 were the driest years. However, for the second year, where accumulated monthly precipitation was
235 higher, rainfall was more important to explain the dissimilarity found among communities than
236 space. When we consider the two regions together we lose the explanatory power of the
237 environmental variables and increase the force of explanation of the space. Recently, França et al.
238 (2017) [44] evaluated the temporal fluctuations in the occurrence and abundance of amphibian
239 species in a portion of the Amazon rainforest, they found that greater species richness and
240 abundance occur during rainy periods, however, they pointed out that species may react differently
241 while some are sensitive to fluctuations, others do not seem to respond easily or do not reduce their
242 abundances at potentially unfavorable times. Similarly, Davis et al. (2017) [45] verified that the
243 persistence and colonization of amphibian metacommunities in the Florida's northwest during a six-
244 year period was affected differently by environmental disturbances with some amphibians being
245 more sensitive to drought and others more sensitive to periods of high precipitation. Péntek et al.
246 (2016) [46] evaluating amphibians in Central Europe in different periods of rain verified a change
247 between years in the relative role of spatial and local processes. All these studies revealed a
248 complex connection of spatial and temporal factors with the structuring the communities. Thereby,
249 determining the periods of fluctuations that species compositions of sites may vary over time and
250 the patterns associated with them is of extreme importance, considering that possible
251 misunderstandings can be generated in the absence of these temporal observations [47, 46, 45].

252 We observed that evaluating all communities together the explanatory power of the
253 environmental variables decreases while the explanation of the space increases. This phenomenon

254 can be explained by a consequent amplification of the biogeographic processes, which can result in
255 stronger limits on the dispersion of individuals, making communities even more differentiated [17,
256 48, 49, 50]. One of the potential determinants of beta diversity is the size of the species pool, which
257 may vary depending on the region considered [51]. Currently we find a climatic variation between
258 the different phytophysionomies of the Atlantic Forest, passing through very humid
259 Ombrophylous Dense forests near the coast and portions of dry Semideciduous Seasonal forest that
260 contact the domain of Cerrado, found more in the interior [24, 29]. This heterogeneity is the result
261 of different historical and biogeographic processes that have occurred over time. Biogeographic
262 processes such as climatic oscillations and periods of glaciations during the Pleistocene and
263 consequent reduction of wetlands (model of refuges) may have generated different evolutionary
264 histories among the species in these regions [52]. Other hypotheses are based on geological
265 changes, such as the isolation of mountains and the emergence of rivers as physical barriers to
266 contribute to the processes of speciation of these sites. However, environmental gradients and
267 altitudinal differences could also have served as ecotones for favoring divergent selection [52].
268 Therefore, these processes were important to determine the difference in species composition
269 among the communities found today in the different physiognomies of the Atlantic Forest.

270 We found that species replacement was the predominant component of anuran beta
271 diversity. Previous studies have already revealed species replacement as the main component of
272 beta diversity distributions [53, 21]. The environmental heterogeneity and the climatic differences
273 found in the coastal and interior regions, such as climate and altitude, are significant, mainly when
274 considered microhabitats used by the anurans. In coastal communities it was found greater species
275 richness as well as higher elevational range compared to the inland communities. These factors may
276 result in an increase of beta diversity values due to physiological limitations of anurans along
277 climate gradients. For example, amphibians have high physiological sensitivity and wide
278 morphological and behavioral diversity, adapted to different climatic and environmental conditions.
279 These characteristics resulted in different reproductive strategies and the use of specific

280 microhabitats during the development and life cycle of this group [54]. However, the variation in
281 the composition of the communities over time may be associated not only to the deterministic
282 processes, such as environmental and climatic changes, which can act as filters for different species
283 (niche perspective), but also in combination to stochastic processes, such as extinction and species
284 colonization, where the distribution of the species locally takes place randomly in response to a
285 possible ecological equivalence between them (neutral dynamic) [1, 55, 56, 57, 58]. Therefore, we
286 must consider a broader view in determining which processes act in the dissimilarity between
287 metacommunities, demonstrating for example that the combination of stochastic and deterministic
288 processes can often provide a better explanation for the distribution of species in a community [59].

289

290 **Conclusions**

291 Our results indicate that Brazilian Atlantic Forest anuran community compositions are
292 dynamic in space and time, and the factors explaining the distribution of species replacement and
293 nestedness-resultant are dependent of the sampling year and spatial extent. Taken together, these
294 results emphasize the importance of including spatial and temporal variables to questions which
295 seek to understand patterns, processes and elements that drive the complex dynamics of factors
296 associated with dissimilarity among ecological communities. Thus, metacommunity studies that do
297 not evaluate different spatial and temporal changes should be cautious about the generality of their
298 biological conclusions.

299

300

301

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452 **Supporting Information**

453

454 **S1 Table. Species composition in the first year sampled.** List of anuran species recorded from
455 December 2014 to February 2015 on 14 protected areas in the Brazilian Atlantic Forest.

456 **S2 Table. Species composition in the second year sampled.** List of anuran species recorded from
457 December 2015 to February 2016 on 14 protected areas in the Brazilian Atlantic Forest.

458 **S3 Table. Species composition in the third year sampled.** List of anuran species recorded on 14
459 protected areas in the Brazilian Atlantic Forest from December 2016 to February 2017.

460 **S4 Table. Species composition for the three years sampled.** List of anuran species recorded on
461 14 protected areas in the Brazilian Atlantic Forest considering three years pooled together.

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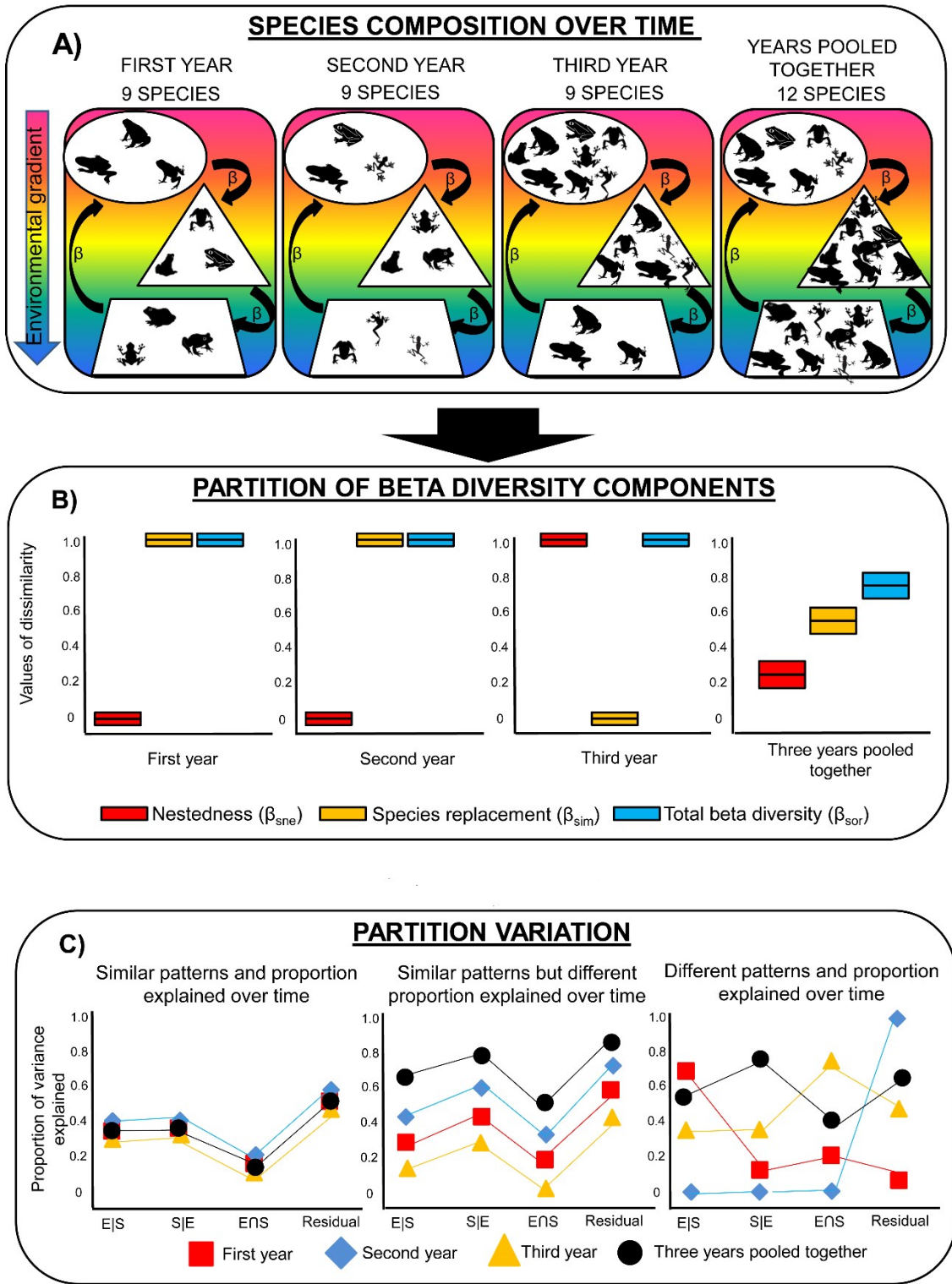
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474 **Figures**

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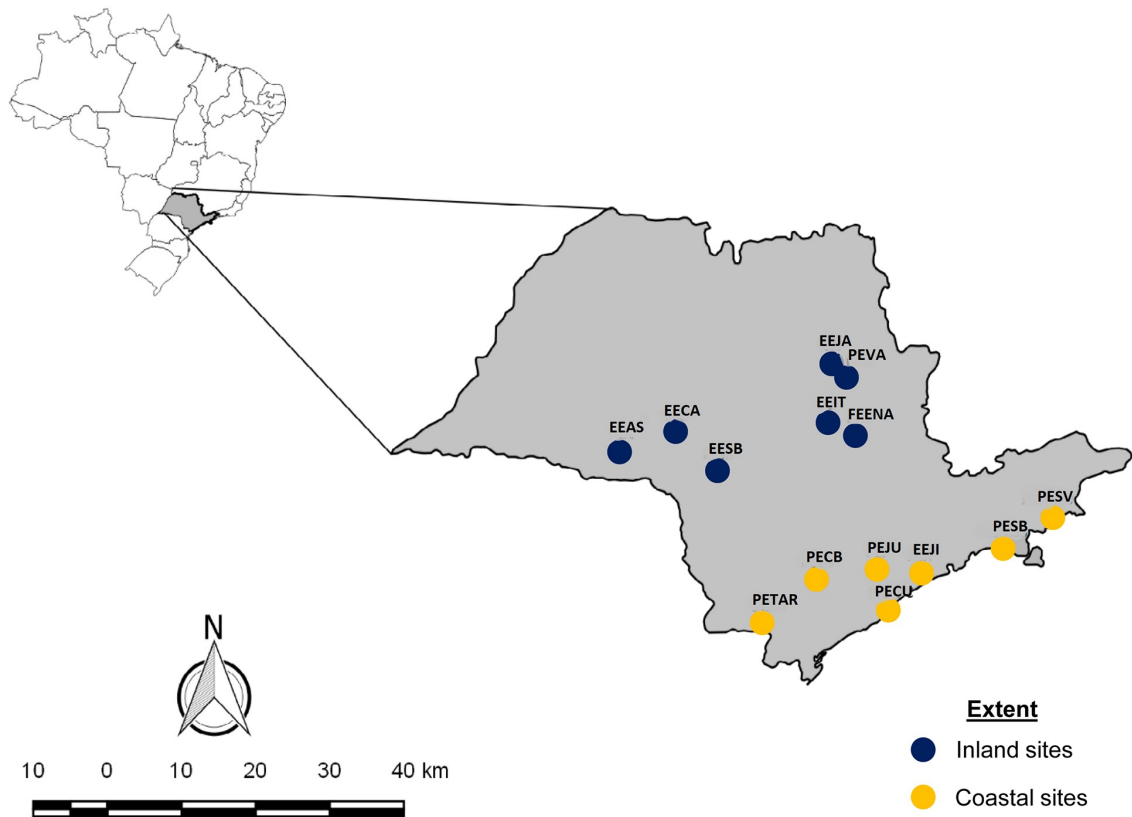
477 **Fig 1. Representative scheme of the approach used in this study.** A) Hypothetical distribution of
 478 anuran species in three different communities (white geometric figures) over three consecutive
 479 years and considering the three years pooled together. Colors represent illustrative environmental

480 gradient influencing anuran species composition. **B)** Four scenarios showing the partition of total
481 beta diversity (β_{sor}) into species replacement (β_{sim}), and nestedness (β_{sne}) components. In the first
482 two scenarios, even the species composition being different between them, we observe high values
483 of turnover indicating that β_{sim} is the main component describing the variation in species
484 composition along the environmental gradient. On the other hand, in the third year, β_{sne} is the main
485 component explaining the variation in species composition among communities. In this case, we
486 observe that some anurans species are lost along the environment gradient, but there is no species
487 replacement between communities. In the fourth year, there is a balance on the importance of β_{sim}
488 and β_{sne} describing the variation in species composition among communities. **C)** Three scenarios
489 showing the relative importance of environmental and spatial factors explaining variation in anuran
490 community composition. In the first scenario, there is congruence about factors and proportion of
491 variance explained over the years. In the second scenario, there is congruence about factors but the
492 proportion of variance explained is dependent on the year. In the third scenario, factors and
493 proportion of variance explained are different among years. $E|S$ = variation explained purely by
494 environment; $S|E$ = variation explained purely by space; $E \cap S$ = spatially structured environment;
495 Residual = variation not explained by the variables used in the study.

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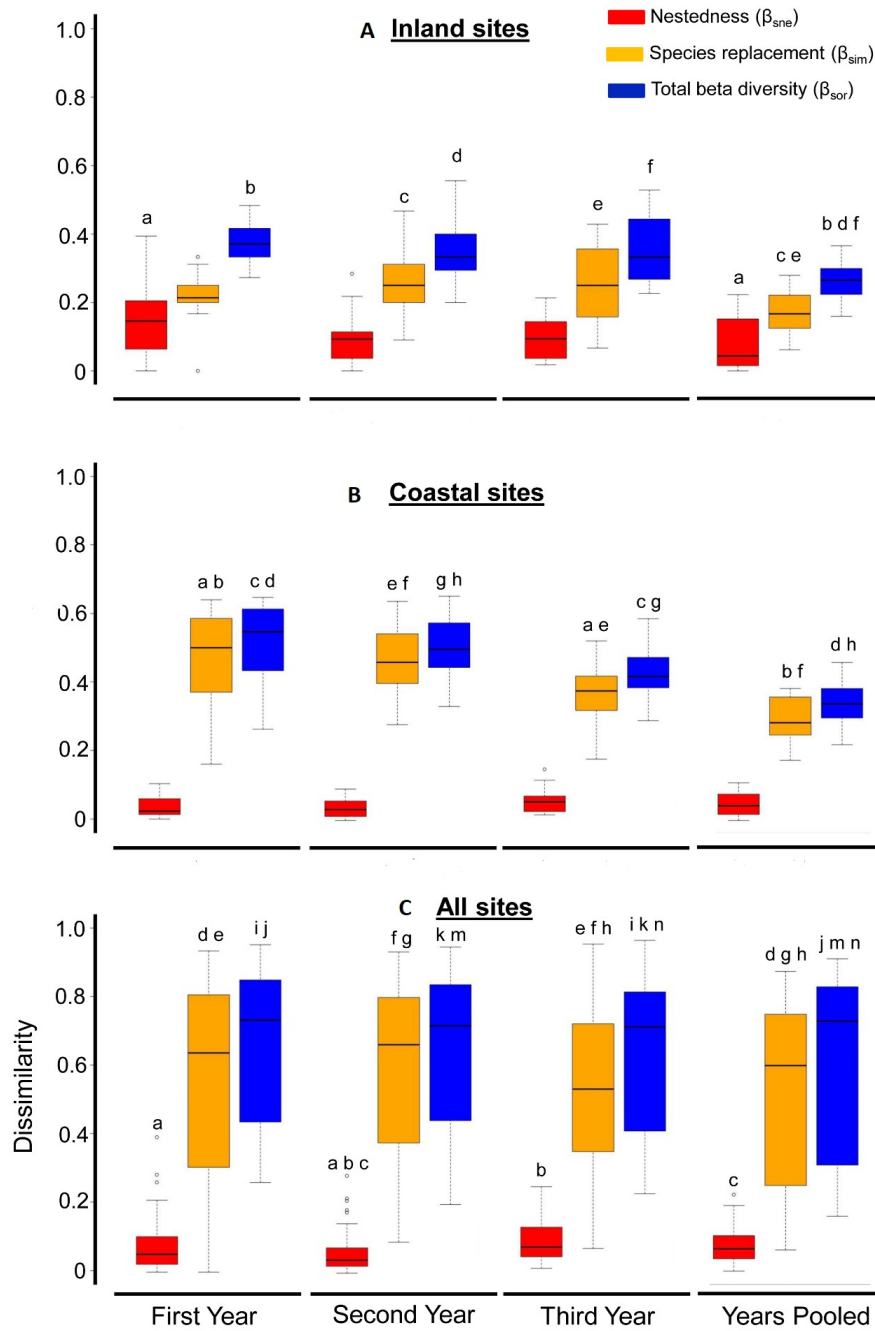
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500 **Fig 2. Study area.** Map showing the state of São Paulo highlighted in Brazil (left) and the protected
 501 areas where we carried out field surveys (right) over three consecutive years. Blue dots represent
 502 the protected areas within inland spatial extent while orange dots represent the protected areas
 503 within coastal spatial extent. Acronyms and consecutive names of protected areas plotted on the
 504 map: EEAS – Estação Ecológica de Assis, EECA – Estação Ecológica de Caetetus, EEIT – Estação
 505 Ecológica de Itirapina, EEJA – Estação Ecológica de Jataí, EESB – Estação Ecológica de Santa
 506 Bárbara, FEENA – Floresta Edmundo Navarro, PEVA – Parque Estadual Vassununga, EECB –
 507 Parque Estadual Carlos Botelho, EEJI – Estação Ecológica Juréia Itatins, PECU – Parque Estadual
 508 da Serra do Mar Curucutu, PEJU – Parque Estadual Jurupará, PESV – Parque Estadual da Serra do
 509 Mar Santa Virgínia, PETAR – Parque Estadual Turístico do Alto Ribeira, PESB – Parque Estadual
 510 da Serra do Mar São Sebastião.

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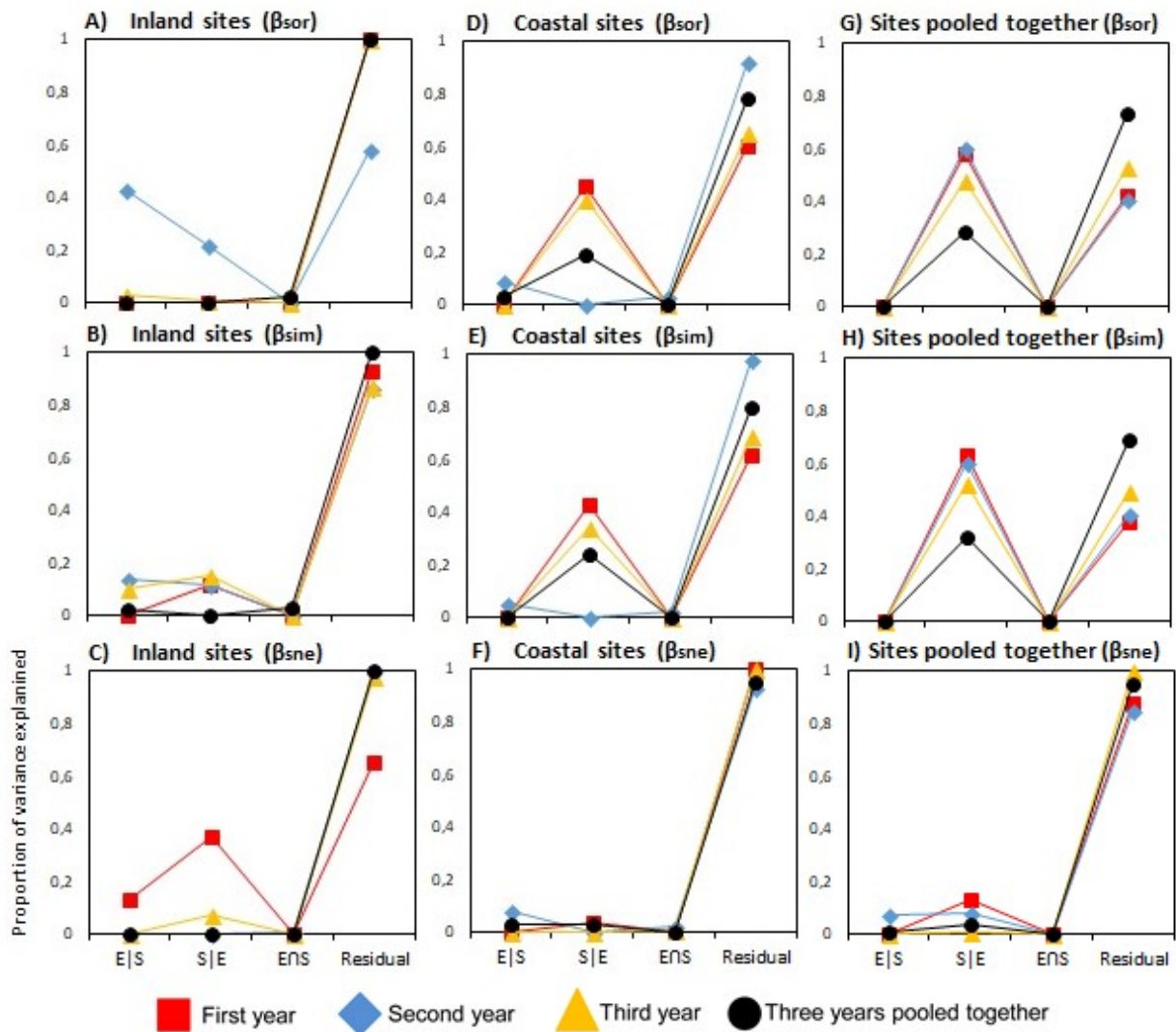
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515 **Fig 3. Results for community dissimilarity.** Boxplot showing the decomposition of pairwise
 516 Sorensen dissimilarity (β_{sor}) into species replacement (β_{sim}) and nestedness (β_{sne}) components over
 517 time considering (A) small spatial extent with seven inland protected areas; (B) small spatial extent
 518 with seven coastal protected areas; and (C) broad spatial extent with all protected areas together.
 519 The horizontal black line and box show the median and 50% quartiles, respectively, and the error
 520 bars display the range of the data. Similar letters indicate significant difference ($p < .05$) between
 521 average dissimilarity values over time.



534 **Tables**

535

Table 1: Accumulated precipitation data (millimeter – mm) for each protected area considering the three months (December , January and February) in which the anuran samplings were carried out along the three sampled years. Data obtained from online governmental platform of the Centro Integrado de Informações Agrometeorológicas (<http://www.ciiagro.sp.gov.br/>).

Sites	Accumulated monthly precipitation by period (mm)								
	Dec. 2014	Jan. 2015	Feb. 2015	Dec. 2015	Jan. 2016	Feb. 2016	Dec. 2016	Jan. 2017	Feb. 2017
Inland									
EEAS	187	211	201	160	261	187	166	215	139
EECA	230	191	197	211	292	285	216	265	181
EEIT	248	89	49	50	328	16	174	326	42
EEJA	186	120	239	79	97	13	0	2	1
EESB	134	117	164	77	210	67	134	288	147
FEENA	134	157	235	124	272	109	175	294	76
PEVA	186	120	239	79	97	13	0	2	1
Coastal									
EECB	254	125	195	106	295	204	1	0	27
EEJI	197	174	118	167	301	328	0	4	0
PECU	160	183	250	227	257	199	0	4	0
PEJU	149	3	1	242	178	83	123	270	113
PESV	107	105	275	191	199	0,2	117	0	27
PETAR	188	96	235	140	235	428	128	217	109
PESB	256	222	310	95	139	98	37	387	61

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Table 2. Precipitation (millimeter – mm) and altitude data for each protected area considered in this study. Precipitation was determined considering the sum of the three months (December , January and February) in which the anuran samplings were carried out and the mean of the three years for each protected area. Precipitation data were obtained from online governmental platform of the Centro Integrado de Informações Agrometeorológicas (<http://www.ciiagro.sp.gov.br/>). Altitude data were obtained from Google Earth (<https://www.google.com.br/intl/pt-BR/earth/>).

Sites	Environmental Variables						
	Sum of precipitation over the three months (mm)				Altitude data		
	First year	Second year	Third year	Mean of the years	Maximum altitude	Minimum altitude	Altitude range
Inland							
EEAS	599	608	521	576	601	450	151
EECA	618	787	662	689	703	452	251
EEIT	386	394	542	441	810	510	300
EEJA	545	189	3	246	788	530	258
EESB	416	355	569	447	740	530	210
FEENA	527	505	545	526	792	598	194
PEVA	545	189	3	246	788	528	260
Coastal							
EECB	574	605	27	402	916	178	738
EEJI	489	796	4	430	1030	0	1030
PECU	593	683	4	427	901	40	861
PEJU	152	503	506	387	920	430	490
PESV	487	391	145	341	1030	600	430
PETAR	520	803	454	592	1001	120	881
PESB	788	332	485	535	930	0	930

545 **Appendix**

546

SUPPLEMENTARY INFORMATION

547

How short-term variation influence the relative importance of environmental and spatial factors associated to anuran dissimilarity composition

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Flávia G. de Mello, Fernando R. da Silva

550

Plos One

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552

S1 Table. Species composition in the first year sampled. List of anuran species recorded from December 2014 to February 2015 on 14 protected areas in the Brazilian Atlantic Forest.

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Species	Inland sites							Coastal sites						
	EEAS	EECA	EEIT	EEJA	EESB	FEENA	PEVA	EECB	EEJI	PECU	PEJU	PESV	PETAR	PESB
<i>Adenomera marmorata</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Adenomera</i> sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Aparasphenodon bokermanni</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Aplastodiscus albofrenatus</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	1
<i>Aplastodiscus albosignatus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Aplastodiscus perviridis</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Bokermannohyla circumdata</i>	0	0	0	0	0	0	0	0	0	1	1	1	0	0
<i>Bokermannohyla astartea</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Bokermannohyla hylax</i>	0	0	0	0	0	0	0	1	0	1	1	1	1	1
<i>Brachycephalus pitanga</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Chiasmocleis leucosticta</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Crossodactylus caramaschii</i>	0	1	0	0	0	0	0	1	0	0	0	0	0	0
<i>Cycloramphus boraceiensis</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Cycloramphus eleutherodactylus</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Cycloramphus lutzorum</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0

<i>Dendrophryniscus brevipolicatus</i>	0	0	0	0	0	0	0	1	0	1	0	1	0	1
<i>Dendropsophus berthaltutae</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	1
<i>Dendropsophus elegans</i>	0	0	0	0	0	0	0	1	1	1	1	0	0	0
<i>Dendropsophus elianeae</i>	0	1	1	0	1	0	0	0	0	0	0	0	0	0
<i>Dendropsophus giesleri</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Dendropsophus jimi</i>	0	0	1	0	1	0	0	0	0	0	0	0	0	0
<i>Dendropsophus microps</i>	0	0	0	0	0	0	0	1	1	0	1	1	1	0
<i>Dendropsophus minutus</i>	1	1	1	1	1	1	0	1	1	1	1	1	1	0
<i>Dendropsophus nanus</i>	1	1	0	1	1	1	1	0	0	0	0	0	0	0
<i>Dendropsophus seniculus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Dendropsophus werneri</i>	0	0	0	0	0	0	0	0	1	0	1	0	1	0
<i>Elachistocleis bicolor</i>	1	0	0	0	1	1	0	0	0	0	0	0	0	0
<i>Elachistocleis cesari</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Fritziana fissilis</i>	0	0	0	0	0	0	0	1	1	1	1	0	1	1
<i>Haddadus binotatus</i>	0	1	0	0	0	0	0	0	1	1	1	1	1	1
<i>Hylodes asper</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Hylodes phyllodes</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	1
<i>Boana albomarginatus</i>	0	0	0	0	0	0	0	1	1	1	1	0	1	1
<i>Boana albopunctatus</i>	1	0	1	1	1	1	1	0	0	1	1	1	0	0
<i>Boana bandeirantes</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Boana bischoffi</i>	0	0	0	0	0	0	0	1	0	1	1	0	1	0
<i>Boana caingua</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Boana caipora</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Boana faber</i>	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>Boana lundii</i>	1	1	0	0	1	1	1	0	0	0	0	0	0	0
<i>Boana pardalis</i>	0	0	0	0	0	0	0	1	1	0	1	1	0	0
<i>Boana semilineatus</i>	0	0	0	0	0	0	0	1	1	0	1	0	0	1
<i>Ischnocnema guentheri</i>	0	0	0	0	0	0	0	1	0	0	0	1	0	1
<i>Ischnocnema henseli</i>	0	0	0	0	0	0	0	1	0	1	1	0	1	0
<i>Ischnocnema parva</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Itapotihyla langsdorffii</i>	0	0	1	0	0	0	0	0	1	0	0	0	0	0

<i>Leptodactylus chaquensis</i>	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Leptodactylus furnarius</i>	1	1	0	0	1	0	0	0	0	1	0	0	0	0
<i>Leptodactylus fuscus</i>	1	1	1	0	1	0	1	0	0	0	0	0	0	0
<i>Leptodactylus labyrinthicus</i>	1	1	0	1	1	1	0	0	0	0	0	0	0	0
<i>Leptodactylus latrans</i>	1	1	1	0	1	0	0	0	1	1	1	0	0	0
<i>Leptodactylus mystaceus</i>	0	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Leptodactylus mystacinus</i>	1	1	1	1	1	0	1	0	0	0	0	0	0	0
<i>Leptodactylus notoaktites</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Leptodactylus plaumanni</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Leptodactylus podicipinus</i>	1	0	0	1	0	0	1	0	0	0	0	0	0	0
<i>Megaelosia bocainensis</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Paratelmatoobius cardosoi</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Paratelmatoobius gaigeae</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Phrynomedusa dryade</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Phyllomedusa distincta</i>	0	0	0	0	0	0	0	0	1	0	1	0	0	0
<i>Phyllomedusa tetraploidea</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Physalaemus atlanticus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Physalaemus bokermanni</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Physalaemus centralis</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Physalaemus cuvieri</i>	1	1	1	1	1	1	1	0	0	1	1	1	0	0
<i>Physalaemus lateristriga</i>	0	0	0	0	0	0	0	1	0	0	1	0	1	0
<i>Physalaemus marmoratus</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Physalaemus nattereri</i>	0	1	0	0	0	0	1	0	0	0	0	0	0	0
<i>Physalaemus olfersii</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus spiniger</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Proceratophrys boiei</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	0
<i>Proceratophrys melanopogon</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Rhinella icteria</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	0
<i>Rhinella ornata</i>	0	1	0	0	1	0	1	1	1	1	1	0	1	1
<i>Rhinella schneideri</i>	0	1	0	1	1	1	1	0	0	0	0	0	0	0
<i>Scinax crospedospilus</i>	0	0	0	0	0	0	0	1	0	0	0	0	1	0

<i>Scinax fuscomarginatus</i>	0	1	1	0	1	0	0	0	0	0	0	0	0	0
<i>Scinax fuscovarius</i>	1	1	1	0	1	0	1	0	0	0	0	0	0	0
<i>Scinax hayii</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	1
<i>Scinax imbegue</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Scinax perereca</i>	0	0	0	0	0	0	0	1	1	1	1	0	1	0
<i>Scinax similis</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Scinax tymbamirim</i>	0	0	0	0	0	0	0	0	1	1	1	0	1	1
<i>Ololygon argyreonata</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Ololygon littoralis</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	1
<i>Ololygon perpusilla</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	0
<i>Ololygon rizibilis</i>	0	0	0	0	0	0	0	1	0	0	1	0	1	0
<i>Sphaenorhynchus caramaschii</i>	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Thoropa taophora</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	1
<i>Trachycephalus mesophaeus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Trachycephalus typhonius</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Vitreorana uranoscopa</i>	0	0	0	0	0	0	0	0	1	1	1	1	1	1

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563 **S2 Table. Species composition in the second year sampled.** List of anuran species recorded from December 2015 to February 2016 on 14 protected
 564 areas in the Brazilian Atlantic Forest.

Species	Inland sites							Coastal sites						
	EEAS	EECA	EEIT	EEJA	EESB	FEENA	PEVA	EECB	EEJI	PECU	PEJU	PESB	PESV	PETAR
<i>Adenomera marmorata</i>	0	0	0	0	0	0	0	0	1	1	1	1	1	0
<i>Adenomera</i> sp.	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Aplastodiscus albosignatus</i>	0	0	0	0	0	0	0	1	0	0	1	0	1	1
<i>Aplastodiscus perviridis</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Bokermannohyla hylax</i>	0	0	0	0	0	0	0	1	0	0	0	1	0	0
<i>Brachycephalus pitanga</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Chiasmocleis albopunctata</i>	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Crossodactylus caramaschii</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Cycloramphus acangatan</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Cycloramphus boraceiensis</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Cycloramphus lutzorum</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Dendrophryniscu brevipolicatus</i>	0	0	0	0	0	0	0	1	0	1	0	0	0	0
<i>Dendropsophus berthallutzae</i>	0	0	0	0	0	0	0	0	1	0	0	1	0	1
<i>Dendropsophus elegans</i>	0	0	0	0	0	0	0	1	1	0	1	0	0	1
<i>Dendropsophus elianeae</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Dendropsophus giesleri</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Dendropsophus jimi</i>	0	0	1	0	1	0	1	0	0	0	0	0	0	0
<i>Dendropsophus microps</i>	0	0	0	0	0	0	0	1	1	0	1	0	1	1
<i>Dendropsophus minutus</i>	1	1	1	1	1	1	1	1	1	1	1	0	1	1
<i>Dendropsophus nanus</i>	1	1	1	1	1	1	1	0	0	0	0	0	0	0
<i>Dendropsophus seniculus</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Dendropsophus werneri</i>	0	0	0	0	0	0	0	0	1	0	1	0	0	1
<i>Elachistocleis bicolor</i>	1	0	1	0	1	1	0	0	0	0	0	0	0	0
<i>Fritziana fissilis</i>	0	0	0	0	0	0	0	1	1	1	1	1	0	1
<i>Haddadus binotatus</i>	0	1	0	0	0	0	0	0	1	1	0	1	0	1
<i>Hylodes asper</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Hylodes phyllodes</i>	0	0	0	0	0	0	0	0	0	0	0	1	1	0

<i>Boana albomarginatus</i>	0	0	0	0	0	0	0	0	1	1	1	1	1	1
<i>Boana albopunctatus</i>	1	1	1	1	1	1	1	0	0	1	1	0	0	0
<i>Boana bandeirantes</i>	0	0	0	0	0	0	0	0	0	1	0	0	1	0
<i>Boana bischoffi</i>	0	0	0	0	0	0	0	1	0	1	1	0	0	1
<i>Boana caingua</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Boana caipora</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Boana faber</i>	1	1	1	1	0	1	1	1	1	1	1	1	1	1
<i>Boana lundii</i>	1	1	0	0	1	1	1	0	0	0	0	0	0	0
<i>Boana pardalis</i>	0	0	0	0	0	0	0	1	0	0	1	0	1	0
<i>Boana semilineatus</i>	0	0	0	0	0	0	0	0	1	0	1	1	0	0
<i>Ischnocnema guentheri</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	1
<i>Ischnocnema henseli</i>	0	0	0	0	0	0	0	1	0	1	1	0	0	1
<i>Itapotihyla langsdorffii</i>	0	0	1	0	0	0	1	0	1	0	0	0	0	0
<i>Leptodactylus furnarius</i>	0	0	0	0	1	0	0	0	0	1	0	0	0	0
<i>Leptodactylus fuscus</i>	1	1	1	1	1	0	1	0	0	0	0	0	0	0
<i>Leptodactylus labyrinthicus</i>	1	1	1	0	1	0	1	0	1	0	0	0	0	0
<i>Leptodactylus latrans</i>	1	1	0	0	1	0	1	0	0	1	0	1	0	1
<i>Leptodactylus mystaceus</i>	0	1	0	1	0	1	1	0	0	0	0	0	0	0
<i>Leptodactylus mystacinus</i>	1	1	1	0	0	1	0	0	0	0	0	0	0	0
<i>Leptodactylus notoaktites</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Leptodactylus podicipinus</i>	1	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Myersiella microps</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Phrynomedusa dryade</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Phyllomedusa distincta</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Phyllomedusa tetraploidea</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Physalaemus atlanticus</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus bokermanni</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus centralis</i>	0	0	1	0	0	0	1	0	0	0	0	0	0	0
<i>Physalaemus cuvieri</i>	1	1	1	1	1	1	1	0	0	1	1	0	1	0
<i>Physalaemus lateristriga</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	1
<i>Physalaemus marmoratus</i>	1	0	1	0	0	0	1	0	0	0	0	0	0	0

<i>Physalaemus nattereri</i>	0	1	1	0	1	0	0	0	0	0	0	0	0	0
<i>Physalaemus olfersii</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Proceratophrys boiei</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	1
<i>Proceratophrys melanopogon</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinella icteria</i>	0	0	0	0	0	0	0	1	1	1	0	0	1	1
<i>Rhinella ornata</i>	0	1	1	1	0	1	1	0	1	1	1	1	0	1
<i>Rhinella schneideri</i>	1	1	1	1	0	1	0	0	0	0	0	0	0	0
<i>Scinax crospedospilus</i>	0	0	0	0	0	0	0	1	0	1	0	0	0	0
<i>Scinax fuscomarginatus</i>	1	1	1	1	1	0	0	0	0	0	0	0	0	0
<i>Scinax fuscovarius</i>	1	1	0	0	1	1	1	0	0	0	0	0	0	0
<i>Scinax hayii</i>	0	0	0	0	0	0	0	0	0	0	0	1	1	0
<i>Scinax imbegue</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Scinax perereca</i>	0	0	0	0	0	0	0	1	1	1	1	0	0	1
<i>Scinax tymbamirim</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Scinax similis</i>	0	0	1	0	0	1	1	0	0	0	0	0	0	0
<i>Ololygon littoralis</i>	0	0	0	0	0	0	0	0	1	0	0	1	0	0
<i>Ololygon perpusilla</i>	0	0	0	0	0	0	0	1	0	1	0	1	1	0
<i>Ololygon rizibilis</i>	0	0	0	0	0	0	0	1	0	1	1	1	0	1
<i>Sphaenorhynchus caramaschii</i>	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Thoropa taophora</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Trachycephalus lepidus</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Trachycephalus typhonius</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Vitreorana uranoscopa</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1

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570 **S3 Table. Species composition in the third year sampled.** List of anuran species recorded on 14 protected areas in the Brazilian Atlantic Forest from
 571 December 2016 to February 2017.

Species	Inland sites							Coastal sites						
	EEAS	EECA	EEIT	EEJA	EESB	FEENA	PEVA	EECB	EEJI	PECU	PEJU	PESB	PESV	PETAR
<i>Adenomera marmorata</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Adenomera</i> sp.	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Aplastodiscus albofrenatus</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Aplastodiscus albosignatus</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	0
<i>Aplastodiscus perviridis</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Bokermannohyla circumdata</i>	0	0	0	0	0	0	0	1	1	1	0	1	1	1
<i>Bokermannohyla astartea</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Bokermannohyla hylax</i>	0	0	0	0	0	0	0	1	1	0	1	1	1	0
<i>Brachycephalus pitanga</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Chiasmocleis albopunctata</i>	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Crossodactylus caramaschii</i>	0	1	0	0	0	0	0	1	0	0	0	0	0	0
<i>Cycloramphus boraceiensis</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Cycloramphus eleutherodactylus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Cycloramphus lutzorum</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Dendrophryniscus brevipolicatus</i>	0	0	0	0	0	0	0	1	1	1	0	0	0	0
<i>Dendropsophus berthaltutzae</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Dendropsophus elegans</i>	0	0	0	0	0	0	0	1	1	0	1	1	0	1
<i>Dendropsophus elianeae</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Dendropsophus giesleri</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	0
<i>Dendropsophus jimi</i>	0	0	1	0	1	0	0	0	0	0	0	0	0	0
<i>Dendropsophus microps</i>	0	0	0	0	0	0	0	1	1	0	1	1	1	1
<i>Dendropsophus minutus</i>	1	1	1	1	1	1	1	1	0	1	1	1	1	1
<i>Dendropsophus nanus</i>	1	1	1	1	0	0	1	0	0	0	0	0	0	0
<i>Dendropsophus sanborni</i>	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Dendropsophus seniculus</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	1
<i>Dendropsophus werneri</i>	0	0	0	0	0	0	0	0	1	0	1	0	0	1
<i>Elachistocleis bicolor</i>	1	0	1	0	0	1	0	0	0	0	0	0	0	0

<i>Elachistocleis cesari</i>	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Fritziana fissilis</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Haddadus binotatus</i>	0	0	0	0	0	0	0	1	1	1	1	0	0	1
<i>Hylodes asper</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Hylodes phyllodes</i>	0	0	0	0	0	0	0	0	0	0	0	1	1	0
<i>Boana albomarginatus</i>	0	0	0	0	0	0	0	1	1	1	1	1	0	1
<i>Boana albopunctatus</i>	1	0	1	1	1	1	1	0	0	1	1	0	0	0
<i>Boana bandeirantes</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Boana bischoffi</i>	0	0	0	0	0	0	0	1	0	1	1	0	0	1
<i>Boana caingua</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Boana caipora</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Boana faber</i>	1	1	1	1	1	1	1	1	1	1	1	0	1	1
<i>Boana lundii</i>	1	1	0	0	1	1	1	0	0	0	0	0	0	0
<i>Boana pardalis</i>	0	0	0	0	0	0	0	0	0	0	1	0	1	0
<i>Boana semilineatus</i>	0	0	0	0	0	0	0	0	1	1	1	1	0	0
<i>Ischnocnema guentheri</i>	0	0	0	0	0	0	0	1	1	1	0	1	1	1
<i>Ischnocnema henseli</i>	0	0	0	0	0	0	0	1	0	1	1	0	0	1
<i>Ischnocnema parva</i>	0	0	0	0	1	0	0	1	1	1	0	1	1	1
<i>Ischnocnema randorum</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Itapotihyla langsdorffii</i>	0	0	0	0	0	1	1	0	1	0	0	0	0	0
<i>Leptodactylus flavopictus</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Leptodactylus furnarius</i>	0	0	0	0	0	0	0	0	0	1	1	0	0	0
<i>Leptodactylus fuscus</i>	1	1	1	1	1	0	1	1	0	0	0	0	1	0
<i>Leptodactylus labyrinthicus</i>	1	1	1	1	1	1	1	0	0	0	1	0	0	0
<i>Leptodactylus latrans</i>	1	1	1	1	0	0	1	1	1	1	1	0	0	1
<i>Leptodactylus mystaceus</i>	0	0	0	0	0	1	1	0	0	0	0	0	0	0
<i>Leptodactylus mystacinus</i>	1	0	1	1	0	0	1	0	0	0	0	0	0	0
<i>Leptodactylus notoaktites</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	1
<i>Leptodactylus plaumanni</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Leptodactylus podicipinus</i>	1	0	1	1	0	0	1	0	0	0	0	0	0	0
<i>Myersiella microps</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0

<i>Paratelmatoobius cardosoi</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Paratelmatoobius gaigeae</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Phrynomedusa dryade</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Phyllomedusa distincta</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	1
<i>Phyllomedusa tetraploidea</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Physalaemus atlanticus</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus bokermanni</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus centralis</i>	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Physalaemus cuvieri</i>	1	0	1	1	1	1	1	0	0	1	1	0	1	0
<i>Physalaemus lateristriga</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	1
<i>Physalaemus maculiventris</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Physalaemus marmoratus</i>	1	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Physalaemus nattereri</i>	1	0	1	0	0	0	1	0	0	0	0	0	0	0
<i>Physalaemus olfersii</i>	0	1	0	0	0	0	0	0	0	0	0	1	1	0
<i>Proceratophrys boiei</i>	0	0	0	0	0	0	0	1	0	0	1	0	1	1
<i>Proceratophrys melanopogon</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinella hoodmoedi</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinella icteria</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Rhinella ornata</i>	0	1	1	1	0	1	1	1	1	1	1	1	1	1
<i>Rhinella schneideri</i>	1	1	1	1	1	1	0	0	0	0	0	0	0	0
<i>Scinax crospedospilus</i>	0	0	0	0	0	0	0	1	0	0	0	1	1	0
<i>Scinax fuscomarginatus</i>	1	1	0	1	1	0	0	0	0	0	0	0	0	0
<i>Scinax fuscovarius</i>	1	1	1	1	0	1	1	0	0	1	0	0	0	1
<i>Scinax hayii</i>	0	0	0	0	0	0	0	0	0	0	0	1	1	0
<i>Scinax imbegue</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Scinax perereca</i>	0	0	0	0	0	0	0	1	1	1	1	0	0	1
<i>Scinax similis</i>	1	1	1	0	0	0	1	0	0	0	0	0	0	0
<i>Scinax squalirostris</i>	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Scinax tymbamirim</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Ololygon argyreonata</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Ololygon littoralis</i>	0	0	0	0	0	0	0	0	1	0	0	1	0	0

<i>Ololygon perpusilla</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Ololygon rizibilis</i>	0	0	0	0	0	0	0	1	1	0	0	1	1	1
<i>Sphaenorhynchus caramaschii</i>	0	0	0	0	0	0	0	0	0	0	1	0	0	1
<i>Thoropa taophora</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Trachycephalus imitatrix</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Trachycephalus mesophaeus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Trachycephalus typhonius</i>	1	0	0	1	0	0	1	0	1	0	0	0	0	0
<i>Vitreorana uranoscopa</i>	0	0	0	0	0	0	0	1	0	1	1	1	1	1

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596 **S4 Table. Species composition for the three years sampled.** List of anuran species recorded on 14 protected areas in the Brazilian Atlantic Forest
 597 considering three years pooled together.

Species	Inland sites							Coastal sites						
	EEAS	EECA	EEIT	EEJA	EESB	FEENA	PEVA	EECB	EEJI	PECU	PEJU	PESB	PESV	PETAR
<i>Adenomera marmorata</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Adenomera</i> sp.	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Aparasphenodon bokermanni</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Aplastodiscus albofrenatus</i>	0	0	0	0	0	0	0	1	0	0	1	1	1	0
<i>Aplastodiscus albosignatus</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Aplastodiscus perviridis</i>	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Bokermannohyla astartea</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Bokermannohyla circumdata</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Bokermannohyla hylax</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Brachycephalus pitanga</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Chiasmocleis albopunctata</i>	1	0	1	0	0	1	0	0	0	0	0	0	0	0
<i>Chiasmocleis leucosticta</i>	0	0	0	0	0	0	0	1	0	0	0	1	0	0
<i>Crossodactylus caramaschii</i>	0	1	0	0	0	0	0	1	0	0	1	0	0	0
<i>Cycloramphus acangatan</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Cycloramphus boraceiensis</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Cycloramphus eleutherodactylus</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Cycloramphus lutzorum</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Dendrophryniscus brevipolicatus</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	0
<i>Dendrophryniscus</i> sp.	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Dendropsophus berthallutzae</i>	0	0	0	0	0	0	0	0	1	0	0	1	1	1
<i>Dendropsophus elegans</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Dendropsophus elianeae</i>	0	1	1	0	1	0	1	0	0	0	0	0	0	0
<i>Dendropsophus giesleri</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	0
<i>Dendropsophus jimi</i>	0	0	1	0	1	0	1	0	0	0	0	0	0	0
<i>Dendropsophus microps</i>	0	0	0	0	0	0	0	1	1	0	1	1	1	1
<i>Dendropsophus minutus</i>	1	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>Dendropsophus nanus</i>	1	1	1	1	1	1	1	0	0	0	0	0	0	0

<i>Leptodactylus mystaceus</i>	0	1	0	1	0	1	1	0	0	0	0	0	0	0
<i>Leptodactylus mystacinus</i>	1	1	1	1	1	1	1	0	0	0	0	0	0	0
<i>Leptodactylus notoaktites</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	1
<i>Leptodactylus plaumanni</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Leptodactylus podicipinus</i>	1	0	1	1	0	0	1	0	0	0	0	0	0	0
<i>Megaelosia bocainensis</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Myersiella microps</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Paratelmatoobius cardosoi</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Paratelmatoobius gaiageae</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Phrynomedusa dryade</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Phyllomedusa distincta</i>	0	0	0	0	0	0	0	1	1	0	1	0	0	1
<i>Phyllomedusa tetraploidea</i>	1	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Physalaemus atlanticus</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus bokermanni</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Physalaemus centralis</i>	0	0	1	0	1	0	1	0	0	0	0	0	0	0
<i>Physalaemus cuvieri</i>	1	1	1	1	1	1	1	0	0	1	1	0	1	0
<i>Physalaemus lateristriga</i>	0	0	0	0	0	0	0	1	0	0	1	0	0	1
<i>Physalaemus maculiventris</i>	0	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Physalaemus marmoratus</i>	1	1	1	0	0	0	1	0	0	0	0	0	0	0
<i>Physalaemus nattereri</i>	1	1	1	0	1	0	1	0	0	0	0	0	0	0
<i>Physalaemus olfersii</i>	0	1	0	0	0	0	0	0	0	0	0	1	1	0
<i>Physalaemus spiniger</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Proceratophrys boiei</i>	0	0	0	0	0	0	0	1	0	0	1	0	1	1
<i>Proceratophrys melanopogon</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinella hoogmoedi</i>	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Rhinella icterica</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Rhinella ornata</i>	0	1	1	1	1	1	1	1	1	1	1	1	1	1
<i>Rhinella schneideri</i>	1	1	1	1	1	1	1	0	0	0	0	0	0	0
<i>Scinax crospedospilus</i>	0	0	0	0	0	0	0	1	0	1	1	1	1	1
<i>Scinax fuscomarginatus</i>	1	1	1	1	1	0	0	0	0	0	0	0	0	0
<i>Scinax fuscovarius</i>	1	1	1	1	1	1	1	0	0	1	0	0	1	1

<i>Scinax hayii</i>	0	0	0	0	0	0	0	0	0	0	0	1	1	0
<i>Scinax imbegue</i>	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Scinax perereca</i>	0	0	0	0	0	0	0	1	1	1	1	0	0	1
<i>Scinax similis</i>	1	1	1	0	1	1	1	0	0	0	0	0	0	0
<i>Scinax squalirostris</i>	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Scinax tymbamirim</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Ololygon argyreolata</i>	0	0	0	0	0	0	0	0	1	0	0	1	0	0
<i>Ololygon littoralis</i>	0	0	0	0	0	0	0	1	1	0	1	1	0	0
<i>Ololygon perpusilla</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Ololygon rizibilis</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1
<i>Sphaenorynchus caramaschii</i>	0	0	0	0	0	0	0	0	0	0	1	0	0	1
<i>Thoropa taophora</i>	0	0	0	0	0	0	0	0	1	0	0	1	0	0
<i>Trachycephalus imitatrix</i>	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Trachycephalus mesophaeus</i>	0	0	0	0	0	0	0	0	1	0	0	1	0	1
<i>Trachycephalus lepidus</i>	0	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Trachycephalus typhonius</i>	1	0	0	1	0	0	1	0	0	0	0	0	0	0
<i>Vitreorana uranoscopa</i>	0	0	0	0	0	0	0	1	1	1	1	1	1	1

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